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OM protein -
protein search, using sw model
                                                               GenCore version 5.1.6
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Scoring table: Sequence: Perfect score: BLOSUM62 US-09-661-992B-106 82 November 7, 2003, 07:21:17; Search time 6,89987 Seconds (without alignments) 368.069 Million cell updates/sec 1107863 seqs, 158726573 residues Gapop 10.0 , Gapext 0.5 1 FRNRGMTALLKVSSCD 16 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

A Geneseq 190m03;

1. /SIDE:/gogdata/geneseq/geneseqg-embl/AA1980.DMT.*

2. /SIDE:/gogdata/geneseq/geneseqg-embl/AA1981.DMT.*

3. /SIDE:/gogdata/geneseq/geneseqg-embl/AA1983.DMT.*

4. /SIDE:/gogdata/geneseq/geneseqg-embl/AA1983.DMT.*

4. /SIDE:/gogdata/geneseq/geneseqg-embl/AA1983.DMT.*

| SIBSI | Godata | Genesed | Genesed | SiBSI | Godata | Sentesed | Genesed | SiBSI | Godata | Sentesed | Genesed | Genesed | Genesed | SiBSI | Godata | Sentesed | Genesed | Gen

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

9	œ	7	0	u	4	. (,,	۵	, µ	No. S	Result
82	82	82	82	82	82	82	82	82	Score	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Score Match Length	Query
740	740	740	740	729	720	368	294	16	Match Length DB	
16	16	16	16	16	16	16	23	22	BB	
AAR73021	AAR76962	AAR76961	AAR76959	AAR74089	AAR74088	AAR73020	AAG79422	AAB20445	ij	
Human Factor-VIII		Human Factor-VIII	Human Factor-VIII/	Factor-VIII heavy	Factor-VIII heavy	Human Factor-VIII	Human factor VIII	Anti-FIX/FIXa anti	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82
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2332	2332	2332	2332	2332	2332	2332	2332	2332	2332	2332	2332	2098	1516	1471	1471	1459	1459	1459	1457	1457	1457	1447	1445	1440	1438	1425	1424	1424	1424	1424	1383	1383	1383	740	740
19	19	18	18	18	18	18	14	8			œ	17	9	22	18	22	22	22	20	19	19	23	23	12	22	9	23	22	10	w	18	18	18	16	16
AAW44132	AAW53483	AAW33226	AAW33225	AAW33224	AAW33223	AAW33222	AAR43257	AAP71729	AAP71728	AAP71727	AAP71726	AAR86863	AAP80265	AAB67959	AAW23414	AAE10833	AAE10832	AAE10827	AAY21675	AAW44372	AAW46246	ABG92541	ABG92540	AAR12971	AAB01262	AAP80267	AA018622	AAB48842	AAP91169	AAP80268	AAW33229	AAW33228	AAW33227	AAR76982	AAR74090
	Human factor VIII.	Procoagulant-activ	Procoagulant-activ	Procoagulant-activ	Procoagulant-activ	Procoagulant-activ	n Factor	VIII:c	VIII:c	VIII:c	ã	Factor-VIII. Homo			B-doma:		factor	VII	Beta-domain delete	Human Factor VIII	Human factor VIII	SArg B-domain-dele	LE B-domain-delete		B-domain deleted f	Modified factor VI	Human mature B-dom	Mutant mature huma	Sequence of 740 Ar	Modified factor VI	Procoagulant-activ	Procoagulant-activ	Procoagulant-activ		Factor-VIII heavy

ALIGNMENTS

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AAB20445 standard; Peptide; 16 AA.

AAB20445;

21-JUN-2001 (first entry)

Anti-FIX/FIXa antibody CDR3.

Reactor IX; FIX; Factor IXa; FIXa; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic datheeis; haemostatic, amidolytic; therapy; mouse; complementarity determining region; CDR.

Mus musculus.

WO200119992-A2

22-MAR-2001.

13-SEP-2000; 2000WO-EP08936

14-SEP-1999; 99AT-0001576

(BAXT) BAXTER AG.

Scheiflinger F, Kerschbaumer R,

Falkner

'n Dorner

WPI; 2001-290358/30

New factor IX/factor IXa antibodies and their derivatives useful for

increasing amidolytic coagulation disorders

activity of factor IXa, and for treating blood such as haemophilia A and haemorrhagic diathesis

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RESULT 2
AAG79422
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of complementarity determining creding in (DRS) of an artibody heaving anti-factor IX (FIX) or anti-activated Pactor IX (FIX) activity. Such artibodies or anti-activated Pactor IX (FIX) activity. Such artibodies or and their derivatives (including their pactor) and their derivatives present CORS apprised have Pactor VIII2 (FIVIII) codector activity of FIX activatives leads to an increase in the procequitate civity of derivatives leads to an increase in the procequitate civity of TXA, even in the procequitation of the artivity of PIXA, even in the presence of FIVIII is inhibitors. The antibodies or their credit allowed activities are used in a claimed pharmaccutical composition for treating partiants with blood obsyllation disorders, especially anomaphilia A and hemosphilia chadhesis.
feators TVII and IX. Region 2 comprises the infernation between N146 of factor YVII and Has and Has and Has of Actor YVIIA, and the interaction between R403 of factor YVIIA and the interaction between R330 of factor YVIIA. Region 3 comprises the interaction between E330 of factor IXa and D712 of factor YVIIA, and Fragments of these polypepides inhibit the interaction between E310 of factor YVIIA.
                                                                                                                                                                        New polypeptide inhibits interaction of blood coagulation factor VIIIa with factor IX a precluding activation of factor X, useful for preventing or treating coagulation disorders, such as thrombosis,
                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                              The sequences given in AAG79422-23 represent regions 2 and 3
                                                                                                                                                              atherosclerosis
                                                                                                                                                                                                                                        WPI; 2002-599771/64.
                                                                                                                                                                                                                                                                      Bajaj
                                                                                                                                                                                                                                                                                                      (UYSL-)
                                                                                                                                                                                                                                                                                                                                    23~JAN-2001; 2001US-263431P
                                                                                                                                                                                                                                                                                                                                                               23-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                               W0200259268-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Factor VIII; factor IX; coagulation; blood; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG79422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 74; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
                                                                                                                           2; Fig 7A; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor VIII region 2/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
16; Conser
                                                                                                                                                                                                                                                                                                    UNIV SAINT LOUIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; protein; 294 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRNRGMTALLKVSSCD
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                                                                                                                                                                                                                                                                   Fay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis; restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                               2002WO-US01724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                              and restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 82,
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                              of human
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325

FRNRGMTALLKVSSCD FRURGMTALLKVSSCD

)-3 16;

16

Conservative

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Mismatches

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Gaps

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RESULT 4

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RESULT 3
AAR73020
ID AAR7
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Query Match
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Matches 16
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Best Local S
Matches 16
                                                                   This is a fragment corresponding to internal Aas 373-740 of human Factor-VIII which may be crosslinked resulting in increased stability and retention of high activity over extended periods of time after activation by thrombin. The polypoptide is used to prevent or treat diseases caused by the absence or deficitly of Factor-VIII in a subject senior as hasmophilia. (Updated on 25-MAR-2003 to correct W field.)
                                                Sequence
                                                                                                                                                                                                      Crosslinked Factor VIII polypeptide which is stable - is prepd, using bis (sulphosuccininydy); suberate or disuccininydy); suberate in the presence of polysorbate 80 to produce a coagulant with long lasting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coagulation factor VIIIa with blood coagulation factor YXa. They alaci hibbit the activation of blood coagulation factor X, or inhibit blood coagulation. These peptide fragments are useful in preventing and/or treating coagulation disorders, in particular cardiovascular disorders such as thromboslie, atheroscierosla and restempsis.
                                                                                                                                                                     Disclosure;
                                                                                                                                                                                              activity
                                                                                                                                                                                                                                                        WPI; 1995-194038/25
                                                                                                                                                                                                                                                                                 Persson
                                                                                                                                                                                                                                                                                                                                  12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                       10-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                       W09513301-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Factor-VIII fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
21-NOV-1995
                                                                                                                                                                                                                                                                                                         (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Factor-VIII;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR73020 standard;
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                                                                                                                                                                                                                                                                                                                                                                                18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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             Similarity
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                                                368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 AA;
                                                                                                                                                                   Page 19; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     blood-clotting; blood; coagulant; haemophilia-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first en
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                                                                                                                                                                                                                                                                                                                                  93DK-0001281
                                                                                                                                                                                                                                                                                                                                                       94WO-DK00424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 82;
Pred. No.
           Score 82;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23;
2.9e-07;
           3.86-07;
                       DB 16;
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                     Length 368;
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Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents N-terminal residues 1-700 of a human Factor-VIII heavy chain. The agagence is abstrar than the Al-Andomania and its produced by treating a polypoptide containing the full Al-A2 domain of full-length Factor-VIII in a produced by treating a polypoptide containing the full Al-A2 domain of full-length Factor-VIII in a chromogenic assay, but activity is a factor of two lower in a clotting assay, and the framework activity is a factor of two lower in a clotting assay, and the framework activity by thrombin at a slower trate and to a lower level ben framework 1740 (AR74098) and plasma Factor-VIII. The framework 1740 (AR74098) and plasma Factor-VIII. The framework by be produced recombinantly to reduce production conts and instability are higher than for the full length form. The fragment may be used to treat particular who have been antibodies against epitopes in the C-terminal part of the heavy chain.
                                                                              04-NOV-1995
                                                                                                          25-MAR-2003
                                                                                                                                                                 AAR74089;
                                                                                                                                                                                                                        AAR74089 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Factor VIII polypeptide(e) comprising a heavy chain shorter than mative Al-A2 domain - are easier to produce recombinantly and retain coagulant activity, may be used to treat patients who have developed antibodies to C-teamnal epitope(e) of Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 24-26; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ezban Rasmussen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12~NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombin cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; Factor VIII; heavy chain; N-terminal fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Factor-VIII heavy chain N-terminal fragment
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04-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                        697
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 FRNRGMTALLKYSSCD 16
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                                                                                                                                                                                                                                                                                                                                                                   FRNRGMTALLKVSSCD 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          720 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                     (updated)
(first entry)
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                                                                                                                                                                                                                    protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                        729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82; DB
Pred. No. 8.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
8.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Factor-VIII heavy chain N-terminal fragment

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                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
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Best Local S
Matches 16
Misc-difference
                        Misc-difference
                                              Misc-difference
                                                                                                                                                                                          25-MAR-2003
09-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents N-terminal residues 1-79 of a human Recor-
VIII heavy chain. The sequence is shorter than the A1-A2 Gomain.
and is produced by treating a polypeptide containing the full A1-A2 domain of full-length Rector-VIII with a protease, e.g. thombin. The fragment has the same coagulant specific activity as full-length Ractor-VIII with a chronogenic assay, and is activated by thrombin at a similar rate. The fragment may be produced recombinantly to reduce production costs and improve safety, and production levels and stability are higher than for the full-length form. The fragment may be used to treat patients who have developed antibodies against be used to treat patients who have developed antibodies against by the A4-A2-A03 to courset By field.)
                                                                      Misc-difference
                                                                                                           Homo sapiens
                                                                                                                                     Factor-VIII;
                                                                                                                                                             Human Factor-VIII/Factor-VIIIa derivative
                                                                                                                                                                                                                              AAR76959;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Factor VIII polypeptide(s) comprising a heavy chain shorter than mative Al-Al domain - are easier to produce recombinantly and retain coagulant activity, may be used to treat patients who have developed antibodies to creaminal epitope(s) of Rector VIII)
                                                                                                                                                                                                                                                    AAR76959 standard; protein; 740 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 27-29; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI, 1995-194037/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ezban Rasmussen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09513300-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombin cleavage; blood-clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; Factor VIII; heavy chain; N-terminal fragment;
                                                                                                                                                                                                                                                                                                                       697
                                                                                                                                                                                                                                                                                                                                           1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                   FRURGMTALLKVSSCD 712
                                                                                                                                                                                                                                                                                                                                                                                                                        729 AA;
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                   therapeutic; blood-clotting
                                                                                                                                                                                     (updated)
(first entry)
                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93DK-0001280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-DK00423
      /label= Asp
                              /label= Asp absent or Asn,
                                                        label= Asp absent or Asn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kjalke M;
                                                                                                                                                                                                                                                                                                                                                                               100.0%;
        absent or Asn,
                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                               Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                   ; DB 16;
. 8.6e-07;
ches 0;
                              Ser,
                                                      Ser,
        Ser,
      Thr,
                                Thr,
                                                      Thr,
                                                                                                                                                                                                                                                                                                                                                                                            Length 729;
                                                                                                                                                                                                                                                                                                                                                                   Indels
      Ala
                                                        Ala
                              Ala
                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                 0
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RESULT 7
AAR76961
ID AAR
XX AAR
XX AAR
AX AAR
DX 09-1
DX Humm
DE Hum
DE Hum
DX Hom
XX Faci
XX Faci
XX Key
FH Miss
FT Miss
FT Miss
FT Miss
FT Miss
FT Miss
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The new Factor-VIII/Factor-VIII derivative comprises a functional A2 domain in which mains eaid residues, as indicated in the Features, are deleted or substituted by another amino acid so as to increase the overall positive charge. Asp-403, Asp-404, Asp-403, Asp-404, Sap-403 are preferably substituted by Asm, Glu-434 and Glu-440 are preferably substituted by Glm. The new derivative has the same activity as the wild-type Factor-VIII but with improved stability (the activity as the wild-type Factor-VIII) are wild decline of the activity of wt Factor-VIII). The new derivative came be used in a composition for treating diseases caused by an absence or deficiency of Factor-VIII separated on 25-War-2001 to correct by Efald.)
                     Misc-difference
                                                     Misc-difference
                                                                                  Misc-difference
                                                                                                                                       Homo
                                                                                                                                                                    Factor-VIII;
                                                                                                                                                                                                    Human Factor-VIII derivative.
                                                                                                                                                                                                                                      09-MAR-1996
                                                                                                                                                                                                                                                                      AAR76961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 11-14; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel factor VIII derivative used to treat haemophilia - and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-255041/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ezban Rasmussen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9518829-A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                      AAR76961 standard; protein; 740 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises a functional A2 domain containing a mutation at one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUL-1995
                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cys residues.
                                                                                                                                                                                                                                                                                                                                                                                        697
                                                                                                                                                                                                                                                                                                                                                                                                              1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                        FRNRGMTALLKVSSCD 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           740 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                    therapeutic; blood-clotting.
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94DK-0000030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-DK00010
                     /label= absent or Gln, Ser, Thr, Val or 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Asp
500
/label= absent or Val, Ala or Ile
                                                                                                    Location/Qualifiers
                                                                  'label= absent or Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Glu absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicolaisen EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     absent or Asn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 82; DB 16;
Pred. No. 8.7e-07;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o
R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or Gln, Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Persson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asn,
                                                                  Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ser,
                                                                  Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 740;
                                                               Gly or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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용
                      S
                                                 Matches
                                                              Query Match
Best Local
                                                                                                                            The new Factor-VIII derivative comprises a functional A2 domain in which Cys-592 is delated or replaced with another amino acid nor residue, preferably Ser (see ARXF952). Alternatively, Glu-720 and Olderdo C substituted with various amino acids (as in the Features). The new derivative has the same activity as the wild-type Factor-VIII but with improved scalability (the activity is maintained for a longer period compared to the rapid decline of the activity of we factor-VIII. The new derivative can be used in a composition for treating diseases caused by an absence or deficiency of Ractor-VIII. especially beenpointied.
                                                                                                                                                                                                                                                                                                               Novel factor VIII derivative used to treat haemophilia - and comprises a functional A2 domain containing a mutation at one
                                                                                                     Sequence
                                                                                                                                                                                                                                                                         Disclosure; Page 14-17; 30pp; English
                                                                                                                                                                                                                                                                                                    more Cys residues.
                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-255039/33
                                                                                                                                                                                                                                                                                                                                                                                                            (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09518827-A1
697
                                                                                                                                                                                                                                                                                                                                                                                 Rasmussen M,
                1 FRNRGMTALLKVSSCD 16
                                                 16;
                                                                Similarity
FRNRGMTALLKVSSCD 712
                                                                                                     740 AA;
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       94DK-0000032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-DK00008
                                                                                                                                                                                                                                                                                                                                                                                   Nicolaisen EM,
                                                              100
                                                              0;
                                                              Score 82;
Pred. No.
                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Persson E
                                                                œ
                                                              DB 16;
8.7e-07;
                                                 0
                                                                          Length 740;
                                                 Indels
                                                 0
                                                                                                                                                                                                                                                                                                                 or
                                                 Gaps
                                                                                                                                                                                                                        and/or
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0
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AAR76962 ID AAR7

AAR76962 standard; protein; 740 8

AAR76962

09-MAR-1996 (first entry)

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Human Factor-VIII derivative

Factor-VIII; therapeutic; blood-clotting

Homo sapiens.

Location/Qualifiers

Misc-difference Misc-difference 692 label= Cys substituted by Ser

Misc-difference label= absent or Gln, Ser, Thr, Val or Ala

/label= absent or Val, Ala or Ile

W09518827-A1

13-JUL-1995

06-JAN-1995; 95WO-DK00008

07-JAN-1994; 94DK-0000032

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
This is the N-terminal fragment of human Factor-VIII which
crossliked resulting in increased stability and retention
activity over extended periods of time after activation by
                                                                                                Crosslinked Factor VIII polypeptide which is stable - is prapd, using this quiphosuccinimydyl, substrate or disuccinimydyl substrate in the presence of polysorbate 80 to produce a cosyulant with long lasting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The new Rector-VIII derivative comprises a functional A2 domain in which typ-692 is replaced with Set. For other (less preferred) substitutions at this site, see AMP76961. Alternatively, Giu-720 and Jacked or substituted with various maino acide (as in the Features). The new derivative has the same activity as the wild-type Ractor-VIII but with improved steability the activity is maintained for a longer period compared to the rapid decline of the activity of expectative of the rector-VIII. The new derivative can be used in a composition for treating diseases caused by an absence or deficiency of Ractor-VIII. especially hemophilia.
                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                              Factor-VIII; blood-clotting; blood; coagulant; haemophilia-A.
                                                                                                                                                                WPI; 1995-194038/25
                                                                                                                                                                                                                                                     12-NOV-1993;
                                                                                                                                                                                                                                                                                1 )-NOV-1994;
                                                                                                                                                                                                                                                                                                           18-MAY-1995
                                                                                                                                                                                                                                                                                                                                       WO9513301-A1
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            Human Factor-VIII N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
21-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR73021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR73021 standard; peptide; 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 18-20; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises a functional A2 domain containing a mutation at one or more Cys residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel factor VIII derivative used to treat haemophilia - and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-255039/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rasmussen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRNRGMTALLKVSSCD 712
                                                         Page 21; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        740 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
(larity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (updated)
(first entry)
                                                                                                                                                                                                                                                     93DK-0001281
                                                                                                                                                                                                                                                                                94WO-DK00424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                            fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 82; DB 16;
Pred. No. 8.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Persson E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
h may be
n of high
y thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glu-720 and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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FRURGMTALLKVSSCD 16

Query Match Best Local Similarity Matches 16; Conserv

Conservative

100.0%; Pr 100.0%; Pr

Score 82; DB 16; Pred. No. 8.7e-07; Mismatches 0;

Length 740;

Indels

0,

Gaps

0,

Sequence

740 AA;

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RESULT 10
AAR74090
ID AAR74
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Best Local S
Matches 16
The sequence represents N-terminal residues 1-40 of a human Recor-
VIII heavy chain. The sequence contains entire N and A2 domains of the produced forms (1-720 in (ANRY4080)) and 1-729 in (ANRY4081)) may be produced by treatment with a processe, e.g. thrombin. The creminally truncated fragments have the same computant specific earth of the computant of the computant of the computant produced production roses and improve safety, giving things recombinantly to reduce production roses and improve safety, giving higher production levels and scability than for the full-length form. The fragments may be used to trest patients who have developed down the fragments against epitopes in the C-terminal part of the heavy chain. (Updated on 25-MRA-2003 to correct by field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
04-NOV-1995
                                                                                                                                                                                                                                                                                                                                                    Sector VIII polypeptide(s) comprising a heavy chain shorter than native A1-A2 domain - are easier to produce recombinantly and retain coagulant activity, may be used to treat patients who have developed antibodies to C-terminal epitope(s) of Factor VIII
                                                                                                                                                                                                                                                                                                            Disclosure, Page 30-32; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-194037/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bzban Rasmussen M, Kjalke M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9513300-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombin cleavage; blood-clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; Factor VIII; heavy chain; N-terminal fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Factor-VIII heavy chain N-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR74090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR74090 standard; protein; 740 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The polypeptide is used to prevent or treat diseases caused by absence or deficiency of Factor-VIII in a subject such as haemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRURGMTALLKVSSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRNRGMTALLKVSSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    740 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93DK-0001280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-DK00423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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В

697

FRNRGMTALLKVSSCD

712

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                                                                                                                                                                             RESULT 11
AAR76982
                                                                                                                                                                                                                              Complias segmence represents the A2 domain of a human factor VIII is a large glycoprotein which is present in plasma at low concentrations. Pactor VIII is an acsential part of the clothan at low concentrations. Pactor VIII is an acsential part of the clothance of the cartinal part of the contentrations of the contentration of the cartinal part of the coleaves of the part of the pactor VIII is susceptible to cleaves of the Cadmain, and other serine processes.

Compared the contentration of the Cadmain, and other serine processes. The cadmain and 2 repeats of the Cadmain, and the Admain, as the A1 cadmain, and 2 repeats of the Cadmain, and the Admain, as the A1 cadmain, and 2 repeats of the Cadmain and 2 repeats of the Cadmain, and 2 repeats of the
                                                                                                          Query Match
Best Local
                                                                                    Matches
                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 11-14; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           deleted/substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel factor VIII derivative with resistance to enzymatic cleavage and comprises a functional A2 domain where Glu720 and/or Tyr729 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ezban Rasmussen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09518828-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Factor VIII; human; haemophilia; thrombin; protein C; plasmin; serine protease; recombination; therapy; deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human factor VIII A2-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR76982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR76982 standard; protein;
                                                                                                                                                                                                                       as
697
                                                                                 16;
                                                                                                          Similarity
FRNRGMTALLKVSSCD 712
                                   FRNRGMTALLKVSSCD 16
                                                                                                                                                                         740 AA;
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94DK-0000031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-DK00009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Val, Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Gln, Ser, Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicolaisen EM,
                                                                                                  100.0%;
                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   740 AA
                                                                                                      Score 82;
Pred. No.
                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Val,
                                                                                                      8.7e-07;
                                                                                                                           DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ala
                                                                                 o,
                                                                                                                        Length 740;
                                                                             0,
                                                                             Gaps
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RESULT 12
AAW33227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant secretion, pro-coagulant mactivity; resistance; activated protein C cleavage; AFC; B domain, A2 domain, A3 domain; oun willebrand factor binding site; binding affinity;
  Amano K,
                                 (UNMI ) UNIV MICHIGAN
                                                                15-MAY-1996;
24-APR-1996;
                                                                                                                 24-APR-1997;
                                                                                                                                                  30-OCT-1997
                                                                                                                                                                              WO9740145-A1
                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                               Disulfide-bond
                                                                                                                                                                                                                                                                                                                                           Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                             Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Procoagulant-active human factor VIII:C (FVIII) mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW33227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW33227 standard; protein; 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro-coagulant active factor VIII; FVIII; haemophilia A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replacement
Kaufman RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                96US-0017785.
96US-0016117.
                                                                                                                 97WO-US06563.
                                                                                                                                                                                                                                                                              /note= "|
528..554
                                                                                                                                                                                                                                                                                                                                           /note= "(
372..373
                                                                                                                                                                                                                                                                                                                                                           /note= "C1
1226..1378
/note= "C2
                                                                                                                                                                                                                                                                                                               153..179
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "A3 domain"
1073..1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           711..746
                                                                                                                                                                                                             note= "wild type Arg replaced with Ala'
                                                                                                                                                                                                                               label= R740A
                                                                                                                                                                                                                                                            /note= "probable"
                                                                                                                                                                                                                                                                                                                            note= "by thrombin"
                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "plastocyanin-like domain
746..1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380..554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187..329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "plastocyanin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Al domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "factor VIIIA light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          741 . . 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "factor VIIIA heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "a spacer of the sequence SPSQNSRHPSTRQKQFNATTIPENDIEKTDPWF ARTTPWFKIQNVSSSDLMLL is inserted between domains A2 and A3"
Pipe SW;
                                                                                                                                                                                                                                                                                             "probable"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "plastocyanin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "plastocyanin-like domain
                                                                                                                                                                                                                                                                                                                                                             domain'
                                                                                                                                                                                                                                                                                                                                                                                            domain'
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WPI; 1997-535830/49

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AAW33228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Co you willebrand satter binding site, a mutation at Argy40 and maddition of an amino acid sequence spaces between the A2 and A3 domains Rector (VIII, along with calcium and phospholipid, acts as a cofactor for factor (CC IXA, when it converts factor X to the activated form (factor A2) evil (CC is the coagultion factor deficient in the X-chromosome-linked bleeding CC disorder hemophilia A. Several other mutant FVIII processing have also been created (see AM33222-29). The FVIII mutant FVIII system for the FVIII wild type FVIII and retains pro-coagulant activity. The FVIII contained the first complete on the first coagulant contained the first complete on purposants of the process in activated process (IAM3322) and RSSX (IAM3322) are resistant to activated process (IAM3222) and RSSX (IAM3322) are resistant to activated contained the first complete on purposants of the first complete on the complete on the first complete on the complete on the first complete on the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                 Misc_feature
                                                                                                                                           Domain
                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant secretion; pro-coagulant activity; resistand activated protein C cleavage; APC; B domain; A2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Procoagulant-active human factor VIII:C (FVIII) mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW33228 standard; protein; 1383 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified human pro-coagulant active factor VIII - can be administered to haemophiliacs, i.e. factor VIII replacement therapy
                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVIII replacement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               von Willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pro-coagulant active factor VIII; FVIII; haemophilia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         using sequences trom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a novel pro-coagulant active factor VII (FVII) mutant protein, comprising a deletion of the B domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page -; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      this sequence does not appear in the specification, it was created sequences from the given references.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRNRGMTALLKVSSCD 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1383 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor binding site; binding affinity;
                                                 /note= ", 711 . 746
                                                                                            /note= "
380..711
                                                                                                                                   /note= "plastocyanin-like domain
187..329
                                                                                                                                                                                                       /note= "A1 domain
                                                                                                                                                                                                                                                  /note= "factor VIIIA light chain'
                                                                                                                                                                                                                                                                                             /note= "factor VIIIA heavy chain"
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
   "a spacer of the sequence SFSQNSRHPSTRQKQFNATTIPENDIEKTDPWF
                                                                       "A2 domain"
                                                                                                              "plastocyanin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82; DB is;
Pred. No. 1.8e-06;
                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
The present sequence represents a novel pro-cosquiant active factor (CVIII (PVIII) mutant protein comprising a deletion of the B domain and CV on Hillebrand factor binding site, mutuations 2018; BSSIX and 1740A and CO an addition of an anima acid sequence spaces between the A2 and A3 condains. Ractor VIII, along with calcium and phospholipid, acts as a CC cofactor for factor IXI, when it converts factor X to the activated form C (factor XA). PVIII is the cosquittion factor deficient in the CX **Chromosome-linked bleeding discorder hemophilia A Several other curtant FVIII proteins have also been created (see AN93222-29). The FVIII CC mutant FVIII proteins have also been created (see AN93222-29) and RSSX (AN93222) are resistant to activated protein C (ApC) cleavage. The FVIII CC mutant continue activated protein and von Hillebrand factor brownising a deletion of the B domain and von Hillebrand factor C binding site, a mutation at Arg740 and an addition of an amino acid configuration, and have an approximate 5-fold increase in specific contribute compared to purified wild type FVIII, while horzeasing their contribute processing affinity to von Millebrand factor improves their stability. The the mutation of the sequence specific contribute process and a provide the process their stability. The post of the process of the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-1996;
24-APR-1996;
                 note: this sequence does not appear in the specification; it was created using sequences from the given references.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09740145-A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
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Modified human pro-coagulant active factor VIII - can be administered to haemophiliacs, i.e. factor VIII replacement therapy
Claim 18; Page -; 57pp; English
                                                                                WPI; 1997-535830/49
                                                                                                                                                (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleavage-site
                                                                                                               Kaufman RJ,
                                                                                                                                                                                 96US-0017785
96US-0016117
                                                                                                                                                                                                                              97WO-US06563
                                                                                                                                                                                                                                                                                                                                                                                                          562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528..554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380..554
/note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153..179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372..373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C1 domain"
1226..1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     746..107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564..711
                                                                                                                                                                                                                                                                                                                       note= "wild type Arg replaced with Ala
                                                                                                                                                                                                                                                                                                                                                                       note= "wild type
                                                                                                                                                                                                                                                                                                                                                                                                                    /label= R336I
/note= "wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "probable"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "by thrombin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note=
                                                                                                                                                                                                                                                                                                                                        label= R740A
                                                                                                                                                                                                                                                                                                                                                                                        label= R562K
                                                                                                            Pipe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "C2 domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "probable"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *plastocyanin-like domain 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "plastocyanin-like domain 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AHRTPMPKIQNVSSSDLLMLL is inserted between domains A2 and A3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A3 domain"
                                                                                                               WS
                                                                                                                                                                                                                                                                                                                                                                         Arg replaced with Lys'
                                                                                                                                                                                                                                                                                                                                                                                                                       Arg replaced with Ile"
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Sequence

1383

B

Length 1383;

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RESULT 14
AAW33229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
       WO9740145-A1
                                            Misc-difference
                                                                      Misc-difference
                                                                                        Disulfide-bond
                                                                                                           Disulfide-bond
                                                                                                                                               Domain
                                                                                                                                                                                                                                                                  Misc_feature
                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                             Cleavage-site
                                                                                                                                                                  Domain
                                                                                                                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant secretion, pro-coagulant activity, resistance, activated protein C cleavage, APC, B domain, A2 domain, A3 domain, and willebrand factor binding site; binding affinity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pro-coagulant active factor VIII; FVIII; haemophilia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW33229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW33229
                                                                                                                                                                                                                                                                                                                                                                                   Kegion
                                                                                                                                                                                                                                                                                                                                                                                                                                       FVIII replacement therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Procoagulant-active human factor VIII:C (FVIII) mutant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; protein; 1383 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRNRGMTALLKVSSCD 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                            /note= "A3 domain"
1073..1221
/note= "C1 domain"
1226..1378
                                                                                                                          /note= "4
                                                                                                           153..179
                                  label= R740A
                                                  /label= F309S
/note= "wild type
                                                                              /note=
                                                                                                 note=
                                                                                                                                                                                  746..107
                                                                                                                                                                                             note=
                                                                                                                                                                                                               notes
                                                                                                                                                                                                                                                                     711..746
                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                note=
                                                                                                                                                                                                                                                                                                                  /note= "plastocyanin-like domain 1"
                                                                                                                                                                                                                                                                                                                                     /note= "Al domain"
                                                                                                                                                                                                                                                                                                                                                       note= "factor VIIIA light chain"
                                                                                                                                                                                                                                                                                                                                                                       /note= "factor VIIIA heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                    note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                       "wild type Arg replaced with Ala
                                                                              "probable"
                                                                                                "probable"
                                                                                                                   "by thrombin"
                                                                                                                                     "C2 domain"
                                                                                                                                                                                          "plastocyanin-like domain 4"
                                                                                                                                                                                                             "plastocyanin-like domain 3"
                                                                                                                                                                                                                                        "a spacer of the sequence SFSQNSRHPSTRQKQFNATTIPENDIEKTDPWF AHRTPMPKIQNVSSSDLLMLL is inserted
                                                                                                                                                                                                                                                                              "A2 domain"
                                                                                                                                                                                                                                                                                             "plastocyanin-like domain
                                                                                                                                                                                                                         between domains A2 and A3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                     Phe
                                                  replaced with Ser'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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The present sequence represents a novel pro-coagulant active factor (III (FVIII) mutant protein comprising a design of the B domain and voter of an amino acid sequence spacer between the A2 and A3 domains. Factor VIII, along with calcium and phospholipid, acts as a cofactor for factor C2 IXA, when it converts factor X to the activated form (factor A2) region (in the C3) representation factor deficient in the X-chromosome-linked bleeding continues the coagulation factor deficient in the X-chromosome-linked bleeding C4 disorder hemophilia A. Several other mutant FVIII proteins have also been created (see ANX3222-29). The FVIII mutant FVIII proteins have also continue to the coagulation factority. The FVIII capable of the protein can thigher levels than typically obsained with wild type FVIII and retains pro-coagulant activity. The FVIII contains a more specific configuration, and have an approximate 5-fold increase in capable of the configuration, and have an approximate 5-fold increase in capable of the first price of the proteins can be absoluted the first price of the first proteins can be an additional can be used to for earse the first price of the 
Query Match
Best Local Similarity
                                                                                            Sequence
                                                                                                                                                 note: this sequence does not appear in the specification; it was created using sequences from the given references.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified human pro-coagulant active factor VIII - can be administered to haemophiliacs, i.e. factor VIII replacement therapy
                                                                                                                                                                                                                     for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Page -; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-535830/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-1996;
24-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaufman RJ,
                                                                                            1383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0017785
96US-0016117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US06563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pipe
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X A X P C R X B X B X B X B X B X B X B X
                                                                                                                                                                                       AAP80268
ID AAP
                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                        片
                                                                                                                                                                                                                                                                                Matches
       31-JUL-1987;
                           11-FEB-1988
                                                                 Homo sapiens
                                                                                                               Modified factor VIII:C sequence with the R740-D1658 deletion
                                                                                                                                     25-MAR-2003
10-OCT-1990
                                                                                                                                                                    AAP80268
                                                                                                                                                                                     AAP80268 standard; protein; 1424 AA
                                              W08800831-A
                                                                                    blood coagulation; RD deletion; procoagulant
                                                                                            Modified factor VIII: C; maturation polypeptide; haemophilia;
                                                                                                                                                                                                                                        697 FRNRGMTALLKVSSCD 712
                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                          1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                    (updated)
(first entry)
       87WO~US01814.
                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                             Gaps
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100.0%; 100

Score 82; DB 18; Pred. No. 1.8e-06;

Length 1383;

01-AUG-1986;

86US-0893375.

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Page 9
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Search completed: November 7, 2003, 07:27:05 
Job time: 7.89987 secs
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 The RD deletion removes the DNA from Ser 741 to Ser 1657.
A major part of the sequence encoding the maturation polypeptide of factor VIIIc 1 is deleted, i.e. Gln 744 - Asp 1563.
The full length Factor VIIIc CDNA has two changes with respect to the published sequence (EFO application 160457):
CTG to CTA at Leu 242 and TTC to CTC change at emino acid residue 1880 (Phe to Leu). The product is produced in approx. 20 times higher yields than previous recombinant produced factor VIII:C and are more easily purified. The peptide is used for treating haemophilia A, both General Approximation of the produced factor and prolonged bleeding.
See also AN80044 and AN80446.
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 60-61-62-63; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA sequences encoding modified factor VIII:C - with deletion of DNA encoding maturation polypeptide, useful for high yield transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1988-049866/07.
N-PSDB; AAN80447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasek MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BIOJ ) BIOGEN NV. (PASE/) PASEK M P.
                                                                                                                  697 FRNRGMTALLKVSSCD 712
                                                                                                                                              1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                   1424 AA;
                                                                                                                                                                                                                            100.0%; silarity 100.0%; I
Conservative 0;
                                                                                                                                                                                                                            Score 82; DB 9; Length 1424;
Pred. No. 1.9e-06;
Pred. No. 1.9e-06; Indels
                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                            Gaps
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OM protein -
                                                                                                                         protein search, using sw model
November 7, 2003, 07:21:18; Search time 1.29506 Seconds (without alignments) 742.581.Willion cell updates/sec
                                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

sequence: Perfect score: US-09-661-992B-5 1 YGNSPKGFAY 10

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR 76:* pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					COLUMNIA	
Result		Query		3	;	
NO.	Score	Match	Length	B	ID	Description
1	42	72.4	626	N	B70749	probable Acv1-CoA
2	41	70.7	389	N	H90083	
ω	41	70.7	453	N	S75579	hypothetical prote
4	41	70.7	2515	N	A41519	
ທ	39	67.2	401	N	H82175	multidrug resistan
ø	39	67.2	568	J -4	A55377	
7	38	65.5	402	N	D90034	prot
89	38	65.5	488	N	AD0735	othe
9	38	65.5	488	N	AG0621	bacterio
10	38	65.5	488	N	B96521	
1.	1 (3)	65.5	583	N	B87204	probable acyl-CoA
12	8	65.5	588	N	JC7206	
: 1:	3/	63.8	205	N	T19356	hypothetical prote
<u>+</u>	3.7	63.8	223	N	B70372	flagellar protein
, L	3.7		306	н	859863	polyA binding prot
16	37	63.8	331	N	D86413	cysteine proteinas
17	37		346	N	C86413	
	37		390	N	G96028	4-hydrox
1	37		390	N	AD3115	
20	37	63.8	394	,-	WHPSBF	4-hydroxybenzoate
22	37	63.8	394	μ	WHPSBA	4-hydroxybenzoate
22	37		422	N	A98172	4-hydroxybenzoate
23	37	63.8	712	N	F97012	hypothetical prote
2.4	1 6	62.1	17	N	167526	CD33 antigen homol
2 10	30	62.1	117	N	C83576	conserved hypothet
2 0	36	62.1	181	N	A96762	probable RNA-bindi
2 4	, 4	62.1	196	N	A95890	
0 0	1 6	62.1	199	ł AZ	\$38867	eggshell protein -
22	36	62.1	381	ĸ,	C90395	

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35	35	35	35	35	35	35	35	35	35	36	36	36	36	36	36	
60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	62.1	62.1	62.1				
285	270	258	217	204	166	157	113	112	109	1928	1414	910	670	611	452	
N	N	ν	Ŋ	N	N	N	N	N	N	N	٢	N	N	N	2	
B82459	AE1497	S25624	T50004	T29489	T39586	S76232	F84671	JU0151	F30607	JS0610	S23809	\$38167	T02019	S60914	\$64211	
hypothetical prote	phoglycerat	coat protein - cas	77		**	•	hypothetical prote	biphenyl-2,3-diol	Ig kappa chain V-I	beta-galactosidase	Ē.	hypothetical prote	-associated	lysine transport p	probable transcrip	

ALIGNMENTS

countor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Churcher, C.; Harris, D.; G Rajandream, M.A.; Rogers, J., Rutter, S.; Seeger, K.; Skelton, S.; Sunatian, N.; Hol Mature 339, 537-544, 1998 A;Authors: Squres, R.; Suleton, J.E.; Taylor, K.; Mitchead, S.; Barrell, B.G. A;Tile: Despinering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500, MUID:98295987; PMID:9634230

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type; DNA. A;Residues: 1-656 <001. A;Cross-references: CGI:274697; GB:AL123456; NID:g3261602; PIDN:CAA98985.1; PID:g A;Experimental source: strain H37Rv

C;Genetics: A;Gene: fadD26

C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology F;103-610/Domain: acetate-CoA ligase homology <ACL>

Query Match Best Local S Matches 7 y Match Jocal Similarity 77.8%; Pred. No. 8.5; Length 626; Local Similarity 77.8%; Pred. No. 8.5; hes 7; Conservative 1; Mismatches 1; Indels 1 YGNSPKGFA 9 1; Indels ٥, Gaps

0;

RESULT 2 H90083

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73 YGSDPKGFA 81

polyademylate-binding protein (imported) - Guillardia theta nucleomorph CiSpecies: nucleomorph Guillardia theta A.Nete: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont CiPate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001 ciAccession: 190083

RiDouglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, Mature 4.0, 1091-1096, 2001
A.Title: The highly reduced genome of an enslaved algal nucleus.
A.Reference number: A99082; MUID:11323671; PMID:11323671

A;Accession: H90083

A; Map position: 1

A;Status preliminary A;Molecule type: DMA A;Residues: 1-399 ZOUJ A;Cross-references: GB:AP.65818; NID:g13794428; PIDN:AAK39803.1; GSPDB:GN00150 C, Genetics:

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                                                                                                                                                                  C; Superfamily: posterior-group protein tudor
                                                                                                                                                                                          A;Cross-references: FlyBase:FBgn0003891
                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-2515 <GOL>
                                                                                                                                                                                                                                                                                                                    R.Golumbeski, G.S.; Bardsley, A.; Tax, F.; Boswell, R.E.
Genes Dev. 5. 2060-2070, 1991
A.;Title: tudor, a posterior-group gene of Drosophila melanogaster, encodes a novel proto
A.;Reference number: A41519, MUID:92038995; PMID:1936993
A.;Accession: A41519
                                                                                                                                                                                                                                                                                                                                                                                                                             postexior-group procein tudor - fruit fly (Drosophila melanogastex)
Cispecies: Drosophila melanogaster
Cipace: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1999
Cipacession, Ads1519, 819019
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A.NOte: the nuclocide sequence was submitted to the MEU nata Library, June 1996
C./Superfamily: hypothetical protein allogate; translation elangation factor Tu homology
C./Keywords: GTP binding: nucleotide binding; P-Loop
C./Keywords: GTP binding: nucleotide binding; P-Loop
F.66-176/Domain: translation elongation factor Tu homology <FTU>
                                                                                                                                                                                                                                                    A;Cross-references: GB:X62420; NID:g8753; PIDN:CAA44286.1; PID:g8754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;68-75/Region: nucleotide-binding motif A (P-loop)
F;173-176/Region: GTP-binding NKXD motif
F;367-369/Region: GTP-binding SAK/L motif
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A; Molecule type: DNA
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o, K., Okumura, S., Shimpo, S., Taksuchi, C., Wada, T., Watanabe, A., Yamada, M., Yasud
DWA, Ress. 3, 109-116, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Date: 25-Apr-1997
C; Accession: 875579
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G:Specises: Symechocystis sp.
G:Date: 25-Apr:1997 #sequence_revision 25-Apr:1997 #text_change 02-Feb-2001
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C;Keywords: nucleomorph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti.
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7; Conserve
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YGNSPKSF 2178
                                            YGNSPKGF 8
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                                                                                    Conservative
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100.0%; Pred. No.
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Pred. No. 7.
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Best Local :
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maltidrug resistance protest VC1634 [imported] - Vibrio cholerse (strain N1696)
CiSpecias: Vibriotance protest revision 20-Aug-2000 #text_change 02-Feb-2001
CiDate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
CiAccessiann: HB2175
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R.Heddelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Claycon, R.A.; Gwinn, M.L.; Dodsc chardson, D.; Emolaeva, M.D.; Vmanthevan, J. Jases, S.; Qin, H.; Dragoi, I.; St. L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Neture 405, 477-483, 2010
A.Fitle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholera A; Reference number: A82035, MUID:20408833; PMID:10952301

A; Molecule type: DNA A; Residues: 1-401 <HEI> A;Status: preliminary

A;Experimental source: C;Genetics: A; Cross-references: GB:AE004241; serogroup GB:AE003852; NID:g9656142; O1; strain N16961; biotype PIDN:AAF94785.1; El Tor

gg

A;Gene: VC1634 A;Map position: 1 C;Superfamily: bicyclomycin resistance protein

Matches Query Match Local Similarity 7; Conserv Conservative 70.0%; 0; Mismatches Score 39; DB Pred. No. 19; ۶, ω, Length 401 Indels 0; Gaps

0

A55377

251

1 YGNSPKGFAY 10

CPE-binding protein - African clawed frog

Wildternate names: cytoplasmic polyadenylation element-binding protein Cybeciss Kanopus laevis (African clawed frog) cylate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 cylate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 cylates: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 cylates: 10-Sep-1999 #sequence in Sep-1999 #sequence number: 10-Sep-1999 #sequence number: A55377; MUID:95042759; EMID:7954828 A; Accession: A55377

A; Molecule type: mRNA A; Status: preliminary; not compared with conceptual translation

A.Pæsidues: 1-586 (HRK) A.Cross-references: GB.U14169; NID:9987224; PIDN:AAA80483.1; PID:9624634 C:Superfamily: African clawed frog CPE-binding protein; ribonucleoprotein repeat F;314-388/Domain: ribonucleoprotein repeat homology <RRM1>

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Length 568;

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Gaps

0

Matches Local 357 GNMPKGYVY 365 2 GNSPKGFAY 10 h 67.2%; Similarity 66.7%; Conservative Mismatches Score 39; DB Pred. No. 28; Indels

hypothetical protein SA2135 [Amported] - Staphylococcus aureus (strain N315) C.Species: Staphylococcus aureus C.Pate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C./Accession: De0034
R.MINGOR, M.; Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, M., A.; Misuteni-U; Y.; Kobayashi, N.; Sawano, T.; Indone, R.; Katico, C.; Gekim C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hizamatsu, K. Lancet 357, 1225-1240, 2001

A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus

A89758; MUID:21311952; PMID:11418146

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A; Molacule type: DNA
A; Molacule type: DNA
A; Molacule type: DNA
A; Cross-references: GB: AL513382; PIDN: CADO5441.1; PID: g16502202; GSpDB: GN00176
                                                                                                                                                                                                                                                          . S.; Moule, S.; O'Gaora, P.
Mature 413 68-882, 2001
Mature 413 68-882, 2001
A:Mathors: Parry, C.; Quali, M.; Rutherford, K.; Simmonde, M.;
A:Mathors: Parry, C.; Quali, M.; Rutherford, C.; Garden, M.;
A:Matherence number: ABOSO2, MUID:2154997; PMID:11677608

A:Reference number: ABOSO2, MUID:2154997; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable bacteriophage protein SYI1048 [imported] - Salmonella enterica subsp. C.Species: Salmonella enterica subsp. enterica serovar Typki A.Note: this species has also been called salmonella typhi C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 10-Nov-2002 C.Accession: AG06211
                                                                                                                                                                                                                                                                                                                                                                                                        R. Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davise, R.M.; Dowd, S.; Noule, S.; O'Gaoza, P.
                                                        C; Genetics:
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C;Superfamily: Haemophilus influenzae hypothetical protein HI1409
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A Photograph Type (1997)
A Procest Eferences (BB BA000018; PID:913702296; PIDN:BAB43437.1; GSPDB:GN00149
A:Cross-references (BB BA000018; N315
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A; Residues: 1-488 < PAR>
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A.Authors: Parry, C.; Quali, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A.Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A.Reference mumber: ABSOS2, MUID:21534977, PMID:18677608
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A;Accession: D90034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YGNSPKGPA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
6, Conservat
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6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGNSPKAY 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGNSPKGF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DE
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                                                                                 Salmonella enterica serov
                                                                                                                                                                                                                                                                                                                                    Skelton,
                                                                                                                                                                                                                                                                                                                                                                                                                                          D.; Wain, J
, L.; White,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                    J.; Stevens,
                                                                                                                                                                                                                                                                                                                                                                                                                                          J.; Churcher
e, N.; Farrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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R;COLe, S.T.; Elgimeicr, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Praser, A.; Hamlin, N.; an, M.A.; Nutherford, K.M.
Nature 409, 1007-1011, 2007

Nature 409, 1007

Nature 409
S
                                                                                                                                                                                           A;Gene: fadD26
C;Superfamily: Synechocystis long-chain-fatty-acid-CoA ligase;
                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL450380; NID:g13093967; PIDN:CAC31874.1; GSPDB:GN00147 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-583 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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                                                                    Matches
                                                                                                      Query Match
Best Local :
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Similarity

65.5%; 75.0%;

Score 38; Pred. No.

DB 2;

Conservative

;

Mismatches

1, Length 583

indels

0

Gaps

0

Squares

YGNSPKGF 8

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protein P21D19.20 [imported] - Arabidopais thaliana
C:Species: Arabidopais thaliana [monse-ear cress]
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C,Accession: B96521
                                                                                                                                                                                                                                                                        C; Superfamily: Haemophilus influenzae hypothetical
                                                                                  RESULT 10
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                        Local
                                                                                                                                     323 FGQSPKGFS 331
                                                                                                                                                                     1 YGNSPKGFA
                                                                                                                                                                                                        Similarity
6; Conser
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                     65.5%;
66.7%;
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                     Score 38; DB 2;
Pred. No. 36;
                                                                                                                                                                                                                                                                        protein HI1409
                                                                                                                                                                                                                                      Length 488
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                                                                                                                                                                                                     Gaps
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0

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RESULT 11
B87204
probable avyl-CoA synthase (imported) - Mycobacterium leprae
Cipacie: 10-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rythoologis, A., Ecker, J.R.; Palm, C.J.; Rederspidel, M.A.; Kaul, S.; White, O., Chin, C.W.; Chung, M.K.; Conn. L.; Connway, A.B.; Connway, A.R.; Connway, T.H.; Dealmen, N.F.; Hughes, B.; Hhitar, L. Wature 408, 818-820, 200
A.; Authors: Hunter, J.L.; Jenkin, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Lid, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurce, J.S.; Maiti, R.; Maizzo, M.; Rooney, T.; Rowley, D.; Sakano, L., Liu, Z.A.; Lurce, J.S.; Maiti, R.; M. A; McLores, Salzeng, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Mu, D.; Yu, G.; Framer, C.M.; Venter, J.C.; Davis, R.W.
Ayilliz: Sequence and analysis of chromosome to the plant Arabidopsis.
Ayselerance number: A86141, MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-488 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005173; NID:g8778515; PIDN:AAF79523.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                              F21D18.20
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                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                6; Conserv
                                                                                                                                                                                                                                                 GNSPKGFAY 10
                                                                                                                                                                                                 GSSPRGFKY 240
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                            65.5%;
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                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                        36;
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                                                                                                                                                                                                                                                                                                                                               Length 488
                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                            Gaps
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RESULT 14
B70372
B70372
F10372
F10372
C.Species: Aquifex acolicus
C.Species: Aquifex acolicus
C.Date: 0.087971998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C.Dates: 0.087971998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C.Dates: 0.087971998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C.Dates: 0.087971999 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C.Dates: 0.08797199 #sequence_revision 08-May-1999
C.Dates: 0.08797199 #sequence_revision 08-May-1999
C.Dates: 0.08797199 #sequence_revision 08-May-1999
C.Dates: 0.08797199 #sequence_revision 0
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus
A;Reference :umber: A70300; MUID:98196666; PMID:9537320
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C.Species: Caenorhabdiris elegans
C.Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: 171956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphoprotein phosphatase (EC 3.1.3.16) (validated) - shitake mushroom C;pace; 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 20-Apr-2001 C;Accession 107206

K;ishizaki, T.; Yokoyama, H.; Kajiwata, S.; Shishido, K. Biosci. Biotechnol. Biochem. 64, 438-442, 2000

A;Title: Basidiomycete fungal gene encoding a regulatory subunit A homologu A;Bacterone number: JC7206; MUID:20139469; PMID:10737208
A;Accession. UC7206
A;Bacterone number: JC7206; MUID:20139469; PMID:10737208
A;Accession. UC7206
A;Bacterone number: JC7206; MUID:20139469; PMID:10737208
A;Accession. UC7206; MUID:20139469; PMID:10737208
A;Accession. UC7206; MUID:20139469; PMID:10737208
A;Accession. UC7206; MUID:20139469; PMID:10737208
A;Accession. UC7206; MUID:20139469; PMID:10737208
A;Accession. UC7206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-205 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library,
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C;Superfamily: phosphoprotein phosphatase 65K regulatory chain
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: CESP:C17E4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:281037; PIDN:CAB02750.1; GSPDB:GN00019; CESP:C17E4.5
A;Experimental source: clone C17E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z19113
A; Accession: T19356
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A; Residues: 1-588 <ISH>
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hes 6; Conserv
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hes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YGNSPKGFAY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSGHPKGFAY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGNTPEGEAF 553
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Pred. No.
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Pred. No. 44;
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Search completed: November Job time : 3.39506 secs

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A;Residiose; 1-206 (ARR).
A)Cross-reference: RMBL:R89969; NID:g1065677; PIDN:ChA62006.1; PID:g1051125
A)Cross-reference: RMBL:R89969; NID:g1065677; PIDN:ChA62006.1; PID:g1051125
A)Mote: the nucleotide sequence was submitted to the RMBL Data Library, July 1999
A;Note: the nucleotide sequence was submitted to the Control of t
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A.Status: pretininary; nucleic acid sequence not shown; translation
A.Wolscule type: DMA
A.Roccidues: 1233 -AOPS
A.Roccidues: 1233 -AOPS
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A.Roccidues: 1234 -AOPS
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A.Paceasion: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: mRNA
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A.THILE: Icolation of genemic and cDNA clones encoding bovine poly(A) binding A.Reference number: 859863; NUID:96071160; PMID:7479061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyA binding protein II - bovine
C:Specias: Ros prinsignius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Nov-1999
C:Accession: S5983
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

kun on: November 7, 2003, 07:21:18; Search time 0.720961 Seconds (without allignments) 652.278 Million cell updates/sec

Sequence: Perfect score: US-09-661-992B-5 58 YGNSPKGFAY 10

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Regult

egult No.	Score	Query Match	Length	엻	10	Description
1	42	72.4	583	۳	FD26_MYCTU	Q10976 mycobacteri
Ŋ	41	70.7	2515	_	TUD DROME	ω
ω	37	63.8	223	ب	FLGA AQUAE	
4	37		394	μ	PHHY_PSEAE	
ÇTI	37		394	H	PHHY PSEFL	
6	37	۳	1180	μ	RNT1_DROME	
7	36	62.1	452	μ	HOS2_YEAST	
8	36		611	۳	LYP1_YEAST	
9	36	62.1	910	H	YK69_YEAST	
10	36	62.1	1928	,_	LPH_RAT	
11	35	60.3	290	μ	TODE PSEPU	
12	35		291	μ	BHC1_RHOGO	P47231 rhodococcus
13	35		332	۳	C1C3_CAVPO	
14	S	60.3	349	μ	RNFD PASMU	
15	35	60.3	373	-ر	NLPD_SALTI	
16	ų, S	60.3	377	μ	NLPD_SALDU	
17	35	60.3	377	۳	NLPD_SALTY	
18	35		379	щ	NLPD_ECOLI	
19	S.		396	н	PRRC_ECOLI	
20	S	60.3	490	۳	JIP1_DROME	
21	35		503	μ	ATE1_YEAST	P16639 saccharomyc
22	ω G	60.3	674	μ	AGUA_THEMA	P96105 thermotoga
23	35		1230	,	UGS4_SOLTU	Q43846 solanum tub
24	34		220	۳	HB7B_XENLA	P04476 xenopus lae
25	34		246	μ	Y625_MYCTU	P96915 mycobacteri
26	34		260	,	COAT_TYLCV	
27	34	58.6	289	μ	HXD8_MOUSE	P23463 mus musculu
28	34		290	μ	HXD8 HUMAN	
29	34		350	-	YL85_PYRAE	-
30	34		427	ب	RU17_ARATH	
31	ω 4		429	,,	THD1_MYCTU	
32	34		1058	μ	U202_ARATH	
(J	Ų.	58.6	1866	Ļ	VGNB_CPMV	Р03600 сомреа пова

45	44	43	42	41	40	39	38	37	36	35	34	
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METK XANCP	METK XANAC	ARGD BACSU	Y36K HALSN	TFB3_HALN1	MIAA AGRTS	CDD HAEIN	COAT CLVN	COAT_CLVK	YB62 THEMA	KV3G HUMAN	YLJ6_CABEL	
Q8pch3 x	Q8pp75 xa	P36839 ba	P14321 h	Q9hhk5 ha	P38436 ac	P44325 ha	P14966 C	P03561 ca	Q9x0p5 tl	P04206 hc		
xanthomonas	xanthomonas	bacillus su	halobacteri	halobacteri	agrobacteri	haemophilus	cassava lat	cassava lat	thermotoga	homo sapien	caenorhabdi	

ALIGNMENTS

Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillanyouth T., Comnor K.,
Badrock K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornaby T., Jagala K., Kropih A., McLean J., Moule S., Murph L.,
Oliver S., Geborne J., Quali M.A., Rajandream M.A., Rogers J.,
Rutter S., Seger K., Skelton S., Squares S., Squares R.,
Sularon J.E., Taylor K., Whitchead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.",

SEQUENCE FROM N.A. STRAIN=CDC 1551 / Oshkosh;

Pelsischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Beterson J., Deboy R., Dodenn R., Gwinn K.L., Haft D., Nickey E., Kolonay J.F., Welson W.C., Umayam L.A., Ernolasva M.D., Salzberg S.L., Delcher A., Utterback T., Waldman J., Khouri H., Gill J., Mikula A.,

"Whole genome comparison of Mycobacterium tuberculosis clinical and

laboratory strains,",
Submitted (Apr-2001) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY; BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME FAMILY.

This SHISS-PROF entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMRIA outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-positi institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an enail to license@dos-sib.ch/). EMBL; AE007122; AAK47327.1; TIGR; MT2999; -. Tuberculist; Rv2930; -. EMBL; 274697; CAA98985.1; ALT_INIT.

InterPro; IPR000873; AMP-bind

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RESULT 2
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P25823;
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                                        DOMAIN
DOMAIN
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HSSP; Q16637; 1G5V.
FlyBase; FBgn0003891; tud.
                                                                                                                                                                                                                                                                                                                This SNISS-PROT entry is copyright It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEZ outeration the EMEZ patestation - the Emropean Bioinformatics Institute. There are no restrictions on the use by non-profit institutions as long as its content is in m way modified and this statement is not resorved. Usage by and for commercial entities requires a license agreement (See http://www.iab-stb.ch/announce/or and on email to oltcomessib-stb.ch/a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Golumbeski G.S., Bardsley A., Tax F., Boswell R.E.;
"Tudor, a posterior-group gene of Drosophila melanogaster, encodes
novel protein and an MRM, localized during mid-oogenesis.";
Genes Dev. 5:2060-2070(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sukaryora; Metazoa, Arthropoda, Hexapoda, Insecta; Pteryota;
Neopoca; Endopteryora; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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PROSTITE; B800455; AMP BINDING; PALSE NEG
BYPOthetical protein; Ligase; Patty ācid
complete proteome.
SEQUENCE 533 AA; 65043 MM; P97CD6E197
                                                                                                                                                                                                               GO; GO:0019090; P:mitochondrial rRNA, mitochondrial export; IMP.
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01-MAY-1992 (Rel. 22, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation updat
                                                                                    DOMAIN
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SMART; SM00333; TUDOR; 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                     interPro
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hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIMODENAL GERM CELLS AND FOR MORNAL ABDOMINAL SEGMENTATION.
DEVELOPMENTAL STAGE: EXPERSESED INFOGUSION IN ELECCRICATION.
MISCELLANGOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR
REGION OF THE DEVELOPING OCCUTE DURING THE EARLY TO MUDILS FIRSTED.
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                                                                                                            protein; Repeat
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PHHY_PSEAE
P20586;
01-FEB-1991
01-FEB-1991
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FLOAD OR AQ 033.
Aquites medicuse Aquificales, Aquificaceae, Aquifex.
NCNI TAXTD 653563;
                                                                                                                                                                                                                                                                                                                                                                              This SHISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the BMH outstation the Buropens Bioinformatics Institute. There are no restrictions on its use by mon-position statement and as a conjent is in no way meet by mon-positi institutions a long as its conjent is in modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-shib.ch/announce/
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-1 FUNCTION: INVOLVED IN THE ASSEMBLY PROCESS OF THE P-RING A PROCESS OF THE P-RING A PROCESS OF THE P-RING A SECURITY BY A SECURITY BY A PROCESS OF THE P-RING A SECURITY BY ANY ACT AS A MODILATOR PROTEIN FOR THE P-RING ASSEMBLY (BY SIMILARITY).

-1 SUMILARITY: BELOANSO TO THE FLAR FAMILY.
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Graham D.E., Owtobeek K., Shead M.A., Kaller M., Aujay M., Huber R.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,
"The complete genome of the byperthermophilic bacterium Aquifex
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                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             067005;
30-MAY-2000
                                                                                                                                                                                                                                                                                               Pfam; PF03240; FlgA;
                                                                                                                                                                                                                                                                                                             InterPro; IPR004924; FlgA.
                                                                                                                                                                                                                                                                                                                             PIR; B70372; B70372.
                                                                                                                                                                                                                                                                                                                                        EMBL; AE000709; AAC06962.1;
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Local Similarity 87.5%;
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                                                                                                                                                                                                                                                                                  Periplasmic; Signal; Complete proteome.
                                                                                                                                                                                                                          223 AA; 26303 MW; 98C0A5189D8254CD CRC64;
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  (Rel. 17, Created)
(Rel. 17, Last sequence update)
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                                            STANDARD;
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Pred. No.
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                                            PRT;
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STPANNANCY 15692 / PAOI,

REDLINE-2047371; RubWed-1094043;

REDLINE-2047371; RubWed-1094043;

RECOVER C. P. Pham X.-Q.T., Exvin A.L., Miscouchi S.D., Warrener P.,

Hickey M.J. Brithman F. S.L., Buffingle W.O., Kowalik D.J., Lagrou M.,

Garber R.J. Goltry L., Tolentino B., Mestbrook-Wedman S. Yuan Y.,

Brody L.L., Collete S.M., Folger K.R., Was A., Larbig K.,

Brith K.J., Spencer D.H., Wang G.K.-S., Wu Z., Paulsen T.T.,

Reiser J., Sake M.H., Hancock R.J. W., Lory S., Olonn M.V.;

"Complete genome sequence of Fasudomonae aeruginosa PAOI, an

poportunistic pethogen.")
                                                                                                                                          This SHESS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMRD contextion the BMRDpean Bioinformatics Institute. There are no restrictions of its use by non-posit institutions as long as its content is in no way notified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseasbs-sib.ch).
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Lah M.S., Palfey B.A., Schreuder H.A., Ludwig M.L.;
"Crystal structures of mutant Baudomonas aeuginosa
p-hydroxyhenroate hydroxylaase: the Tyr201Phe, Tyr385Phe,
Asn300Asp Variants.";
                                                                                                     EMBL; M23173; AAA88455.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 33:1555-1564(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "pH-dependent extuctural changes in the active site of proton and phytoxybenzoate hydroxylase point to the importance of proton and water movements during catalysis."; https://doi.org/10.100/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001
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Gatti D.L., Entsch B., Ballou D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gatti D.L., Palfey B.A., Lah M.S., Entsch B., Massey V., Ballou D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95025875; PubMed=7939628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJNE=89138003; PubMed=2465205;
Briech B., Nan Y., Meaich K., Scott K.F.;
"Sequence and organization of pobA, the gene coding for p-
hydroxybenzoate hydroxylase, an inducible enzyme from Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monooxygenase)
POBA OR PA0247
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P-hydroxybenzoate hydroxylase (EC 1.14.13.2) (4-hydroxybenzoate 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 266:110-114(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The mobile flavin of 4-OH benzoate hydroxylase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                  SUBUNIT: Homodimer.
SIMILARITY: TO P. PUTIDA SALICYLATE HYDROXYLASE.
                                                                                                                                                                                                                                                                                                                                                                            CAPALYTIC ACTIVITY: 4-hydroxybenzoate + NADPH + O(2) protocatechuate + NADP(+) + H(2)O. COPACTOR: PAD.
// AE004463; AAG03636.1; -.
JT0334; WHESBA.
1DOB; 30-NOV-94.
1DOC; 30-NOV-94.
1DOD; 30-NOV-94.
                                                                                                                                                                                                                                                                                                                                                        PATHWAY: DEGRADATION OF BENZOATE TO SUCCINATE AND ACETYL-COA
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DR PDB: 1105; 30-30V-54.

DR PDB: 1105; 30-3NR-96.

DR PDB: 1107; 03-ARR-96.

DR PDB: 1107; 03-ARR-96.

DR PDB: 1107; 03-ARR-96.

DR PDB: 1107; 03-ARR-96.

DR PDB: 1107; 20-3NR-96.

DR PDB: 1107; 20-3NR-96.

DR PDB: 1107; 20-3NR-96.

DR PDB: 1208; 32-78B-95.

DR PDB: 1208; 32-7
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PO0438;
CRel. 01, Cast sequence update)
01-ARR-1993 (Rel. 15, Last sequence update)
02-REB-2003 (Rel. 41, Last annotation update)
28-REB-2003 (Rel. 41, Last annotation update)
29-REB-2003 (Rel. 41, Last annotation update)
2-REB-2003 (Rel. 41, Last annotation update)
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SEQUENCE OF CNBR PEPTIDES AND STRUCTURE OF MEDLINE=83209623; PubMed=6406227; Weijer W.J., Hofsteenge J., Beintema J.J.,
                                                                   Reference J., Weijer W.J., Jekel P.A., Beintema J.J., "Phyldroxybenzoate hydroxylass from Pseudomonas fluorescens. Completion of the elucidation of the primary structure."
                                                                                                                                                              Vereijken J.M., Hofsteenge J., Bak H.J., Beintema J.J.;
"The anino-scie dequance of the three smallest CSBr peptides from Tydroxybenzoate hydroxylase from Pseudomonas fluorescens.";
Bur. J. Blochem. 113:151-157(1890).
                                                                                                                                                                                                                                                                                  "primary and tertiary structure studies of p-hydroxybencoate hydroxylase fire Peaudomonas fluorescens. Isolation and alignment of the CMEr peptides; interactions of the protein with flavin adenine dimodeoride."
                                                                                                                                                                                                                                                                                                                                           MBDJINB-81114230; PubMed=6780352;
Hofsteenge J., Vereijken J.M., Weijer W.J., Beintema
Wiezenga R.K., Drenth J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           van Berkel M., Westphal A., Eschrich K., Eppink M., de Kok A.; 

"Substitution of Arg214 at the substrate-binding site of p-

tydroxybenzoate hydroxylase from Pseudomonas fluorescens.";

Eur. J. Biochem. 210:411-419(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSEFL
                                                                                                                 SEQUENCE OF CNBR PEPTIDES AND TERTIARY STRUCTURE MEDLINE=83209654; PubMed=6406229;
                                                                                                                                                                                                                          MEDLINE=81114232;
                                                                                                                                                                                                                                      SEQUENCE OF 1-52; 53-65 AND 66-110.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 111-138 AND 270-280
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Weijer W.J., Hofsteenge J., Vereijken J.M., Jekel P.A., Beintema J.J., Primary structure of p-hydroxybenzoate hydroxylase from Fseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=82257502; PubMed=6809053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonadaceae;
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                                                            Biochem.
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                                                         133:91-108(1983).
                                                                                                                                                                                                                        PubMed=6780353;
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327
327
386
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66.7%;
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Pred. No. 2
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                            ACTIVE SITE
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Wierenga R.K.,

Drenth J.;

2PHH; 1PBB; 1PBC; 1PBD; 1PBE; 1PBF;

15-JAN 93 15-APR 92 30-SEP-94 30-SEP-94 30-SEP-94 30-SEP-94 31-MAR-95 12-AUG-98

A90643; WHPSBF 1PHH; 15-JAN-9 X68438; CAA48483.1;

1PDH;

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                                                                                                                                                                                                                                                                                                                                                                                                    WEDLINE-98217889; PubMed-9579477;
BPpiik M.H., Schreuder, H.A., van Berkel W.J.;
Brysik and Ser42 variants of p-hydroxybenzoate hydroxylase from
Flyskl and Ser42 variants of p-hydroxybenzoate sesential for NADPH
Pseudomonas fluoreseens reveal that Aryd 1 is essential for NADPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BppKink M.H., Schreuder H.A., van Berkel M.J.,
"Structure and function of mutant Apy441ys of 4-hydroxybenzoate
Nydroxylase implications for NapPH binding.";
bur. J. Biochem. 231.157-155(1995).
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Hol M.G.J. Dennth J.
"Crystal structure of the reduced form of p-hydroxybenzoate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-80029705; PubMed=40036; Wierenga R.K., de Jong R.J., Kalk K.H., "Crystal structure of p-hydroxybenzoate J. Mol. Biol. 131:55-73(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "p_hydroxybenzoate hydroxylase from Pseudomonas fluorescens. 2. Fitting of the amino-acid sequence to the tertiary structure.", Bur. J. Biochem. 133:109-118(1983).
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
MEDLINE=99148809; PubMed=10025942;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95354684; PubMed=7628466;
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Proteins 14:178-190(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Crystal structure of p-hydroxybenzoate hydroxylase complexed with its reaction product 3,4 dihydroxybenzoate.";
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                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO E.COLI UBIH/VISB AND VISC.
                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: DEGRADATION OF BENZOATE TO SUCCINATE AND ACETYL-COASUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. 253:194-201(1998).
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hydroxylase
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Ffam; PF01494; PAD_binding_3; 1.
Ffam; PF01490; Monocygenase; 1.
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FADI
                                                                                                                                                                        NADP, 3D-structure.
33 FAD (POTENTIAL).
286 FAD (POTENTIAL).
344 W -> Y (IN REF. 2).
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RESULT 6
RNT1_DROME
Makana M. Delcher S.E. Bolt R. A. Evans C.A. Gocayne J.D.

Ra Mahama M.D. Seinikus S.E. Bolt R. M. Boskins R. A. Galla R. R.

Ra Manamatides P.G., Scheres B.E. Li E.M. Boskins R. A. Galla R. R.

Ra Gocaye R.A. Lewis S.E. Richards S. Amblumar M. Henderson S.M.

Ra Sutcon G.G., Wortman J.R., Yandall M.D., Zhang G., Chen L.X.

Ra brandon R. C., Roges Y.+H.C. Blaze'R G., Champe M., Pfeiffer B.D.,

Ra brandon R. G., Wortman J.R., Yandall M.D., Zhang G., Chen L.X.

Ra brandon R. G., Boyes Y.+H.C. Blaze'R G., Walker C.R., MALOS J.G.,

Ra haril J.F., Ragbaynih A. An H.-J., Andrews Franchook C., Baldouin D.,

Ra bladwa R.H., Basu A., Baxandale J., Bayakhurojai L., Bearley B.M.

Bellow R.H., Basu A., Baxandale J., Bayakhurojai L., Dest J., Barley R.M.,

Bellow R.H., Basu A., Baxandale J., Bayakhurojai L., Dest J., Barley R.M.,

Bellow R.H., Basu A., Barler H., Cadisu B., Center A., Chandra I.,

Ra Hartis K.C., Basem D.A., Buller H., Cadisu B., Center A., Chandra I.,

Ra Chetry J.M., Cowley S., Downes M., Dugan-Rocha S., Duhove S.,

Ra Bartis R.J., Rough L.E., Downes M., Dugan-Rocha S., Duhove S., Chunn P.,

Ra Dodon K., Dough L.E., Downes M., Dugan-Rocha S., Duhove S., Chunn P.,

Ra Dodon K.J., Brangdisteu C.G., Ferras C., Ferriera S., Flasichmann W.,

Ra Posker C., Gabriellan A.E., Gang N.S., Gelbart M.M., Glasser K.M.,

Ra Hartis M.J., Harvey D., Halman T.J., Hernmeder J.R., Houch C.,

Ra Hartis M.J., Harvey D., Kaster K., Kanyire S., Mallp D., Lai Z.,

Ra Hartis M., Kalladon K., Marushi M., Kalladon D., Malaci M., Marushi M., Walladon K., Marushi M., Walladon K., Marushi M., Walladon J.R., Polladon M., Wellon D., Welladon M., Bartis M.J., Kalladon D., Welladon M., Welladon M., Bartis M.J., Welladon M., Welladon M., Standel B., Welladon M., Standel B., Welladon M., Standel B., Welladon M., Welladon D., Welladon M., Standen M., Welladon M., 
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Drospyhila melanogaster (Fruit fly).
Bikaryota: Metasos, Arthropoda; Hexapoda: Insecta: Pterygota:
Neoptera: Endopersyota: Dipera; Bradhycera; Muscomorpha;
Ephydroida; Drospyhilidae; Drosophila.
Mchil (Taxib=127)
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G9Y63, Q9S669;

16-CCT-2001 (Rel. 40, Created)

28-F2B-2003 (Rel. 41, Last sequence update)

28-F2B-2003 (Rel. 41, Last amotation update)

Regulator, of momesme transcripts 1 homologs
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STRAINHBEYELEY;

KEDLINE-2243669; PubMed=12537572;

KEDLINE-2243669; P. A. Mungall C.J., Matthews B.B., Campbell K.S.,

Hasza S., Croeby M. X. Maninber J.S., Millburn G.H., Prochnik S.E.,

Hradeoby P., Haugy Y. X. Maninber J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

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RESULT HOSE YES NOT THE PROPERTY OF THE PROPER
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Stapleron M. Envokesin P. Hong L. Agbayani A. Carlson J.W.
Change M. Charez C. Dorest V. Farfan D. Friee E. Goorge R.A.

Gonzalez M. Goartin H. Lib FW. Liao G. Miranda A. Mangall C.J.

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Nunco J. Perleb J.M. Parass V. Bark S. Phousensworg S.

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Submitted (NCT-2001) to the BMBL/GenBank/DDBJ databases

1 BURCTUS Eliminates the production of momense-containing

MANS UP SERVICE CONTROL OF 
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Coglievina M., Klima R., Bertani I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOS2 OR YGL194C OR G1130.
Saccharcmycas cerevisiae (Baker's yeast)
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EMBL; AY061379; AAL28927.1; -.
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                         Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Dryadale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart M.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            systematic review.
              MEDLINE=97121415; PubMed=8962081;
                                                                                                                  SENE NAME
                                                                                                                                                                                                                                                                Yeast 13:55-64(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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1261 protein; Hydrolase, Helicase, ATP-binding, Sinc-finger.

108 136 C2H2-TFPE (ATPFICAL). (FOTENTIAL).

109 140 ATP (FOTENTIAL).

110 GIV-RICH.

110 GIV-RICH.
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6; Conser
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Pred. No. 66;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zaccaria P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Requirement of Hos2 histone decetylase for gene activity in yeast.", Science 298:1412-1414(2002). Consent 298:1414(2002). Consent 298:1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pijnappel M.H.M.P., Schaft D., Roguev A., Shevchenko A., Tekotte H.,
Wilm M., Rigaut G., Sexephin B., Assland R., Stewart A.F.;
"The S. cerevisiae SET3 complex includes two histone deacetylases,
Mos2 and Hetl, and is a mejotic-specific repressor of the sporulation
gene program."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grunstein M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rundlett S.E., Carmen A.A., Kobayashi R., Bavykin S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang A., Kurdistani S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=12434058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUNCTION, AND MUTAGENESIS OF 195-HIS-HIS-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DENTIFICATION IN A COMPLEX WITH SET3; HST1; SNT1; SIF2; CPR1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15:2991-3004(2001).
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions at long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensessib-sib.ch/). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CO; GO:000118; C:histone deacetylase complex; IFI.

GO; GO:001136; F:NAD-dependent histone deacetylase activity; IDA.

GO; GO:0045129; F:NAD-independent histone deacetylase activity; IDA.

GO; GO:0016575; P:histone deacetylation; IDA.

GO; GO:0016575; P:histone deacetylation; IDA.

GO; GO:0015335; P:negative regulation of meiosis; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 272716; CAA96906.1; -.
EMBL; X91837; CAA62950.1; -.
    SEQUENCE
                                                      CONFLICT
                                                                                  Transcription regulation; Activator:
DOMAIN 26 340 HISTONI
ACT SITE 197 BY SUN-
MUTAGEN 196 197 HH->AA.
                                                                                                                                                                                                Hydrolase; Nuclear protein; Chromatin regulator;
                                                                                                                                                                                                                                Pfam; P700850; Hist deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                       InterPro; IPR000286; His_deacetylse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       $64211, $64211.
$0003162; HOS2.
    452 AA;
    51455 MW;
                           1; CAA62950)
                                                                                  HISTONE DEACETYLASE.
BY SIMILARITY.
HH->AA: LEADS TO HYPERACETYLATION
                                                           PFRDSFGPDYSLY -> HSGTHSGRIIHFI
024E8AEA0A445A08 CRC64;
                                                           REF
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RESULT 8 LYP1_YEAST ID LYP1_YEAST

STANDARD;

611 AA

F

163 NSPSGFCY 170 3 NSPKGFAY 10 6,

Matches Query Match Best Local

Local Similarity

62.1%; 75.0%;

DB 1;

Length 452; Indels

0 Gaps

0

Conservative

0; Mismatches Pred. No. 39;

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                                                                                                                                                                                                                                                                                PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
Transport; Amino-acid transport; Transmembrane.
TRANSMEM 116 136 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002293; AA/rel_pormease1.
InterPro; IPR004840; AAC_permease.
InterPro; IPR004861; Permease.
InterPro; IPR004762; Yeaet_AA_porm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X67315; CAP47729.1; -.
EMBL; X97494; CAP63230.1; -.
EMBL; X97494; CAP6325175.1; -.
FIR; S60914; S60914
SGD; S0005212; LYP1.
GO: CO: 00152174. Service British
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Suropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send on email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEG outstation the Suropean Bioinformatics; institute, there are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIMS-288c / FY1679;
MEDLINE-6531051; PubMed-8740475;
MEDLINE-6531051; PubMedline-653105; PubMedl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sychrova H., Chevallier M.R.;

"Cloning and sequencing of the Saccharomyces cerevisiae gene LYP1

coding for a lysine-specific permease.";
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00324; aa permeases;
TIGRFAMs; TIGR00913; 2A0310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0015174; F:basic amino acid transporter activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetacese; Saccharomyces.
NCBI_TaxID=4932;
                                                                               TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10654085;
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STRAIN=ATCC 28583 / FL100;
MEDLINE=93377414; PubMed=8368011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lysine-specific permease.
LYP1 OR YNL268W OR N0790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996
15-SEP-2003

    -!- SIMILARITY: Belongs to the amino acid permease family.

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(Rel. 34, Last sequence update)
(Rel. 42, Last annotation update)
POTENTIAL.
                                                                                                                                                                                                                                                           POTENTIAL.
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LPH_RAT ID LPH AC QOZ DT 01-

LPH_RAT STANDARD; Q02401; Q63712; Q63719; Q1-JUL-1993 (Rel. 26, Created)

PRT;

1928 AA

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RESULT
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                              This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMRI-Quittation - the European Bloinformatics Institute. There are no restrictions on its use by non-potic institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amounce/or send an enail to licenses@ib-sib.oh/s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEXOURNCE FROM M.A. Baladron V. Esteban P.F., Santos M.A., Bou G., (Barcia-Cantalajo J., Baladron V., Esteban P.F., Santos M.A., Bou G., Remenba M.A., Fervalta J.T., Ballesta J.P.G., Jimenet A., del Rey F., "The complete sequence of an 18,002 bp segment of Saccharomyces carevisiase chromosome XI. Contains the 1851, XMP-100 and PRP16 games, carevisiase chromosome XI. Contains the 1851, XMP-100 and PRP16 games,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-UNH-1994 (Ral. 29, Created)
01-UNH-1994 (Ral. 29, Late Sequence update)
16-CUT-2010 (Ral. 40, Last amotation update)
18-CUT-2010 (Ral. 40, Last amotation update)
1800950 ON YEA409.

    -i- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
    -i- SIMILARITY: TO YEAST YMR313C AND S.POMBE SPCC1450.16C.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and six new open reading frames."; Yeast 10:231-245(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Saccharomyceto; Engl; Ascomycota; Saccharomycetina; Saccharomycetas;
Saccharomycetales, Saccharomycetaceae; Saccharomyces.
KCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YK69_YEAST
P36165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                         SEQUENCE
                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                             Pfam; PF01734; Patatin; 1
                                                                                                                                                                                                                                               InterPro, IPR002641; Patatin.
                                                                                                                                                                                                                                                           ; Z27116; CAA81640.1; -.; Z28314; CAA82168.1; -. S38167; S38167. S0001797; YKR089C.
                                         710 YGRSPSGF 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 GNAPKQFGY 438
                                                                   н
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                                                                                               4
                                                                                                               Similarity
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                                                                   YGNSPKGF 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     611 AA;
                                                                                               Conservative
                                                                                                                                                                                   protein; Transmembrane.
282 302 POTENTI
310 326 POTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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93
561
                                                                                                           62.1%;
                                                                                                                                                       102716 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.1%; Score 36; DB 1; Length 611; 66.7%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW; 4E7AF6F7P5F1461B CRC64;
                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                             Score 36; DB
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 % +
                                                                                                                                                       POTENTIAL.
1: 1CFC03C4A6E64B9C CRC64;
                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                   POTENTIAL
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MI)
MI)
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                                                                                                                         1; Length 910;
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                                                                                                                                                                                                                      PROPER
                                                                                                                                                                                                                             Procom, PD000659, dlyco hydro 1; 4.

PROSITE, P800757, GKYOÖKL PKYBROL, Fl 1; 1.

PROSITE, P800653, GKYOOKL_FYDBOL, Fl 2; 2.

PYGHOLASE, GOlycosidase, Symogan, Signal, Transmembrane, Ropeat.

SIGNAL 1 13 E SIMIMATIT.
                                                                                                                                                                                                                                                                                                       InterPro; IPR001360; Glyco_hydro_1.
Pfam; PF00232; Glyco_hydro_1; 5.
PRINTS; PR00131; GLHYDRLASE1.
                                                                                                                                                                                                                                                                                                                                                EMBL; X56748; CAA40070.1; -.
EMBL; X56747; CAA40069.1; -.
EMBL; L04635; AAA41539.1; -.
EMBL; JS0610; JS0610.
HSSP; P26205; 1CBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley;
MEDLINE=93091244; PubMed=1339333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Wistar; TISSUB-Intestine;
MEDLINE-91365258; PubMed=1909681;
Duluc I., Boukamel R., Mantei N., Semenza
"Sequence of the precursor of intestinal
"Sequence of the precursor of intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The rat LPH gene 5' region: comparative structure with the human gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 103:275-276(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boukamel R., Freund J.-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-192 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0-MNY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last amcration update)
Lactase-phiorizin hydrolase precursor (Lactase-glycosylceramidase)
[Includes: Lactase (EC 3.2.1.108); Phlorizin hydrolase (EC 3.2.1.62)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: INTESTINE.
DOMAIN: THE SEQUENCE EXHIBITS 4 REGIONS (1-
HOMOLOGY: THEREFORE LEH MIGHT HAVE EVOLVED
PARTIAL GENE DUPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-acylsphingosine.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fetal rat."
                                                                                                                   1884
1903
89
365
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1928
1883
1902
1902
1928
1842
175
1849
1366
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1274
1539
PROTON DONOR (POTENYIAL),
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (POTENTIAL).
NUCLEOPHILE (BY SIMILARITY).
A -> R (IN REF. 1; AAA41539).
Q -> E (IN REF. 1; AAA41539).
                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                    BETA-GLUCOSIDASE.
LACTASE-PHLORIZIN HYDROLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                              APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 REGIONS (1-IV) OF
HAVE EVOLVED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Semenza G., Raul F., Freund J.-N.;
estinal lactase-phlorizin hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                            noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and the EMBL outstation
re no restrictions on it
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TODE_PSEPU
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   Query Match
Best Local S
Matches 6
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SMISS-PROT entry is copyright. It is produced through a collaboration and the MBML outstart between the Swiss Institute of Bioinformatics and the MBML outstart the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                SEQUENCE
                                                                                                                 METAL
                                                                                                                                                                                            ProDom; PD000977; Xd1ol dioxygnse; 1,
PROSITE, PS00082; EXTRADIOL_DIOXYGENAS;
Oxidoreductase; Dioxygenase; Aromatic hy
                                                                                                                                                                                                                                                                   EMBL, J04996; AAA26010.1; -.
FIR; F36516; F36516.
HSSP; P17297; IDBY.
InterPro; IFR004360; Gdy bleo diox.
InterPro; IFR00486; Xdiol_dioxygnse.
F26m; F800903; Glyoxalase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TODE PSEPU
P13453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-methylcatechol 2,3-dioxygenase (EC 1.13.11.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PACHWAY: Tolucne degradation; third step.
SUBUNIT: HOMOCLEAMER:
SIMILARITY: BELONGS TO THE EXTRADIOL RING-CLEAVAGE DIOXYGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2,4-heptadienoate.
COFACTOR: FERROUS ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1375
       Similarity
6; Conser
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209
259
       Conservative
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                                                                                            AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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259
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                        60.3%;
                                                                                            32078 MW;
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60.0%;
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Score 35; DB
Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥ 10
                                                                                                              IRON (BY SIMILARITY)
IRON (BY SIMILARITY)
IRON (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB
Pred. No. 1.6e
1; Mismatches
                                                                                            4752380FA5C249A9 CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        It is produced through a collaboration
                 . 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290
                                                                                                                                                                                                       nydrocarbons catabolism; Iron
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                                          Length 290
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Indels
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                 C1C3 CAVPO STANDARD; PRT; 332 AA.
090276;
16-0CT-2001 [Rel. 40, Created]
16-0CT-2001 [Rel. 40, Last sequence update)
15-5EP-2003 [Rel. 42, Last samotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ul. 1882-1996 (Bal. 23, Greated)
01-882-1996 (Bal. 33, Last saquence update)
15-JUL-1999 (Rel. 38, Last antocation update)
Elphenyl-2,3-doil,2-dioxygenase I (EC 1.13.11.39)
oxygenase I) (2,3-dihydroxybiphenyl dioxygenase I)
ERICA
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                           T-cell surface glycoprotein CD1c3 precursor (CD1-c3 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004360; Gly_bleo_diox.
InterPro; IPR000486; Xdiol_dioxygnse.
Pfam; PF00903; Glyoxalase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X75633; CAA53297.1; -. PIR; B53419; B53419. HSSP; P47228; 1HAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Suropean Hobinformatics Institute. There are no restrictions on its 
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or send an email to licensee@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assurias J.A., Eltis L.D., Prucha M., Timmis K.N.; "Ansurias J.A., chive cyclophenyl 1,2-dioxygenases found Rhodococcus globerulus P6. Identification of a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHOGO
BHC1_RHOGO
                                                         CDIC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Dioxygenase;
METAL 146 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000977; Xdiol_dioxygnse; 1.
PROSITE; PS00082; EXTRADIOL_DIOXYGENAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P47231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           extradiol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94171820; PubMed=8126007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=33008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterineae; Nocardiaceae; Rhodococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodococcus globerulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAMILY.
                                                                                                                                                                                                                                                                                                                                                                  250 YGATPSGFA 258
                                                                                                                                                                                                                                                                                                                                                                                                                  1 YGNSPKGFA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dioxygenases."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32081 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB
Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRON (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aromatic
IRON (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104F189FE1EDDA6A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hydrocarbons catabolism; Iron.
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DS 1; Length 291;
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Pasteurella multocida. RNFD OR PM0384.

SEQUENCE FROM N.A.

NCBI_TaxID=747;

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellaceae; Pasteurella.

Pasteurellales;

OGONRY.

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last amnotation update)

Electron transport complex protein rmfb.

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PASMU

RNFD_PASMU

STANDARD;

PRT;

349 AA

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Query Match
Best Local Similarity
Matches
                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Sudsa Institute of Bloinformatica and the EMBL outstation - the Buxpean Bioinformatica Institute. There are no restrictions on its use by non-pposit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-stb.ch/announce/or send an email to license@ib-stb.ch/s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRÄINHARTLEY, and NIH 2, TISSURATHYMNE;
MEDLINE-20021685, pubMed-1553074,
Bascher C.C., Hiromatsu K., Naylor J.W., Brauer P.P., Brown K.A.,
Stocky J.R., Behart S.W., Kawasaki E.S., Porcelli S.A., Brenner W.B.,
                                                       SEQUENCE
                                                                                  CARBOHYD
                                                                                                  CARBOHYD
                                                                                                                              DISULFID
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF145489; AAF12744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia
                                                                                                                                                                                                                                          Multigene
                                                                                                                                                                                                                                                        Glycoprotein; Signal; Transmembrane; Immunoglobulin domain
                                                                                                                                                                                                                                                                   SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                               interPro,
                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                             HSSP; P11609; 1CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Conservation of a CD1 multigene family in the guinea pig.";
J. Immunol. 163:5478-5488(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: NOT KNOWN.
                                                                                                                                                                                                                                                                                                               IPR007110; Ig-like.
IPR003597; Ig_c1.
IPR003006; Ig_MHC.
                                                                                                                                                                                                                                            family.
Conservative
                                                       Š
         60.3%;
66.7%;
                                                       37437 MW;
,
                                                                     Pred, No. 44;
                                                                                                                            BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                          T-CELL SURFACE GLYCOPROTEIN CD1C3.
                                                       19DA52E30CC05DFC CRC64;
Mismatches

    Indels

                         Length 332;
                                                                                (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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Gaps
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                      Parkhill J. Dougan G. James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentleys B.D., Holden M.T.G., Sabshika M.J. Baker S., Basham D., Brooke K., Chillingworth T., Connerton D., Cronin A., Davis P., Davise R.M., Dowd L., Milte N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holtoyd S., Jagels K., Krögl A., Laren T.S., Leathor S., Moule S., O'Goxa P., Parry C., Otali M., Butherford K., Simonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat Lipoprotein nupl precursor.
NLEP OR STY3050 OR T2826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLPD SALTI
Q56131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SALTI
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InterPro; IPR004338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SHISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute, There are no restrictions is in no way modified and this statement is not removed. Usage by, and for commercial modified and this statement is not removed. Usage by, and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella typni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE006074; AAK02468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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'Complete genome sequence of Passeurclian multoxida Ph70','
Proc. Natl. Acad. St., U.S.A., 98:3460-3465(2001).
PROC. Natl., Acad. St., U.S.A., 98:3460-3465(2001).
CHAMPION M.W. ybe part of a membrane complex involved in electron cranagort [By similarity].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                         MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=601
                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
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    -!- SIMILARITY: BELONGS TO THE NORB/RNFD FAMILY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Composed of at least six subunits; rnfA, rnfD, rnfE and rnfG (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 YGNYPDGVAF 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pro; IPR004338; NQR2 RnfD RnfE, PF03116; NQR2 RnfD RnfE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YGNSPKGFAY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o transport;

M 42

M 69

M 125

M 125

M 214

269

269

27
genome sequence of a multiple drug resistant Salmonella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 35, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38470 MW;
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 AA
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                                                                                                                                                                                                  , J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-7/2 / AFCC 700931,

MEDILINE-9911815; PubMed-991662;

MEDILINE-9911815; PubMed-991662;

MEDILINE STAILS V., MOZEL F.;

Gobbe-Saule V., MOZEL F.;

FERS McCObiol, Lett. 107:141-143[199].

1- PUNCTION: MAY BE INVOLUTED IN STOTIONARY-PHASE SURVIVAL.
                                                                                                                                                                                                                                                                      Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The live oral typhoid vaccine Ty21a is a rpoS mutant and susceptible to various environmental stresses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plumkett G. III
Burland V., Kodoyianni V., Schwartz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
[2]
                                                                                                                SEQUENCE
                                                                                                                                              REPEAT
                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                     InterPro; IPR002886; Peptidase_M37.
                                                                                                                                                                                                                                                                                                                                MEROPS; M37.UPW; -.
InterPro; IPR002482; LysM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - I- SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS LPPB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEMS Microbio1. Lett. 126:171-176(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robbe-Saule V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Ty21a;
MEDLINE=95220644; PubMed=7705608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 255-373 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE OF 269-373 FROM N.A.
                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 185:2330-2337(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Attached to the inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anchor (Potential
103 YGNIPKG 109
                                                                                                                                                                                                                                                                                                                                                               X81641; CAA57297.1; -
Y17610; CAA76806.1; -
                                                                                                                                                                                                                                                                                                                                                                                             AL627276; CAD06031.1; -. AB016843; AA070383.1; -.
                            1 YGNSPKG 7
                                                        6,
                                                                      Similarity
                                                                                                                                                                                                                                                               PS00013;
                                                        Conservative
                                                                                                                Ŋ,
                                                                                                                                                                                                                                              Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coynault C.,
                                                                                                                                                                                                                     39183 MW;
                                                                   60.3%;
                                                        0
                                                                   Score 35; DB
Pred. No. 49;
                                                                                                                                                                                      LIPOPROTEIN NLPD.
N-ACYL DIGLYCERIDE (BY SIMILARITY)
4 X 7 AA APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norel F.;
                                                                                                                DD075BB440098FF7 CRC64;
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                III, Mayhew G.F., Rose D.J., rtz D.C., Blattner F.R.,
                                                                                      멂
                                                                                    Length 373;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by a
                                                        0;
                                                     Gaps
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Search completed: November 7, Job time : 2.72096 secs

2003, 07:28:04

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18, Search time 3.2973 Seconds (without alignments) 782.516 Willion cell updates/sec

Title: Perfect score: US-09-661-992B-5 58

Scoring table: Sequence: Gapop 10.0 , Gapext 0.5 BLOSUM62 1 YGNSPKGFAY 10

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	φ	œ	7	6	IJ	44	w	N	۳	No.
39	39	39	39	39	39	39	40	40	41	4	41	42	42	43	44	Score
67.2	67.2	67.2	67.2	67.2	67.2	67.2	69.0	69.0	70.7	70.7	70.7	72.4	72.4	74.1	75.9	Query
568	566	561	559	559	491	401	1312	291	2515	453	389	833	160	294	120	Length DB
13	4	11	13	13	4	16	16	ຫ	ഗ	16	00	ω	w	16	11	B
Q91572	Q9BZB8	P70166	Q9DED5	Q9YGX5	Q9BZB7	Q9KRK6	Q98NH6	6HIA60	Q9W2J8	P74064	Q98RZ7	013620	COLLAI	Q8XN61	Q920E8	IB B
Q91572 xenopus lae	Q9bzb8 homo sapien	P70166 mus musculu	Q9ded5 carassius a	Q9ygx5 brachydanio	Q9bzb7 homo sapien	Q9krk6 vibrio chol		Q9vth9 drosophila	Q9w2j8 drosophila	P74064 synechocyst	Q98rz7 guillardia	Ol3620 schizosacch	Q9utul schizosacch	Q8xn61 clostridium	Q920e8 mus musculu	Description

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366	, ω	36	36	36	36	37	37	37	37	37	37	37	37	37	37	37	37	37	37	38	38	38	38	38	38	3.8	39	
62.1	62.1	62.1	62.1	62.1	62.1	63.8	63.8	63.8	63.8	63.8		63.8		63.8			63.8	63.8	63.8	65.5	65.5	65.5	65.5	65.5	65.5	65.5		
183	183	181	173	117	69	746	712	422	390	390	346	331	306	306	302	292	258	255	205	588	583	488	488	488	402	402	600	
11	4.	10	4	6	11	16	16	16	16	N	10	10	6	4	11	11	v	ω	ψ1	ω	<u>1</u> 6	16	16	10	16	16	13	
070307	060572	Q9FX45	Q96G09	Q915X3	Q8CF51	Q8KG23	Q97KK5	Q8U7B0	Q92TL6	Q59744	Q9LP39	Q9LP40	Q28165	043484	035935	080056	Q9W086	Q9P4V6	Q93233	Q9P982	Q925K5	Q8Z622	Q8Z7V6	Q9LNG1	95AN8Ö	Q99RS8	093386	
0970t9 mus musculu 070307 mus musculu	Omo	Q9fx45 arabidopsis	Q96g09 homo sapien		Q8cf51 mus musculu				Q92tl6 rhizobium m	Q59744 rhizobium l	Q91p39 arabidopsis	Q9lp40 arabidopsis	Q28165 bos taurus	homo	Bum	σ	Q9w086 drosophila		Q93233 caenorhabdi	-		Q8z622 salmonella				Q99rs8 staphylococ	093386 brachydanio	

ALIGNMENTS

음 성	3 M O	8778		228	43236	3888		I SE
101 YGNSPWGFAY 100	Onery Match Bast Local Similarity 90.04; Pred Mo. 1.4; Length 120; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps	PROSITE P850836; IG_LIKE; 1. NON_TER 120 120 NON_TER 120 120 SEQUENCE 120 AA; 13204 MW; DC4834ABIDE56F3C CRC64;	InterPro; PR9007110; 1g-1ike. InterPro; PR9003006 Ig JMC. InterPro; PR9003596; Ig_V. Pfam; PR90047; Ig; 1. SMART; SMO466; Idv; 1.	th remmentative LAS. ; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AP307936; AAL09420.1;	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Jennings I.G., Horaitis O., Cotton R.G.H.; SEXINITION of the inicope of Pterin-Manacking Antibodies Expressed Desiration of the foliocope of Pterin-Manacking Antibodies Expressed	rragment). Nus muscullus (Mouse). Rukaryota, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Butharia, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI TaxTha,1090;	092088; 01_BGC-2001 (TrEMBLrel. 19, Created) 01_BGC-2001 (TrEMBLrel. 19, Last sequence update) 01_MBC-2001 (TrEMBLrel. 29, Last sequence update) 01_MBC-2003 (TrEMBLrel. 23, Last smootation update) Pterin-mimicking anti-idiotope heavy chain variable region	RESULT 1 Q220E8 ID Q20E8 PRBLIMINAXY; PRT; 120 AA.

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99 AC 
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Query Match
Best Local Similarity
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Proc. Mail. Aond. Sci. U.S.A. 99:996-1001(2002).
BrBir. APO01366; BABB01831;
Intertror. IBB001173; Glyco-trans 2.
Pfam; PF00535; Glycos_transE_2; I.
PfamfErzase; Complete processe.
SEQUENCE 294 AAJ, 34358 Mrj. 390BF593B712CA35 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TREMBLEE). 20, Created)
01-MAR-2003 (TREMBLEE). 20, Last sequence update)
01-MAR-2003 (TREMBLEE). 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "darge-scale screening of intracellular protein localization in living fassion years cells by the use of a GFP-fusion genomic DNA library."; guess cells 15:15-190(200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical 18.1 kDa protein (Fragment). 2257512.
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Bacteria; Firmicutes; Clostridia, Clostridiales, Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSXN61;
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                                                                                                                                                                                                                                                            InterPro; IPRO00504; RNA_rec_mot.
Pfam; pF00076; rrm; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ding D.Q., Tomita Y., Yamamoro A., Chikashige Y., Haraguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=968 h90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizogaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimizu T., Oheani K., Hirakawa H., Ohebima K., Yamashita A.,
Shiha T., Ogasawara M., Hattori M., Xhhara S., Hayashi H.,
"Complere genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPE0477
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                                                                                                                    SEQÜENCE
                                                                                                                                                           Hypothetical protein.
NON_TER 1
NON_TER 160 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB028003; BAA87307.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20223868; PubMed=10759889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1502;
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                                                                                                             160
160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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                                                                                                             180
18116 MW; 168A1F1D5D5A94F5 CRC64;
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72.4%; Score 42; DB 3;
87.5%; Pred. No. 4.6;
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Pred. No.
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Mismatches
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                                      Length 160;
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Best Local
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                                                                                                                                                                                                                                                                                                  09827;
01-0CT-2001 (TrEMSLrel. 18, Last sequence update)
01-0CT-2001 (TrEMSLrel. 23, Last annotation update)
01-MAR-2003 (TrEMSLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ol-JMM-1998 (TERBILIZE). 05, Created)
Ol-JMM-1998 (TERBILIZE). 05, Last sequence update)
Ol-JMM-2003 (TERBILIZE). 22, Last amortation update)
Hypothetical 37.7 Mos protein (RNA binding protein,
recognition MOTIES).
1029 GR SPB217.00C.
Schilosaccharomyces pombe (Fission yeast).
Bukaryote; Pungli Ascomycet; Schilosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murpby L., Harris D., Wood V., Radandress M.A., Barrell
Submitted (NR-2001) to the BNBL/GemBank/DDBJ databases.
BNBL, ABO04535; BAAJ108-L; .
BNBL, ALS004535; BAAJ108-L; .
BNBL, ALS004535; BAAJ108-L; .
LITEAFPO; IPEN00564; RNM, Tec. mot.
PEam; PE00076; PTM; 5.
SMART; SMO0350; PRM; 5.
SEQUENCE FROM N.A.
MEDILINE=1123349; PubMed=11323671;
Douglas S., Zauner S., Frauhholz M.,
Douglas S., Zauner S., Frauhholz M.,
Mu K., Neith M., Cavalier-Smith T., Maier U.G.;
"The highly reduced genome of an enalayed algal
                                                                                                                                                                  NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kushida M., Yamazaki S., Yanaka T., Jinno K., Haikawa Y., Yamazaki, Yamamebo S., Sekino M., Ogotia A., Nagali Y., Sakia M., Aokim. S., Ogura K., Otsuka R., Kudoh Y., Yanagida M., Wachida M., Zhang M.Q., Sukutted (MX-1997) to the REEL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             013620
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                                                                                                                                                                                                                 Nucleomorph
                                                                                                                                                                                                                                          Guillardia theta (Cryptomonas phi).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q98RZ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00030; RRM RNP 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=972h-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=972 H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4896;
                                                                                                                                                                  Sukaryota, Cryptophyta; Cryptomonadaceae; Guillardia.
NCBI_TaxID=55529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 NNPKGFAY 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   833 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 3; Length 833;
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64FE767D43E02FE4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                       Penny S., Deng L.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barrell B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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nucleus.";

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RESULT 7
Q9W2JE
ID Q9W2
AC Q9W2
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 100-
DE TUD
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P74064
P74064;
P74064;
01-FEB-1997
01-FEB-1997
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECURNCE FROM N.A.

WELLINE-7061201; Publed-8905231;

WELLINE-7061201; Publed-8905231;

WEARNEY T., Sato S., Kotanii H., Türnaka A., Asamizu E., Nakamura Y.,

Miyajina H., Hitroawa M., Sugiura M., Sasanoto S., Kimura T.,

Myajina H., Hitroawa M., Sugiura M., Nakazaki N., Naruo K., Okumura S.,

Hosouchi T., Matsuno A., Maraki A., Nakazaki N., Naruo K., Okumura S.,

Muraki H., Watanaba H., Yasuda M.,
                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Haxapoda, Insecta; Pterygota;
Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                  TUD OR CG9450.
                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                            Q9W2J8,
                                                                                                                                                                                                                                                                                                                                                                             Q9W2J8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005225; Small_GTP.
TIGRFANG; TIGG00231; small_GTP; 10
Hypothetical protein; Complete proteome.
SEQUENCE 453 AA; 49154 MM; 4CFDPAED77536F59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prequency analysis of the genome of the unicelular cyanobonetethe
synequency as strain for Co6603. It sequence determination of the
mattire genome and assignment of potential protein-coding regions.",
DNA Res. 3:109-136(1396).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein sll0804
SLL0804.
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SMARY; SN00360; RRM; 3.
PROSITE; PS50102; RRM; 3.
PROSITE; PS00030; RRM; RNP 1; 1.
SEQUENCE 389 AA; 45171 MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF165818; AAK39803.1; -.
InterPro; IPR000504; RNA_rec_mot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1148;
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SEQUENCE FROM N.A.
                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMBL; D90911; BAA18140.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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(TrEMBLrel 02, Last seq
(TrEMBLrel 21, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.7%; Score 41; DB 16; Length 453; 100.0%; Pred. No. 23;
                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                        2515 AA.
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Q9VT19
ID Q9VT19
ID Q9VT19
AC Q9VT1
AC Q9VT1
AC Q9VT
AC Q9VT
CG11-0
DT 01--4
DT 01--0
DB CG11
GN CG1
GN CG

OSVTH9 PRELIMINARY;

OSVTH9;

OSVTH9;

O1-MAY-2000 (TREMBLE-01.13, C:
O1-MAY-2000 (TREMBLE-01.13, L:
O1-UN-2002 (TREMBLE-01.21, L:
CG1/26 protein.

Created)
Last sequence update)
Last annotation update)

291 AA

Drosophila melanogaster (Pruit fly).
Bakaryota / Metasua, Atthropoda; Haxapoda; Insecta; Pterygota;
Meoptera, Endopterygota; Juptera, Brachycera; Muscomorpha;
Sphydroides, Drosophilidae, Drosophila.
NCBI_TaxID-7217;

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w serwind solvester, pubbled 19731122;

Wadman M.D. Jochnikers S.E., Bolt R.A., Evens C.A., Goccayne J.D.,

R. Admant M.D. Jochnikers S.E., Bolt R.A., Evens C.A., Goccayne J.D.,

R. Admant M.D. Jochnikers S.E., Hichards S., Asbburster M., Hendersen S.M.,

R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

R. Strandon R.C., Rogers W.-H.C., Blazel R.G., Change M., Felffer B.D.,

R. Hardlon R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

R. Sandon R.C., Rogers W.-H.C., Blazel R.G., Change M., Felffer B.D.,

R. Mahril J.F., Spöbyani A., An H.-J., Andrews-Falmhoch C.R., Miklog G.L.G.,

R. Mahril J.F., Spöbyani A., An H.-J., Andrews-Falmhoch C.R., Miklog G.L.G.,

R. Mahril J.F., Spöbyani A., An H.-J., Andrews-Falmhoch C.R., Miklog G.L.G.,

R. Mahril J.F., Spöbyani A., An H.-J., Andrews-Falmhoch C.R., Miklog S.M.,

R. Baselon K.F., Benos P.V., Berna B.P., Bandath D., Bootlar P.,

R. Barty J. W., Benos P.V., Berna B.P., Bandari D., Bootlar P.,

R. Barty J. W., Benos P.V., Benos B.P., Bandari D.,

R. Barty J. W., Benos P.V., Benos B.P., Bandari D.,

R. Barty J. W., Benos P.V., Benos B.P., Benos P.V.,

R. Barty J. W., Benos P.V., Benos B.P., Benos P.V.,

R. Dander K., Doup L.E., Boones M., Gary N.S., Galbart W.M., Glasser K.,

R. Golder A., Gong F., Gorrell J.H., Gu Z., Gluan P., Harris M.,

R. Golder A., Gong F., Gorrell J.H., Hernandes J.R., Houck J.,

R. Harris M.L., Harvey D., Helman T.J., Hernandes J.R., Houck J.,

R. Harris M.L., Harvey D., Helman T.J., Hernandes J.R., Houck J.,

R. Harris M.L., Harvey D., Helman T.J., Hernandes J.R., Houck J.,

R. Harris M.L., Mauhr F., Garpin G.H., Kelled M.P., Hopherson D.L.,

R. Harris M.L., Mauhr F., Garpin G.H., Kelled M.P., Hopherson D.L.,

R. Harris M.L., Mohr H., Wohley M., Holled M.P., Hopherson D.L.,

R. Harris M.L., Moy M., Murphy J.B., Murphy J.M., Mohr H.P.,

R. Harris M.L., Moy M., Murphy J.B., Murphy J.M., Mohr H.
            Matches
                                          Best Local
                                                                                                                                                                                                                              InterPro; IPR001097; Maternal_tudor.
InterPro; IPR002999; Tudor.
Pfam; PP00567; TUDOR; 10.
SMART; SM00333; TUDOR; 9.
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0003891; tud.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BERKELEY;
                                                Similarity
                                                                                                                                                                                                PSS0304; TUDOR; 9
                                                                                                                                                            2515 AA;
            Conservative
                                                87.5%;
                                          70.7%; Score 41; DB 5;
87.5%; Pred. No. 1.5e+02
                                                                                                                                                            285264 MW; 1218700174D66701 CRC64;
      0; Mismatches
                                          5e+02;
                                                                              Length 2515;
      0
Gaps
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Kato T., Samura T.,

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Q98NH6
ID Q98N
AC Q98N
AC Q98N
DT 01-0
DT 01-0
DT 01-0
DT Ribo
GN MILO
OS Rhiz
OC Back
OC Bayl
OX NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MADDAM MODERNALDON, PLANMENTON, DVANE C.A., GOORYDE J.D.,
NA MADDA M.D., OSCINIKA S.E., HOLL R.A., BYANG C.A., GOORYDE J.D.,
RA MADDA M.D., OSCINIKA S.E., RICHAYGE S., ARLANDEY M., Hondries P.R.,
RA SHILLOR G.G., WOFTMENN J.E., RICHAYGE S., ARLANDEY M., HORSTEIN F.R.
RA SHILLOR G.G., WOFTMENN J.E., YANGEL M.D., Zhang C., Chen L.X.,
RA BERNADOR R.C., ROGREF Y.H.C., BLAZEJ R.G., Champe M., Feliffer B.D.,
RA HARN K.H., Doyle C., BRAKET E.G., Helle G., Walson C.R., MALOS G.L.G.,
RA HARN K.H., Doyle C., BRAKET E.G., Helle G., Walson C.R., MALOS G.L.G.,
RA HARN K.H., Doyle C., BRAKET E.G., Helle G., Walson C.R., MALOS G.L.G.,
RA HARN K.H., Doyle C., BRAKET E.G., Helle G., Walson C.R., MALOS G.L.G.,
RA HARN K.H., Doyle C., BRAKET E.G., Helle G., Walson C.R., MALOS G.L.G.,
RA HARN K.H., Doyle C., BRAKET E.G., Helle G., Walson C.R., MALOS G.L.G.,
RA HARN K.H., Doyle C., BRAKET E.G., Helle G., Walson C.R., MALOS G.L.G.,
RA HARN K.H., Doyle C., BRAKET E.G., Helle G., Walson C.R., MALOS G.L.G.,
RA HARN K.H., Doyle C., BRAKET E.G., Walson D., LOHN T., WOHLE G., BRAKET E.G.,
RA HARN K.H., Doyle C., BRAKET E.G., WALOS G.L., WALOS G.L.,
RA HARN K.H., DOYLE C., BRAKET E.G., WALOS G.L., WALOS G.L.,
RA HARN K.H., DOYLE C., BRAKET E.G., WALOS G.L.,
RA HARN K.H., DOYLE C., BRAKET E.G., WALOS G.L.,
RA HARN K.H., DOYLE C., BRAKET E.G., WALOS G.L., DANN P.,
RA HARN K.H., CAMPAY G., WALOS G.L., DANN P.,
RA HARN K.H., CAMPAY G., WALOS G.L., DANN P.,
RA HARN K.H., CAMPAY G., WALOS G.L., DANN P.,
RA HARN K.H., WALOS G.L., WALOS G.L., C., RETTER S., RALOS G.L.,
RA HARN K.H., WALOS G.L., WALOS G.L., GURRER S., PALOS G.L.,
RA HARN K.H., WALOS G.L., WALOS G.L., WALOS G.L., DANN P.,
RA HARN K.H., WALOS G.L., WALOS G.L., WALOS G.L., WALOS G.L.,
RA HARN K.H., WALOS G.L., WALOS G.L., WALOS G.L., WALOS G.L.,
RA HARN K.H., WALOS G.L., WALOS G.L., WALOS G.L., WALOS G.L.,
RA HARN K.H., WALOS G.L., WALOS G.L., WALOS G.L., WALOS G.L.,
RA HARN K.H., WALOS G.L., WALOS G.L., WALOS G.L., WALOS G.L.,
RA HARN K.H., WALOS G.L., WALOS G.L., WALOS G.L., WALOS G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                               Q98NH6;
01-OCT-2001 (TrEMBLrel. 18,
01-OCT-2001 (TrEMBLrel. 18,
01-OCT-2001 (TrEMBLrel. 18,
Ribonucleotide reductase.
Mijoj3.
Rhizobiun, protoi (Wesorhizobium loti).
Bacteria, protobacteria, hphappoteobacteria, Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                              Q98NH6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART, SM00360; RRM; 1.
PROSITE; PSS0102; RRM; 1.
PROSITE; PSS0030; RRM; RNP 1; 1.
SEQUENCE 291 AA; 32307 MW;
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STRAIN=BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                  119 GKRPKGFAY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNSPKGFAY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.0%; Score 40; DB
77.8%; Fred. No. 21;
tive 0; Mismatches
                                                                                                                                                                                                                        Created)
                                                                                                                                                               Last annotation update)
                                                                                                                                                                                         Last sequence update)
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                                                                                                                                                                                                                                                                              1312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o,
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Q9KRK6
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                                                                                                          Matches
                                                                                                                                Query Match
Best Local
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MEDLINE=21082930; PubMed=11214968;
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SEQUENCE FROM N.A.
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SCORRES REAL REPRESENTATION OF THE PROPERTY OF

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Query Match 69.0%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAILMENT TO TM.656! / Serotype OI;
MEDLINE-2006833 PubMed-10552011;
Heidelberg J.F. Eisen J.A., Nelson M.C., Clayton R.A., Gwinn M.L.,
Dodaon R.J., Heit D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Dodaon R.J., Nelson X. P., Read T.D., "Peteslin H., Richardson D.,
Ermolaeva M.D., Wamathevan J., Base S., Qin H., Paradion D.,
McDonald L., Utterbeck T., Peischmann R.D., Niemann W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mehlangs J.J., Venner J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005828; Sub_transporter.
Pfam; Pr00083; sugar_tr; 1.
Pfam; Pr00083; eugar_tr; 1.
TIGREAMS; TIGR00710; efflux_Bcr_CflA; 1.
PR0SITE; PS50850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB004241; AAF94785.1; -. TIGR; VC1634; -.
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01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP002994; BAB47785.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunako T., Makamura K., Sato S., Asamiru E., Kato T., Sasamoto S., Katnabo A., Ideaswa K., Ishikawa A., Kawashina K., Kimura T. S., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Mcchinaki Y., Makayama S., Makazaki N., Shimpo S., Sujimoto M., Takauchi C., Yamada M., Tabata S., Takauchi C., Yamada M., Takauchi C., Takauchi C., Yamada M., Takauchi C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004812; Efflux_Bcr_CflA.
InterPro; IPR007114; MFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 406:477-483 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multidrug resistance protein.
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Pfam; PF02867; ribonuc_red_1gC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO1183; RIBORDTASEM).
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                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                           proteome
YGNSPKGFAY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1312 AA; 143398 MW; 409464CB9F709F38 CRC64;
                                                                                                                                                                                                                                                                                                  401 AA;
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                  42914 MW;
                                                                                                                                         67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation update)
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                                                                                                                                         Score 39; DB 16; Length 401;
Pred. No. 47;
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                                                                                                                                                                                                                                                                                                  814CD7A2A86E3BDB CRC64;
                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 AA
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                                                                                        Gaps
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RESULT 12

OPYGOXS
ID OPYGOX
AC QUARTER
DT 01-W
DT 01-W
DT 01-W
DT 01-W
DT 02-W
DT 02-
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Q9BZB7
ID Q9BZB
AC QFED

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                                                                                                                      Query Match
Best Local :
Matches
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Best Local S
Matches 6
                                                                                                                                                                                                                                                  EMBL; ABO11680; BAA75637.1; --
ZEYIN; ZDB-GBME-999527-1; ZOTDB-
InterPro; IPRO00504; RNA_rec_mot
SWART; SM00360; RRN; 1.
PROSTTE; PRS0102; RRN; 1.
SEQUENCE 559 AA; 62255 MM; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9BZB7;
01-JUN-2001
01-JUN-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suzuki H., Maegawa S., Murakawa M., Hoshijima K.,
Yasuda K., Inoue K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata
Actinopterygli; Neopterygli;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999
01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Healt J.F., Charlescorth A., Smith G.D., MacNicol A.M.;
'Identification and characterization of the gene encoding human
cytoplasmic polyadenylation element binding protein.";
Gene 263:113-121(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Covary, and Brain;
MEDLINE=21125222; PubMed=11223249;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZORBA OR ZOR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003
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InterPro; IPR000504; RNA rec_mot.
PROSITE; PS50102; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of zebrafish maternal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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348
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                                                             N
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                                                                                                                      Similarity
6; Conserv
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6; Conserv
GNMPKGYVY 356
                                                        GNSPKGFAY 10
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                                                                                                                           Conservative
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(TrEMBLrel. 17,
(TrEMBLrel. 23,
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                                                                                                                 Score 39; DB
Pred. No. 68;
1; Mismatches
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element-binding protein
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
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Pred. No.
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                                                                                                                                                                                                                                                       36CF42E1AC70A377 CRC64;
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59;
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01-MAR-2001
01-MAR-2001
01-MAR-2003
                                                                                                                                                                                                         SEQUENCE
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Gebause F. Richter J.D.;

"Mouse cytoplasmic polydenylation element binding protein: An 
"Mouse cytoplasmic polydenylation element of con-
evolutionarily conserved protein that interacts with the cytopl-
polydenylation elements of c-mos mRNA.";

Proc. Natl. Acad. Sci. U.S.A. 93:14602-14607(1996).

BMBL, V00260; CAA65988.1;

BMBL, V00260; CAA65988.1;

BMBL, ROSSO(SSI, RNA, rec_mot.

BMBL, RNA, RNA, rec_mot.

BMBLT, RNOSSO() RNH. 1.

BMBLTT, RNOSSO() RNH. 1.

BMBLTT, RNOSSO() RNH. 1.
                                                                                                                                                                                                                                                                                                                                      TISSUE=Ovary;
MEDLINE=97121433; PubMed=8962099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel. 02) Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MRR-2003 (TREMBLrel.) 23, Last subcation update)
01-MRR-2003 (TREMBLRel. 23, Last smootation update)
CYCoplasmic polyadenylation element-binding protein
CPEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CPBB):Its intracection with CRE of cyclin B mRNA and phr by cdk and 822 protein kinases.", cyclin B mRNA and phr sbantted (JMR-2000) to the BMSU/GenBank/DDBJ databases. BMSU, AB04534; BAN19051.1; -
InterPro, 1PR00504; RNA_TSC_mot. SWART; SM00360; RNA_TS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FKKOM R.A. (Gawa K., Nagahama Y.;
Kateu Y., Yamashita M., Ogawa K., Nagahama Y.;
"Goldfish cytoplasmic polyadenylation element binding protein
"Goldfish cytoplasmic polyadenylation element binding protein B mRNA and phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukarycta, Metazosi Chordato, Craniato, Vertebrata, Butelcostomi,
Actinopterygii, Meopterygii; Teleostesi, Ostariophysi, Cypriniformes,
Cyprinidae; Carassius.
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559 AA; 62122 MW;
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(TrEMBLrel. 16,
(TrEMBLrel. 23,
                                                                                              61917 MW;
                         67.2%;
66.7%;
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                             Pred.
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Pred. No.
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   Mismatches
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Best Local Similarity 66.7
Matches 6; Conservative
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TISSUE-CVEY, and Exim,
TISSUE-CVEY, and Exim,
WEDLINE-20155227, PubMed-11223249,
Welk U.F. Charlesworth A., Smith G.D., MacNicol A.M.;
"Identification and characterization of the gene encoding human
cyroplasmic polyodemylation element binding protein.";
Gene 26:113-121(2001)
EMBLI, MR324942, J.F.
EMBLI, MR324942, JAK01239-1, F.
EMBLI, MR326942, JAK01239-1, F.
EROSTE, PSS01021, RKN; 28-2185BOECS9DA87 CRC64;
SEQUENCE 566 AA; 62594 WM; 98-4185BOECS9DA87 CRC64;
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08228.

09228.

01-JIN-2001 (TrEMBLEE1. 17, Lorested)

01-WAY-2001 (TrEMBLEE1. 17, Lorested)

01-WAY-2003 (TrEMBLEE1. 21, Lorested)

01-WAY-2003 (TrEMBLEE1. 21, Lorested)

01-WAY-2003 (TrEMBLEE1. 23, Lorested)

01-WAY-
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Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Bureleostomi;
Mammalia; Butheria; Primates; Catarrbini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
355 GNMPKGYVY 363
                                                                                                                                                      2 GNSPKGFAY 10
                                                                                                                                                                                                                                                                                                                                                                            67.2%; Score 39; DB 4; Length 566; 66.7%; Pred. No. 69;
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Search completed: November 7, 2003, 07:34:27 Job time: 6.39773 secs

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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ABP08836
AAY43866
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Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Frotein encoded by
Drosophila melanog
Drosophila melanog
Dunan ORFX protein
Heavy Chain (WI) g
Human breast speci
                                                                                                       Description
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	60	60.3	66.	60.3	60.3	60.3	60.3	60.3	60.3	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1 1	62.1	63.8		63.8
22	21	21	22	21	21	22	21	21	22	22	22	21	23	22	22	24	22	22	22	21	21	22	22	21	22	22	23	21	23	19	22
AB010811 ABB68852 ABP62216	AAG32223 AAG18544	AAG18545	AAG19069	AAG35352	AAG35353	AAG10160	AAG32222	AAG49954	AAG10161	ABB63009	ABB67398	AAW90940	ABP40557	AAB65770	AAM39480	ABU11773	AAM41266	AAB93180	ABG15228	AAY70220	AAY84429	ABG00682	AAB92806	AAY70228	ABG15227	ABG00681	ABP03818	AAG02102	ABG95556	AAW59884	ABB68781
	sis thal	Zea mays protein f	protein	Zea mays protein f				Arabidopsis thalia	n		mela	Pyrococcus sp. str	Staphylococcus epi		Human polypeptide		_		Novel human diagno	Human RNA-associat			Human protein sequ	RNA-as	_	human	Human ORFX protein	secre	novel		Drosophila melanog

ALIGNMENTS

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AAB20388 standard; Peptide; 10 AA.

AAB20388;

21-JUN-2001 (first entry)

Anti-FIX/FIXa antibody 193/AD3 CDR3.

Ractor IX; FIX; Factor IXa; FIXa; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia h; haemorrhayic dathresis; haemostatic, amidolytic; therapy; mouse; complementarity determining region; CDR.

Mus musculus.

WO200119992-A2

22-MAR-2001.

13-SEP-2000; 2000WO-EP08936

14-SEP-1999; 99AT-0001576

(BAXT) BAXTER AG.

Scheiflinger F,

Kerschbaumer R, Falkner F,

Dorner F;

WPI; 2001-290358/30

New factor IX/factor IXa antibodies and their derivatives useful for

Claim 7; Page 74; 138pp; English.

increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis

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RESULT 2
AAB20444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
WPI; 2001-290358/30
                                                                                   14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                             Paetor IX, FIX, Factor IXa, FIXa, antibody, procagulant;
Paetor VIII ofactor, blood coagulation disorder, haemophilia A,
haemorrhagic diathesis, haemostatic, amidolytic, therapy, mouse;
complementarity determining region; CDR.
                                                                                                              13-SEP-2000; 2000WO-EP08936.
                                                                                                                                            22-MAR-2001
                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB20444 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                         Scheiflinger F,
                                                       (BAXT ) BAXTER
                                                                                                                                                                        WO200119992-A2
                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-FIX/FIXa antibody CDR3.
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                                                                                   99AT-0001576
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                         Kerschbaumer R,
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                                                                                                                                                                                                                                                           note=
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                                                                                                                                                                                                                                                                                         amino acid"
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Pred. No. 0.0012;
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                         Falkner F,
                         Dorner
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Claim 7; Page 74; 138pp; English.
                                                                                                                                                                        New factor IX/factor IXa antibodies and their derivatives useful for increasing aniodytric activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic disthesis
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activating activity. Administration of the antibodies of their derivatives leads to an increase in the proceedinal activity of FIXA, even in the presence of FVIIIa inhibitors. This allows for rapid blood cogulation even in the absence of EVIII or FVIIIa, and the case of FVIII inhibitor patients. The antibodies or their derivatives are used in a claimed pharmaceutical composition for treasting patients with blood cosgulation disorders, especially hemosphilia A and hemonrhagic databases. The present sequence is that of complementarity determining region 3 (DM3) of an antibody having anti-Factor IX [FIX) or anti-activated Factor IX [FIXA) activity. Such antibodies and their derivatives (including those that comprise the present CDB3 peptide) have Factor VIIIa [FIII.a) cofactor activity or FIXA

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The present sequence is that of complementarity determining region (2) (CDE3) of the heavy chain of an antibody expressed by mouse by pridoma 193/ADS. This anxibody has anti-Patrior IX (FIX) or anti-activated Factor IX (FIXA) activity. It is an example of anti-ACTIVATEA antibodies of the invention. Such antibodies and their derivatives (including those that comprise the present CDE3 activating lateral to the present CDE3 activating lateral to the comprise the present CDE3 activating lateral to the present of the complete comprise the present CDE3 activating lateral to the present of the complete com

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Matches
                                           Query Match
Best Local :
                                   10;
             1 YGNSPKGFAY 10
                                             Similarity
YGNSPKGFAY 13
                                   Conservative
                                           100.0%;
                                   0
                                          Score 58; DB 22;
Pred. No. 0.002;
                                   Mismatches
                                   Indels
                                                    Length 16
                                   ٥,
                                   Gaps
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Sequence

16 AA;

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Anti-FIX/FIXa antibody 193/AD3 scFv
                                       21-JUN-2001
                                                                                                                 AAB20433 standard; Protein; 242 AA.
                                                                               AAB20433;
                                       (first entry
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Factor IX, FIX, Factor IXa; FIXa; scFv; antibody; procagulant, Factor VIII cocfactor; blood cosgulation disorder; haemophilia h, haemorrhagic diatheeis; haemostatio; amidolytic; therapy; mouse.

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ARESULT 3
ARESTULT 3
ARESTULT 2
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                                                                                                                                    (BAXT ) BAXTER AG.
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/label= VL
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'label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= CDR3
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WPI; 2001-290358/30

Scheiflinger F,

Kerschbaumer R,

Falkner F,

Dorner F;

AAF30723

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ARBGG140

ARBGG140

ARBGG140

ARBGG140

ARGG140

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Best Local :
                                                        Screening a mutant library for mutants unable to grow under specific conditions and for identifying loci involved in pathogenicity,
                               comprises using signature tagged transposon mutagenesis
                                                                                                                                                                                                   N-PSDB; AAF31627.
                                                                                                                                                                                                                                                                                                              Gicquel B,
                                                                                                                                                                                                                                                                                                                                                                                               (INSP ) INST PASTEUR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis; attenuated microorganism; fad26; Rv2930; signature tagged transposon mutant; mutant library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Mycobacterium tuberculosis fad26 (Rv2930) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-2001
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increasing amidolytic activity of factor IXa, and for treating blood
coagulation disorders such as haemophilia A and haemornhagic diathesis
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                                                                                                                                                                                                                                                                                                              Guilhot C,
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99US-0142833
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                                                                                                                                                                                                                                                                                                              Camacho L;
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identifying and isolating metants of attinomorphics and for identifying compounds that have antibiotic activity. The method is used to identify metants of microogranisms, prefeably. The method is used to identify metants of microogranisms, professely an evitinomorphic such as M. tuberculosis, M. buylar, M. avitinomorphic conditions. M. paratheberculosis, M. buylar, M. avitinomorphic specific conditions. It is especially useful for identifying joe under specific conditions. It is especially useful for identifying joe understoodled by a generally. It can screen inhorate such as screen multiple libraries concurrently. It can screen inhorate such as predafting the produced by a gene which is disrupted by the insertion of the 18 1096 transposon to produce an attenuated mutant of Mycobacterium whenever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is given in a specification relating to a method for screening a library with insertions in genes and/or regulatory sections of the organisms of interest, where the insertion contains a cog and/or transposen associated with a teg. The mutants are identified by a hybridisation of the tags to known sequences. The method is useful for treating an individual suffering from a mycobacterial infection, suspected of being infected with a Mycobacterial, which which been exposed to an infectious Mycobacterium. It is a also useful for identifiant of the infectious Mycobacterium. It is a also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8; Fig 5A; 159pp; English.
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##88888888888888888888888888888

7; Conserv YGSDPKGFA 81 YGNSPKGFA 9 Conservative 72.4%; . 88 ; Score 42; Pred. No. Mismatches 60; 22; ۲, Length 626; Indels °, Gaps 0;

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73

Matches Query Match Best Local

Sequence

626 AA;

RESULT 5 ABB64427 ID ABB6 26-MAR-2002 ABB64427; ABB64427 standard; Protein; 2515 AA (first entry)

Drosophila melanogaster polypeptide SEQ ID NO 20073

Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster. pharmaceutical.

27-SEP-2001. W0200171042-A2

23-MAR-2001; 2001WO-US09231

23-MAR-2000; 2000US-191637P 11-JUL-2000; 2000US-0614150

(PEKE) PE CORP NY.

Venter JC, Adams M, Ľ. PWD, Myers EW

N-PSDB; ABL08530. 2001-656860/75

New isolated nucleic acid genes from Drosophila and detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell

Disclosure; SEQ ID NO 20073; 21pp + Sequence Listing; English

The invention relates to an isolated nucleic acid detection reagent

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Matches
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                                                                                                                           capable of detecting 1000 or more genee from Drosophila. The inventue that in developmental biology and in elucidating cell signaling cell-cell interactions in higher enkaryotes for the development of insecticides, therapeatics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLAST-G-BAIDST), expressed DNA sequences (ABLAST-G-BAIDST), expressed DNA (ABBAST-33-ABD72073).
                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 16890; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
Sequence
                                              at ftp.wipo.int/pub/published_pct_sequences
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABB57737-ABB72072)
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Pred. No. 3.9e+02
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RESULT 7
ABP08836
ID ABP
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Best Local S
Matches 7
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                                              ABP08836;
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Human ORFX protein sequence SEQ ID NO:17654.
                                                                                                                        119 GKRPKGFAY 127
                                                                                                                                                                   l Similarity
7; Conserve
                                                                                                                                             2 GNSPKGFAY 10
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Human; open reading frame, ORFK; gene therapy; cancer; cirrhosis; hyperproliferative disorder; peoriasis; benign unmour; hamorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hyportemation; hyportyroddism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; immune deficiency; immune defi myasthenia gravis. autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;

8 S

Homo sapiens.

WO200192523-A2

06-DEC-2001

29-MAY-2001; 2001WO-US10836.

30-MAY-2000; 2000US-206132P 29-AUG-2000; 2000US-228716P

(CURA-) CURAGEN CORP. Leach MD

Shimkets RA, 2002-106308/14

N-PSDB; ABN24588.

Novel human polypeptides and polypucleotides useful for disgnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders

Disclosure; SEQ ID 17654; 1037pp; English

Contribute present investion describes substantially purified human proteins of treferred to as open reading frame, OREX, when X is 1 1103 1 105 (c) in the specification). ABMIJ762 to ABMIJ762 monde the human orex of the proteins given in ABBIJ761 to ABMIJ762 monde the human orex of the contribute of the proteins given in ABBIJ761 to ABMIJ762 monde the human orex of the contribute of the proteins (see Table 1 a

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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                         (Wi) gene sequences from antibodies against Bacillus antiración spores. The antibodies are produced by different hybridomas. The specification describes monoclonal antibodies (specially 1968) antibodies) which are highly specific and can discriminate between the spores of the Bacillus Sanily. The antibodies are produced by exposing mice to Bacillus spores. The humoral immune response to Bacillus spores shows a conservation of W gene usage which is distinct for each spore, birding tragments derived from the antibodies are also capable of the bacillus spores in the interval of the spores. The humoral things the spore capable of the spore of the spor
                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anthrax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody specific for Bacillus spores, used to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-1998;
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at fip wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY43866 standard; Peptide; 129
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les 7; Conserv
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                                                                                                                                                                                    l Similarity
7; Conserv
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                                                      YGNYPAWFAY 86
                                                                                                                   YGNSPKGFAY 10
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                                                                                                                                                                                                                                                                                                                             129 AA;
                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                     70.0%;
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77.8%;
                                                                                                                                                                               Score 38; DB
Pred. No. 56;
0; Mismatches
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Pred. No. 34;
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                                                                                                                                                                                                                     56;
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Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 33135
                                                                                                                                                                                                                                                               ABB68781 standard; Protein; 258
                                    Drosophila melanogaster
WO200171042-A2
                                                                                                                                                                                      26-MAR-2002
                                                                                                                                                                                                                                 ABB68781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides human breast specific coding sequences and proteins. These are useful for detecting breast tissue and for detecting and treating breast cancer and other breast diseases. The present sequence is a breast specific polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel breast-specific polypeptides and polymucleotides encoding polypeptide, useful for identifying, disgnosting, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 219; 243pp; English
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22-NOV-2000; 2000US-252563P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABJ01013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 2 GNSPKGFA 9
                                                                                                                                                                                                                                                                                                                                                                             GNGPRGFA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macina RA,
                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Length 151;
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Gaps 0

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RESULT 11
ANM5984
ID AAM59884
AC AAM598
AC AAM59
AC AAM59
AC AAM50
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Best Local
                                                        Feng P,
Su JY;
     N-PSDB; AAV41925
                     WPI; 1998-414099/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The useful in developmental biology and in elucidating cell signaling realities of the development in biology and in elucidating cell signaling realities in the development in higher waterprotes for the development of insecticides, therapputies and pharmaceutical fungs. The invention discloses genomic PNA sequences (AELSA 76-AELSOSII) supressed DNA requences (AELSA 77-AELSOSII) supressed DNA requences (AELSA 77-AELSOSII) and the encoded proteins
                                                                                                                                                           21-JAN-1997;
                                                                                                                                                                           21-JAN-1997;
                                                                                                                                                                                                           21-JAN-1998;
                                                                                                                                                                                                                                              23-JUL-1998
                                                                                                                                                                                                                                                                           WO9831800-A2
                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABB57737-ABB72072)

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid
genes from Drosophila and
interactions -
                                                                                                                                                                                                                                                                                                                                         Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW59884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW59884 standard; Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 33135; 21pp + Sequence Listing; English.
                                                                                                                        (AUCK-) AUCKLAND UNISERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
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                                                                                                        HUMAN
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                                                                     Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGNAPVGF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGNSPKGF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-191637P
2000US-0614150
                                                                                                        GENOME
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                                                                                                                                                        97US-0034205.
97US-0034204.
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                                                                     Krissansen
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                                                                                                        SCI
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                                                                                                                                                                                                                                                                                                                                                                                            cDNA clone Bcl-like (HAICH29).
                                                                                                                        CID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37;
Pred. No.
                                                                     GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                     Z
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1.7e+02;
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                                                                     Rosen CA;
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malling and
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Best Local S
Matches 6
                                                                                                                                                                                07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
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07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
                                                11-APR-1997
11-APR-1997
                                                                             11-APR-1997
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                                                                                                                                                11-APR-1997,
11-APR-1997,
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                                                                                                                                                                                                                                                                                                                                                                       16-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                         US6420526-BJ
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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New isolated polynucleotides and encoded polypoptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, aller
       allergies
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12A-12D; 120pp; English

This is the maino acid sequence of the cDNA clone Bc1-like (HACT29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polymerides. They can be used for e.g. treating chronic behalf of the polymerides. They can be used for e.g. treating chromic diseases, inflammatory diseases, various allergies, and as anti-lifectious agents. The products can also be used for detection and dispossis.

365 AA;

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Similarity
6; Conserv
 YGNSPKGFAY
             Conservative
10
                   60.0%;
                   Score
Pred.
             Mismatches
                   37;
No.
                   2.5e+02;
                          DB 19;
                         Length 365
             Indels
            0;
            Gaps
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0

standard; Protein; 365 AA

(first entry)

Human novel secreted protein gene 120 polypeptide #1

Human; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;

oerabrovascular disorder; cerebral ischaemia, angiogenesis; smiburi, nervous system disorders; Albeimer's disease; infection; coular disorder; cormeal infection; wound healing; tissue regeneration; optimelia, cell projiteration; organ transplantation; food additive;

preservative; nutritional.

97US-040161P. 97US-040162P. 97US-040163P. 97US-038621P 97US-040161P 98US-0149476

97US 97US 97US 97US 97US S-040333P. S-040334P. S-040336P. S-040626P.

97US-043312P. 97US-043313P. 97US-043314P. 97US-043315P. 97US-043568P. 97US-043569P. 97US-043576P. 97US-043578P. 97US-043580P. 97US-043669P.

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16 - UL. 1997

10 - NUG - 1997

22 - NUG - 1997

22 - NUG - 1997

23 - NUG - 1997

24 - NUG - 1997

25 - NUG - 1997

26 - NUG - 1997

27 - NUG - 1997

27 - NUG - 1997

28 - NUG - 1997

29 - NUG - 1997

20 - NUG - 1997

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24 - NUG - 1997

25 - NUG - 1997

26 - NUG - 1997

27 - NUG - 1997

27 - NUG - 1997

28 - NUG - 1997

29 - NUG - 1997

20 - NUG
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23-MAY-1997;
23-MAY-1997;
06-JUN-1997;
06-JUN-1997;
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23-MAY-1997;
23-MAY-1997;
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23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
9708-95631P

9708-95632P

9708-95635P

9708-956369

9708-95663P

9708-95662P

9708-95662P

9708-95682P

9708-96682P

9708-95682P

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9708-
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97US-048964P.
97US-048974P.
97US-049610P.
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97US-047615P.
97US-047617P.
97US-047618P.
97US-047632P.
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9708-047589P
9708-047592P
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97US-052874P.
97US-055724P.
97US-056630P.
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97US-043671P.
97US-043672P.
97US-043674P.
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Competition relates to an isolated protein that is one of 186 human competition to the protein of the man competition to accorded by one of the protein of the protein is used condition of the protein is used condition in a pharmaceutical compestion used to prevent treat or ameliorate a condition in e.g. humans, mice, rabbits, goats, horses, dats, condition in e.g. humans, mice, rabbits, goats, horses, dats, condition in e.g. humans, mice, rabbits, goats, horses, dats, condition in e.g. humans, mice, rabbits, goats, horses, dats, condition in e.g. humans, mice, rabbits, goats, horses, dats, condition in e.g. humans, mice, rabbits, goats, horses, dats, condition in e.g. humans of the breast or liver, cardiovascular disorders e.g. cardatal ischammia, condition caused by bacteria, viruses and fungi and ocular disorders e.g. Albainers of disease, conditions caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can alab be used as a food additive or preservative to components of maintain organic backwards and other untrilional components of the present sequence represents one of the movel human corrected proteins of the inventions caused to be conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
05-SEP-1997;
05-SEP-1997;
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or preservative .
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Column 103; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-634796/68.
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Duan R, Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-1997
02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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GA, Yu G, Ni J,
''' J, Florence KA, Ott
365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-056909P.
97US-056911P.
97US-05761P.
97US-057650P.
97US-057650P.
97US-057669P.
97US-058785P.
97US-061060P.
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id, Feng P, Young PE, Greene NM, Fen
nce KA, Olsen HS, Ebner R, Brewer LA;
fleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bednarik DR;
Ferrie AM;
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Best Loc
Matches
                                                   Query Match
Best Local Similarity
 267
                    1 YGNSPKGFAY 10
                                         6,
FSGHPKGFAY 276
                                        Conservative
                                                63.8%;
                                      Score 37; DB 23; Length 365;
Pred. No. 2.5e+02;
1; Mismatches 3; Indels
                                      ٥,
                                      Gaps
                                      o
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RESULT 13
AAG02102
ID AAG03
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AAG02102 standard, Protein; 92 AA
AAG02102;
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Human secreted protein, SEQ ID NO: 6183

06-OCT-2000

(first entry)

2X8X22X2X2 Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.

Homo sapiens

EP1033401-A2

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RESULT 14
ABPOJS18
ID ABPOJS18
XX
ABPOJS18
XX
ABPOJS18
XX
ABPOJS18
XX
ABPOJS18
XX
ABPOJS18
XX
Human
XX
Human
XX
Human
XX
Human
XX
Homos
XX
Homos
PN
WO201
PD
PD
PD
PD
PS
29-M
XX
30-M
RR
ABPOJS18
ABPOJS1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular disease, diabetes mellitus, systemic lupus erythematosus, 
hypertension, hypothyroidism, cholesterol ester storage disease, 
immune deficiency, immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; 
hyperproliferative disorder; peoriasis; benign tumour; haemorrhage 
degenerative disorder; osteoarthritis; naurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence rag (5' BST) for obtaining cDNAs and genemic DNAs that correspond to 5' BSTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
30-MAY-2000; 2000US-206132P
                                                                                     29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                          WO200192523-A2
                                                                                                                                                                                                                                                                                                                                          Homo sapiens:
                                                                                                                                                                                                                                                                                                                                                                                                                         myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX protein sequence SEQ ID NO:7618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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Pred. No. 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
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EXEXEESS

Novel human diagnostic protein #672

13-FEB-2002 ABG00681;

(first entry

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

XXXXXXX

11-OCT-2001. WO200175067-A2 Homo sapiens

30-MAR-2001; 2001WO-US08631

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YGRSPSGF 50

Matches

Conservative

ç,

0, Gaps

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ABG0068 RESULT 15

ABG00681 standard; Protein; 118 AA

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The present invention describes substantially purified human proteins of referred to as open reading frame, ORPX, where X is 1,1491 (see Table 1) or fetered to as open reading frame, ORPX where X is 1,1491 (see Table 1) or treating type and in Repool to Ambition 20 conde the human open corrections given in Ambount of the human open corrections of the thing of the human open corrections of the correction o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autonmmune disorders
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID 7618; 1037pp; English
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                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
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                                 Similarity
                                                                                                                             117 AA
                                 62.1%;
75.0%;
Score 36; DB 23; Length 117;
Pred. No. 1.1e+02;
0; Mismatches 2; Indels
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Query Match
Best Local Similarity
"arches 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polymucleotide (I) and coplymeriae (II) sequences (II) is useful as phyticial station probes, polymeriae chain reaction (PRR) primers, oligomers, and for chromosome copulymeriaes chain reaction (PRR) primers, oligomers, and for chromosome copulymicleotides are also used in disposition as expressed sequence tags for identifying expressed genes, (I) is useful an interest the expressed primers (I) is useful for generating antibodies against it, detecting or (III). (III) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical companies involving abstrant process expression or biological activity. It is not the polypeptide and polymucleotide sequences have applications in the polypeptide and polymucleotide sequences and of materiors and composition of materiors. Account of the polypeptide and polymucleotide sequences in the printed composition and assume the sequence data for this patent did not appear in the printed of specification, but was obtained in electronic format directly from MIPO or from the polyment of the printed of the property of the printed of the property in the polyment of the printed of the property of the printed of the property in the printed of the property of the printed of the property in the printed of the property of the printed of the property of the property in the printed of the property of the property of the property of the printed of the property of the printed of the
Search completed: November 7, 2003, 07:26:56
Job time : 5.31242 secs
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diagnostics, Forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                     46 YTRRPRGFAY 55
                                                                                                                                                                                                                                                                                                   1 YGNSPKGFAY 10
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                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.1%;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 22; Length 118;
Pred. No. 1.1e+02;
1; Mismatches 3; Indels
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Result
No.
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                               Score
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1 cgn2 6/prodate // Joubpas/USO7 PUBCOMB. pep:

2 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

3 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

4 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

5 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

6 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

7 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

8 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

9 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

10 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

11 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

12 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

13 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

14 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

15 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

16 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

17 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

18 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

19 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

19 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

10 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

11 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

12 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

13 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

14 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

15 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:

16 cgn2 6/prodate // Joubpas/USO7 RMW FUB. pep:
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Match Length
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58
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                      151
249
306
365
365
373
373
1038
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1197
1197
       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                   Description
sequence 96, Appl
sequence 120, App
sequence 120, App
sequence 55, App
sequence 55, App
sequence 55, App
sequence 1215, App
sequence 1215, App
sequence 12, Appl
sequence 12, Appl
sequence 12, Appl
sequence 12, Appl
sequence 40, Appl
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US-10-001-887-96

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US-10-121-032-16
US-10-093-037-16
Sequence 174, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 11, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 113, Appli Sequence 113, Appli Sequence 113, Appli Sequence 114, Appli Sequence 115, Appli Sequence 16, Appli
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Sequence 96, Application 187/10001887

Publication No. US200015546A1

GREERAL INFORMATION:

APPLICANT: Macina, Roberto
APPLICANT: Macina, Roberto
APPLICANT: Salveda, Susmana
APPLICANT: Salveda, Roberto
APPLICANT: Sun Younghing
APPLICANTO CAfferbey, Robert
APPLICANT: Sun Younghing
APPLICANTO WINERER: 187/10/001,897

CURRENT APPLICATION MUMBER: 187/10/001,897

CURRENT APPLICATION MUMBER: 60/449,998

PRIOR FLING DATE: 2000-11-20

PRIOR APPLICATION MUMBER: 60/552,563

PRIOR PLING DATE: 2000-11-20

PRIOR APPLICATION MUMBER: 60/552,563

PRIOR PLING DATE: 2000-11-20

PRIOR PLING DATE: 2000-11-20

PRIOR PLING DATE: 2001-11-20

PRIOR P
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                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Homo sapien US-10-001-887-96
                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                      GNSPKGFA 9
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                   75.0%;
                                                                                                                                                                                               ; Score 37; DB
; Pred. No. 46;
1; Mismatches
                                                                                                                                                                                                                                                   46;
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0

RESULT 2 US-10-153-668-118

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APPLICANT: MIRSAWSU, Shuji
APPLICANT: MIRSAWSU, Shuji
APPLICANT: ISHIZAMA, KRUYA
TITLE OF INVENTION: CTATG ACTIVATING Gene
FILE REFERENCE: 1254-027P
CURRENT FILING DATE: 2007-05-24
PRIOR REPLICATION NUMBER: US 60/299,172
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-05-25
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US-10-153-668-118
                                                                                                                    SEQ ID NO 120
LENGTH: 306
TYPE: PRT
ORGANISM: Homo sapiens
-10-153-668-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
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Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 488
SOFTWARE: PatentIn Ver. 2
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR FILING DAYE: 2001-08-30
PRIOR APPLICATION UNMBER: JP 2001-313175
PRIOR FILING DAYE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FLING DATE: 2001-08-31
PRIOR PLICATION NUMBER: US 60/328,403
PRIOR FLILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: UP 2001-157043
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MATSUDA, Akio
APPLICANT: MUZAMATSU Shuji
APPLICANT: ISHIZAMA, Kenya
TITLE OF INVENTION: STATE ACTIVATING Gene
FILE REFERENCE: 1254-0207P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 118, Application US/10153668
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PRIOR FILME DATE: 2001-08-30
PRIOR APPLICATION NUMBER: UP 2001-313175
PRIOR FILME DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
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Local Similarity 60.0%;
hes 6; Conservative
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Pred. No.
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US-09-882-171-696
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US-09-809-391-696
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PRIOR PILING INTE 1998-0-06

PRIOR PILING INTE 1998-0-06

PRIOR PILING INTE 1997-0-07

PRIOR REPLICATION INDERER 60/040.626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 696, Appli
Publication No. US2
GENERAL INFORMATION
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APPLICANT: Ruben et al.
TITLB OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002PZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 696
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Publication No. US20030049618A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/809,391
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/149,476
PRIOR FILING DATE: 1998-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT PILING DATE: 2001-03-16
Frior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 761
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nes 6; Conserv
                                                                                                    APPLICATION NUMBER: 60/040,334
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
                                         APPLICATION NUMBER: 60/047,600 FILING DATE: 1997-05-23
                                                                                   FILING DATE: 1997-03-07
                                                                                                                                                                                                                       FILING DATE: 1997-03-07
FILING DATE: 1997-05-23
                    APPLICATION NUMBER: 60/047,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 FSGHPKGFAY 276
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o. US20030175858A1
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Pred. No. 1.1e+02;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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60/047,597

RAIOR FILING DATE: 1997-05-23

RAIOR APPLICATION NUMBER: 60/017-613

RAIOR FILING DATE: 1997-05-23

RAIOR APPLICATION NUMBER: 60/047-612

RAIOR FILING DATE: 1997-05-23

RAIOR APPLICATION NUMBER: 60/047-63

RAIOR FILING DATE: 1997-05-23

RAIOR STATUM NUMBER: 80/047-601 COR APPLICATION NUMBER: 66/043,568
COR APPLICATION NUMBER: 66/043,314
COR APPLICATION NUMBER: 66/043,314
COR APPLICATION NUMBER: 66/043,569
COR APPLICATION NUMBER: 66/043,569
COR APPLICATION NUMBER: 66/043,311
COR APPLICATION NUMBER: 66/043,471
COR APPLICATION NUMBER: 66/043,671
COR APPLICATION NUMBER: 66/043,674
COR APPLICATION NUMBER: 66/043,674
COR APPLICATION NUMBER: 66/043,674
COR APPLICATION NUMBER: 66/043,674
COR APPLICATION NUMBER: 66/043,669 OR PELLING DATE: 1997-05-23
OR OR FILING DATE: 1997-08-22

OR RPELICATION NUMBER: 60/556,889

OR FILING DATE: 1997-08-22

OR APPLICATION NUMBER: 60/056,893

DR FILING DATE: 1997-08-22

OR APPLICATION NUMBER: 60/056,630 NE APPLICATION NUMBER: 60/043,315
NE HILING DATE: 1997-04-1
NE APPLICATION NUMBER: 60/048,974
NE FILLING DATE: 1,997-06-20,056,886
NE APPLICATION NUMBER: 60/056,877
NE APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,313
FILING DATE: 1997-04-11 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,492 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,598 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11 NUMBER: 60/047,633 NUMBER: 60/047,502 1997-05-23 ON PELLIAND NATE 1997-08-23
ON ON FILIME DATE: 1997-08-22

ON APPLICATION UNUBER: 6(0/156,878

ON APPLICATION UNUBER: 6(0/156,6678

ON APPLICATION UNUBER: 6(0/156,6672

ON APPLICATION UNUBER: 6(0/156,672

ON APPLICATION UNUBER: 6(0/156,872

ON APPLICATION UNUBER: 6(0/156,882

ON FILIME DATE: 1997-08-22

ON APPLICATION UNUBER: 6(0/156,637)

ON APPLICATION UNUBER: 6(0/156,637)

ON APPLICATION UNUBER: 6(0/156,903)

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US-10-219-220-285
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CUBRENT PILING DATE: 2002-08-14
PRIOR APPLICATION WINBER: U.S. No. US20030082724A1 09/325,932
PRIOR PILING DATE: 199-06-04
NUMBER: OF SEC ID NOC5 290
SOFTWARE: PattSEQ for Windows Version 3.0
SEQ ID NO 265
SEQ ID
Taguarde Tis Tagual ention 18/1021920

**Education Marco 100082744A1

**Education Marco 100082744A1

**Education Marco 10008274A1

**APPLICANT: Limitan, Annette

**APPLICANT: Limitan, Annette

**TITLE OF INVENTION: death and their use in the modification of plant development FILE REPERENCE: 11000.1022-05-19

**CIMERENT APPLICATION NOMERS: US/10/219,220

CURRENT FILENDAME: 3002-06-19
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APPLICANT: Liasham, Annette
APPLICANT: Liasham, Annette
TITLE OF INVENTION: death and their use in the modification of plant development
TITLE OF INVENTION: death and their use in the modification of plant development
TITLE OF INVENTION:
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PRIOR APPLICATION NUMBER: 60/056,887
PRIOR FILING DATE: 1997-08-22
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Local Similarity 60.0%;
hes 6; Conservative
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/057,650
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,669
FILING DATE: 1997-09-05
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,862
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,909
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6; Conservation
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Pred. No.
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Pred. No. 1.8e+02;
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APPLICANT: SHIEM, TANAVOSHII
APPLICANT: SHIEM, TANAVOSHII
APPLICANT: HATTORI, MASAHIRA
APPLICANT: HATTORI, MASAHIRA
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVESTION: AVERLE POLYMUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
FRICA FILING DATE: 2002-05-29
FRICA FILING DATE: 2001-05-30
FRICA FILING DATE: 2001-05-30
FRICA FILING DATE: 2001-05-02
FRICA FILING DATE: 2001-05-03
FR
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; ORGANISM: Pinus radiata
US-10-219-220-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-032-585-7154
Sequence 7154, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
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Best Local S
Matches 6
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PRIOR FILING DATE: 1999-06-04
NUMBER OF EEQ ID NOS: 299
SOFTWARE: FRATESEQ for Windows Version 3.0
SEQ ID NO 133
LENGTH: 396
                        APPLICANT: Terry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Charles, 1018-005-095
CURBENT PILING DAITS: 2001-12-20
NUMBER OF SEX 1D NOS: 8001-12-20
NUMBER OF SEX 1D NOS: 8001-10-005
SOPTWARE: PARCELLIN VERSION 3.1
SEX 1D NO 713-6
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Publication No. US20030119018A1
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
LENGTH: 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 62.1%;
Local Similarity 60.0%;
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6; Conserva
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Pred. No. 1.9e+02;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 15; Length 1038;
Pred. No. 5.2e+02;
1; Mismatches 1; Indels
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ORGANISM: Candida albicans

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Sequence 12, Application US/10284668

Publication No. US20030106100A1

GENERAL INFORMATION:
                                                                                                                                                    US-10-284-668-12
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                           Matches
                                                                                                                Query Match
                                                                        Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                 TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DANA:
PRIOR APPLICATION UNMER: US/08/836,567
PILING DATE: 24-JUL-1997
APPLICATION UNMER: PCT/EP95/04415
PILING DATE: 09-NOV-1995
                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: DE P 44 41 408.0 FILING DATE: 10-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/284,668
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION DAN MOLECULES THAT COODE FOR RECYPES EACTERIA TRANSGENIC PLANT CELLS AND FLANTS CONTAINING SAID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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45 GSSPKGF 51
                                 2 GNSPKGF 8
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                                                                                                                                                                                                                                                                                                                                                               NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                             LENGTH: 1197 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                          TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10020
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                                                                           Conservative
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Abel, Gernot
                                                                                          60.3%;
                                                                        Score 35; DB 15;
Pred. No. 9e+02;
1; Mismatches
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Pred. No. 3.8e+02;
                                                                                                                DB 15;
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                                                                                                             Length 1197;
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RESULT 11

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Query Match
Best Local Similarity
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US-09-852-870A-12
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                                                                                                                                                         US-09-852-870A-12
                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09852,870A
CURRENT FILING DATE: 1001-05-10
PRIOR APPLICATION NUMBER: US 09/384,601
PRIOR REFLING DATE: 1099-08-26
NUMBER OF EED ID NOS: 24
NUMBER OF EED ID NOS: 24
SED ID NO 12
SED ID NO 12
SED ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09852870A Patent No. US20020165132A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOPTWARE: PatentIn ver. 3.0
SEQ ID NO 4750
LENGTH: 1257
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Best Local Similarity 50.0%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goodman, Murray
APPLICANT: OSapay, George
TITLE OF INVENTION: Lanthic
FILE REFERENCE: LKR 9122-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 249-125
CURPENT APPLICATION NUMBER: US/09/738,626
CURPENT FILING DATE: 2000-12-18
FRIOR APPLICATION NUMBER: UF 99/377484
FRIOR FILING DATE: 1999-12-16
FRIOR FILING DATE: 1999-12-16
FRIOR FILING DATE: 1990-12-16
FRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                  PEATURE: OTHER INFORMATION: Cys-Ser lanthionine bridge
                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                   ENGTH:
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1 YGNSPKG 7
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3 FGNSPRG 9
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F: OZAKI, AKIO
INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANDO, SEIKO
HAYASHI, MIKIR
OCHIAI, KEIKO
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SENOH, AKIHIRO
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                                                                              Conservative
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                                                                           58.6%; Score 34; DB 10;
71.4%; Pred. No. 5.8e+05;
tive 2; Mismatches 0
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Pred. No. 9.5e+02;
3; Mismatches 2;
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APPLICANT: Microbial Technics Limited APPLICANT: Gilbert, Christophe inted APPLICANT: Gilbert, Christophe inted APPLICANT: Handbro, Philip M
TITLE OF INVENTION: Froteins
FILE REFERENCE: PMC/P21129MO
CURRENT APPLICATION WMOSER: UB/09/765,787
TORRENT PRILITATION WMOSER: UB/09/765,787
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PRICE FILING DATE: 1996-03-27
PRICE FILING DATE: 1996-03-27
SEQ ID NO 40
SEQ ID NO 40
LENGTH FAR
                              RESULT 15

Sequence 18, Application US/10272419

Publication No. US20030087403A1

GENERAL IMPORMATION:
APPLICANT: CIERN, 0100G

APPLICANT: CIERN, 0100G

APPLICANT: HOMAS, STUART

APPLICANT: MAGABAJAN VASANTHA

TITLS OF INVESTION: MICHOEN DEFORMATION OF ADIPIC ACID AND TITLS OF INVESTION: MICHOEN APPLICANT

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US-09-769-787-40
US-09-769-787-40
; Sequence 40, Application US/09769787
; Publication No. US20030091577A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-40
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-953
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US-09-764-864-953
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Parent No. US2002012753A1
PARTICON: RESEARCH INFORMATION:
APPLICANT: RESEARCH STATE OF INVESTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23 MORBER: US/09/764,864
CUREBUT 15/10X DATE: Z001-01-11
CUREBUT 15/10X DATE: Z001-01-11
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NUMBER OF SBQ ID MOS: 1792
SOFTWARE: FatentIn Ver. 2.0
SBQ ID NO 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Owery March 58.6%; Score 34; DB 11; Length 284; Best Local Similarity 66.7%; Pred. No. 3e+02; Matches 6; Conservative 2; Mismatches 1; Indels
CURRENT ACPLICATION NUMBER: US/10/272,419
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I TYPE: PRT
ORGANISM: Acinetobacter sp.
US-10-272-419-18
                                                         Matches
                                                                     Query Match
Best Local Similarity
                                                                                                                                                                         SOPTWARE: Microsoft Office 97
SEQ ID NO 18
                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/252,553
PRIOR FILING DATE: 1999-02-19
                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 32
31 PSNTPKGF 38
                           1 YGNSPKGF 8
                                                         Conservative
                                                                     58.6%;
                                                       2; Mismatches
                                                                     Score 34; DB 15;
Pred. No. 3.5e+02;
                                                                                     DB 15;
                                                                                   Length 324;
                                                         Indels
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Gaps

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Search completed: November 7, 2003, 08:16:49 Job time: 10.7717 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
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seq length: 2000000000
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1 /cgm2_6/pcodata/1/isa/58_COMB.psp:*
22 /cgm2_6/pcodata/1/isa/5E_COMB.psp:*
33 /cgm2_6/pcodata/1/isa/6E_COMB.psp:*
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42 /cgm2_6/pcodata/1/isa/6E_COMB.psp:*
43 /cgm2_6/pcodata/1/isa/beTig_COMB.psp:*
44 /cgm2_6/pcodata/1/isa/beTig_COMB.psp:*
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(without alignments)
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Copyright (c) 1993 - 2003 Compugen Ltd.
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WS-00-522-9111-12973
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WS-00-522-9111-12973
WS-00-125-9111-12973
WS-00-125-9111-12971
WS-00-618-671-12
                                                   78.70.784.0044.11
18-09-648.004.18
18-09-107-522.633
18-09-107-522.633
18-09-127-522.7104
18-09-252.991.72104
18-09-52.991.72104
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18-09-441.507-71
18-09-441.507-11
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2, Appli
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32215, A
19973, Ap
15973, Ap
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12, Appl
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US-09-149-476-696
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Patent No. 6430556
GENERAL IMPORMATION:
APPLICANT: ROSen et al luman Secreted proteins
FITHE 0P INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PRODE!
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CURRENT FILING DATE: 1998-09-08
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EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
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ESS PILLING DATE: 1997-05-20/047,633
ESS PILLING DATE: 1997-05-20/047,633
ESS PILLING DATE: 1997-05-23
ESS PILLING DATE: 1997-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ER PILING DATE: 1997-03-07

BER APELICANION UNUBER: 60/047,600

BER PILING DATE: 1997-05-23

BER PILING DATE: 1997-05-20/047,615

BER PILING DATE: 1997-05-20/047,597

BER APELICATION UNUBER: 60/047,597

BER PILING DATE: 1997-03-2147,597
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,584
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/038,621
FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
FILING DATE: 1997-03-07
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Minimum DB Maximum DB

Searched: Scoring table: Sequence: Perfect score:

on:

US-06-928-692-57
US-09-339-972-67
US-09-139-972-67
US-09-17-5228-3103
US-08-611-577-21
US-08-18-9138-21
US-08-18-9138-21
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57, Appl 370, Appl 370, Appl 21, Appl 21, Appl 21, Appl 32, Appl 32, Appl 32, Appl 35, Appl 15, Appl 15, Appl 15, Appl 15, Appl 15, Appl

US-09-107-532A-5048 US-08-639-237-2 US-09-134-078-16

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

5048,

ALIGNMENTS

US-09-025-769B-16 US-09-252-991A-31838

16, Appl

Result No.

Score

Query

EARLIER EARLIER

RE APPLICATION NUMBER: 60/047,500
RE FILING DATE: 1997-05-23
RE APPLICATION NUMBER: 60/047,587
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APPLICATION FILING DATE	LING	FILING DATE	APPLICATION	APPLICATION	FILING DATE	FILING DATE	APPLICATION	APPLICATION	FILING DATE	APPLICATION	APPLICATION	FILING DATE	APPLICATION	APPLICATION	FILING DATE	APPLICA	FILING	PILING	APPLICA	FILING	FILING	APPLICA	FILING	FILING	APPLICA	FILING	FILING	APPLICA	FILING	FILING	APPLICA	APPLIC	FILING	APE	APPLICA	APPLICA	FILING	APE	APPLICA	FILING	APPLICATION	APPLICAT	FILING DA	APPLICATION	APPLICATI	FILING DA	APPLICATI	APPLICAT	FILING DA	APPLICAT	FILING DA	FILING D
NUMBER: 60/056	: 1997-09-05	1997-06-06	NUMBER: 60	NUMBER: 60	1997-08-22	1997-08-22	NUMBER: 60/05	NUMBER: 6	: 1997-08-22	NIEMBER: 60/	NUMBER: 6	1997-08-22	NUMBER: 6	NUMBER: 60/056	: 1997-08-22	NUMBER	1997	1997-05-23	NUMBER	: 1997-04-11	1997-04-11	NUMBER: 60	: 1997-05-23	: 1997-05-23	NUMBER: 60	1997	: 1997-05-23	NUMBER: 60	. 1997	1997-05-23	NUMBER: 60	NUMBER: 6	1997-05-23	1997-	NUMBER: 60	. 1997-05-	: 1997-08-22		NUMBER: 60	: 1997-08-	: 1997-08-22	NUMBER: 60	: 1997-08-22		NUMBER: 60	1997-08-22	Į,	NUMBER: 60	: 1997-08-22	NUMBER: 60	: 1997-08	: 1997-08-22

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TITLE OF INVENTION NUCLEIC ACID AND MINO A
TITLE OF INVENTION NUCLEIC ACID AND MINO A
TITLE OF INVENTION ABOURTNOS FOR DIAGNOSTI
FILE REFERENCE 107.196.126 (19/05/25,991A
CURRENT PILING DATE: 1999-02-18 (19/074,788
PRIOR PEPILING DATE: 1999-02-18 (19/074,788
PRIOR PILING DATE: 1999-02-18 (19/074,190
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEG ID NOS: 33142
SEO ID NO 32215
                                                                                        ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-19973
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US-09-252-991A-32215
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                                              Query Match
                                                                                                                                                            SEQ ID NO 19973
LENGTH: 149
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.
TITLS OF INVENTION: NICLEIC ACID AND MINO ACID SEQUENCES RELATING TO PREUDOMONAS
TITLS OF INVENTION: ARROGINGAN FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 10719-136
CURRENT APPLICATION MYMERS: US/09/252,991A
CURRENT FLING DATE: 1999-07-18
FRIOR APPLICATION MYMERS: US 60/074,788
PRIOR APPLICATION MINERS: US 60/074,788
PRIOR APPLICATION MINERS: US 60/074,789
PRIOR APPLICATION MINERS: US 60/074,780
REGOR FILING DATE: 1998-07-27
REGOR FILING DATE: 1998-07-27
REGOR FILING DATE: 1998-07-27
REGOR FILING DATE: 1998-07-27
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Matches 6; Conserv
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Patent No. 6551795
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ERALIER FILING DATE: 1997-09-05
ERALIER APPLICATION NUMBER: 60/049,610
ERALIER APPLICATION NUMBER: 60/061,060
ERALIER APPLICATION NUMBER: 60/061,060
ERALIER ERILING DATE: 1997-10-02
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   . MACCH Similarity 62.1%; Score 36; DB 4; Length 149; Local Similarity 66.7%; Pred. No. 29; Pred. No. 29; Indels 6; Conservative 1; Mismatches 2; Indels
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6; Conserv
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Pred. No.
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Pred. No.
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: Sequence 29391, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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                                                                                                                                                                                                                                   US-09-252-991A-29391
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APPLICANT: LATUR DOUGETE-Stamm et al

TITLE DF INVENTION: NUCLEIC ACID AND ANIMO ACID SEQUENCES RELATING TO STAPRHY

TITLE DF INVENTION: NEIDERMINIS FOR DIAGNOSTICS AND THERAPEUTICS

THE REFERENCE: GTC-007

CURRENT PILLING DATE: 1990-08-13

PRIOR REPLICATION NUMBER: US 60/054,964

PRIOR PILLING DATE: 1997-11-08

PRIOR PILLING DATE: 1997-11-08

PRIOR PILLING DATE: 1997-10-08

PRIOR TILLING DATE: 1997-08-13

PRIOR TILLING DATE: 1997-08-16

PRIOR TILLING 
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LENGTH: 484
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CURRENT FILLING DATE: 199-06-04
NUMBER OF SBO ID NOS: 206
SOFTWARE: SEASED for Windows Version 3.0
SBO ID NO 153
LENGTH: 360
APPLICANT: MACC J. RUBERTSAIG et al.
TITLE OF INVENTION: HULGER ACTO AND MAINO ACTO SEQUENCES RELATING TO PSEUDO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
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Patent No. 6451604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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les 6; Conserv
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66.7%;
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Pred. No. 1e+02;
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Pred. No. 83;
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                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 000
PRIOR APPLICATION NATA.
APPLICATION NATURE: 007001-1918
PRIOR APPLICATION NATURE: 007001-1918
PRIOR APPLICATION NATURE: 007001-1918
REFERENCE DOCUMENT NATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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LENGTH: 474
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                                                                                                                                              INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1197 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT SILING DATE: 1999-02-18 00/074,788
PRIOR HPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
PRIOR PRICHETING DATE: 1998-07-27
NUMBER: 05 5850 LD NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                   COLECULE TYPE:
                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DIA MOLECULES THAT CODE FOR ENZYMES
TITLE OF INVENTION: INVOLVED IN STRANGE SYMPHESTS VECTORS BACTERIA TRANSGENIC
TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Springer, Franziska
APPLICANT: Abel, Gernot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                 TYPE: am:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 NAPKGFA 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10020
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                                                                       amino acid
XGY: linear
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                                                                                                                                                                                                                                                              212-596-9090
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                                   protein
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Pred. No. 1.5e+02
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Query Match

60.3%; Score 35; DB 3;

Length 1197;

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Best Local Similarity
---hes 6; Conserv
                                                                                                                   US-08-968-542C-35
                                                                      ; Sequence 35, Application US/08968542C; Patent No. 5981728
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Patent No. 6483010
GENERAL INFORMATION:
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Matches 6; Conservative
                          GENERAL INFORMATION:
APPLICANT: Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
       APPLICANT: Myers,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READMED FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: LING FC Compatible

OPERATING SYSTEM: FC-D05/MS-D05

CURRENT APPLICATION: GUML-2010

CLAMSIFICATION: GUML-2010

CLAMSIFICATION: GUML-2010

PRIOR APPLICATION: GUML-2010

PRIOR APPLICATION: GUML-2010
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FILMS ADTS. CINKONDY /835,567
FILMS ADTS. CINKONDY /835,567
FILMS ADTS. 10.500,1994
ATTORREY/AGENT INFORMATION: 10.500,1994
MANS: HALey Jr., James F.
MESISTRATION NUMBER: 27,794
TELECOMPURENCE/DOCKET MANGER: AGTEVO-4
TELECOMPURENCE/DOCKET MANGER: AGTEVO-4
TELECOMPURENCE/DOCKET MANGER: AGTEVO-4
TELECOMPURENCE/DOCKET MANGER: AGTEVO-4
TELECOMPURENCE/J212-596-90100
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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INVOLVED IN STRACH SYNTHESIS VECTORS BACTERIA TRAN
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
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ADDRESSEE: FISH & NEAVE
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                                                                                                                                                                                                                    45 GSSPKGF
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                                                                                                                                                                                                                                                         2 GNSPKGF 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1197 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                             Conservative
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Abel, Gernot
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                          et al
dull1 Codes For A No. 5981728el Starch
                                                                                                                                                                                                                                                                                                      60.3%; Score 35; DB
85.7%; Pred. No. 4.1e
tive 1; Mismatches
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1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                4.le+02;
                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 1197;
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TITLE OF INVENTION:

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; MOLECULE TYPE:
; DESCRIPTION: ami
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE:
; PRAGMENT TYPE:
US-08-968-542C-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-750-152A-2
                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08750152A Patent No. 5977331
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: ASAKURA, YOKO
APPLICANT: KINURA, EIICHIRO
APPLICANT: ABB, CHIZU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (713) 777-2321
TELEPAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
ZIP: 22152
COMPUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: 06LOW, SEPVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WAMS. Benjamin Aaron Adler, Ph.D.,
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D6036
TELECOMUNICATION INCREMATION:
TELEPHONE: (713) 777,2321
                                                                                                                                                                                                                                 PEPLICANT: KAWAHARA, YOSHYO
REPLICANT: KAWAHARA, YOSHYO
TITLE OF INVENTION: ALPHA-KSTOGLUTARATE DEHYDROGENASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/968.542C
FILING DATE: No. 5981728ember 12, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: C...
CITY: Houston
TATE: TX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Word 6.0.1 for Macintosh CURRENT APPLICATION DATA:
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                                                                                                            COUNTRY:
                                                                                                                                               CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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    1: 1230 amino acid residues
amino acid
XY: linear

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8011 Candle Lane
                                                                                                            USA
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85.7%;
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Pred. No. 4.2e+02;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1230;
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US-08-467-472C-12
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Best Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08467472C Patent No. 6028168 GENERAL INFORMATION:
                          TELEX: NONE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    PRION APPLICATION DATA:

APPLICATION NUMBER: US 0/742,908

PILLANG DATE: 9-ANGUSF-199;

APPLICATION NUMBER: US 08/021,606

PILLANG DATE: 28-JANUARY-199;

APPLOREE/JACETY INFORMATION.

NAMES __ROBINSON_WILLIAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: COMPAQ - IBM CON-
OPERATING SYSTEM: M5-DOS V
SOFTWARE: ASCII
CURRENT APPLICATION UNDER: US/08/
APPLICATION UNDER: US/08/
PILING DATE: 6-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRLEFAX: 703-413-2220
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10040
COMPOTER READABLE FORM:
MEDIUM TIPE: 3.5" FLORPY DISC
MEDIUM TOPE: OCMPAQ - IBM COMPATIBLE
MEDIUM TOPE: OCMPAQ - IBM COMPATIBLE
MEDIUM TOPE OF THE TOPE
                                                                                                                                                                                                                       REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                     TELEPHONE: (212) 557-5635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 99 PARK AVENUE
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              883 FANTPEGFNY 892
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OLECULE TYPE:

TYPE: AMINO ACID TOPOLOGY: LINEAR

DESCRIPTION:

PEPTIDE

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US-08-467-472C-12
                              Matches
                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANYI-SUNSE: N/A
FRACHENT TYPE: INTERNAL
ORIGINAL SOURCE: NMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.
ORIGINAL SOURCE: 100 MARKET STREET, PHILADELPHIA,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL:
                                                                                                   PUBLICATION DATE:
RELEVANT RESIDUES
RELEVANT RESIDUES
                                                                                                                                                DOCUMENT NUMBER:
                                                                                                                                                                                                                                        JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL:
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VOLUME:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD:
1 YGNSPKG 7
                          Similarity
5; Conserv
                                                                                                                                                                             1990
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1990
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: PROCEEDINGS OF THE 11TH AMERICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUPPLEMENTARY
                                                                                                                                                                                                                                                                                                             IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 - 519
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                            Conservative
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                                        58.6%;
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                       Score 34, DB 3; Le
Pred. No. 2.5e+05;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12:
                                                                                                 12: CYS-SER
STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                         CYS-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYS-SER
                                                    Length 9;
                       Indels
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á 무 RESULT 12

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US-09-384-061-12
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CRETTER READABLE FORM:
CMEDITER READABLE FORM:
MEDITM TYPE: 3.5" FLOPPY DISC
MEDITM TYPE: 3.5" FLOPPY DISC
CMEPUTER: COMPAQ - IEM COMPATIBLE
CREMET APPLICATION DATA:
NORTH TOWN NUMBER: US/09/384,061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09384061 Patent No. 6268339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: N/A
FRACHENT TYPE: INTERNAL
GRACINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
GRACINAL SOURCE: INC.
GRACINAL SOURCE: INC.
GRACINAL SOURCE: ORGENIEST STREET, BHILADELPHIA,
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
                                                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME: 
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: US 08/02
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BROCKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GOODMAN,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                          AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH STLFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
                                                                             DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NONE
                                                                                                                865 - 869
                                                                                                                                                    ESCOM (LEIDEN 1990)
                                                                                                                                                                     SYMPOSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 557-5635
                                                                                                                                                                                                                                                                                                                                                                                                                                       SYNTHESIZED PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                      N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LANTHIONINE BRIDGED PEPTIDES
                                                                                                                                                                                                                                                                             a -S- bridge is present between Cys and Ser
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                       12:
                    CYS-SER
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Query Match
Best Local Similarity
""" (Conserved)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 464, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Black, Michael
APPLICANT: Modgrom, John
APPLICANT: Knowles, David
APPLICANT: Knowles, Richard
APPLICANT: Stodols, Richard
APPLICANT: Stodols, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDED ADDRESS:
MICHAEL AD
                                                                                                                                                                                                                                                                           COUNTRY: UNM399
ZIF: 19406-0939
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Diskette
"AMBUTTER: IEM Compatible
"AMBUTTER: DE COMPATION DOS
APPLICATION NUMBER: U8/08/858,
PILING DATE: 09-MAY-1997
CLASSIFICATION: 435-
PRIOR APPLICATION DATA:
APPLICATION UNBER: 60/017670
FILLING DATE: 14-MAY-1996
                                                                                                                                                                                                            COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESD for Windows Version 2.0
CHERENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12:
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PUBLICATION DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ
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DATE: 1990
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL:
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CHEMISTRY OF LANTHIONINE PEPTIDES
BIOPOLYMERS
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Pred. No. 2.5e+05;
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STRUCTURE
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Best Local Similarity
Watches 6; Conserv
PEPLICANT: CHEN, QIONG
APPLICANT: THOMAS, STUART
APPLICANT: HIGHES, STUART
APPLICANT: NEARABANAN, VASANTHA
APPLICANT: NEARABANAN, VASANTHA
APPLICANT: NEARABANAN, VASANTHA
APPLICANT: OF INVENTION: APPLICATION: APPL
                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6498242
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Best Local &
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FILING DATE: 29-JAN-1993
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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APPLICANT: Method of Controlling Plant Pathogenic Fungi
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REFERENCE/DOCKET NUMBER: PS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Local Similarity 85.7%;
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Pred, No. 1.2e+02;
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Pred. No. 49;
2; Mismatches
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CURRENT APPLICATION NUMBER: US/09/648,004

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CURRENT FILING DATE: 2000-04-25
FRIOR REPLICATION NUMBER: 09222,553
FRIOR FILING DATE: 199-02-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Microsoft Office 97
JESQ ID NO 18
JENGTH : 324
TYPE: PRI TYPE: TYPE: TYPE: TYPE: 1004-18
Search completed: November 7, 2003, 07:30:05  
Job time: 2.46862~{\rm secs}
                                                                                                                                                                 Query March 58.6%; Score 34; DB 4; Length 324; Best Local Similarity 62.5%; Prod. No. 1.5e+02; Marches 5; Conservative 2; Mismatches 1; Indels
                                                                                    1 YGNSPKGF 8 : |:|||| 31 FSNTPKGF 38
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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
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               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     %
Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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72
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                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5,1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length DB
                                                                                       H32513
T04310
G01859
A45350
F96770
C27115
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B45466
A45466
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T28808
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PH1733
PH1738
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A90672
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                  glycine/tyrosine r
glycine/tyrosine r
glycine/tyrosine r
Ig heavy chain V-I
Ig heavy chain V-I
Ig heavy chain pre
strong gravity str
RNA binding motif
matrix protein RNI
protein RNA-bindin
K-kiningen, LNM p
                                                                                                                                                                                                                                                                                                                                                         glycine/proline-ri
hypothetical prote
protein (imported
probable iron-sulf
hypothetical prote
hypothetical p
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FUN2 protein - yea
Ig heavy chain V r
                                                                                                                                                                                                                                                                                                                                         hypothetical prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycine/proline-tich protein - Arabidopeis thaliana
NiAlternate names; protein KIOA@ 130
C.Specias: Arabidopeis thaliana (mouse-car creas)
C.Specias: Arabidopeis thaliana (mouse-car creas)
C.Jates 18-Nay-2000 #sequence_revision 18-Nay-2000 #text_change 18-Nay-2000
C.Jacession: T51469
R.Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamiru, E.; Kotani, H.; Tabata
Namitted to the Protein Sequence Database, August 2000
A.Scension: Type: 23394
A.Scension: Type: 23394
A.Scension: Type: DNA
A.Status; preliminary
                                                           A; Gene: CC3024
Query Match
Best Local Similarity
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39	39	39	39	39	39	39	39	39	39	39	40	40	40	40	40
54.2	54.2	54.2	54.2	54.2	54.2	54.2	54.2	54.2	54.2	54.2	55.6	55.6	55.6	55.6	55.6
480	399	385	353	321	313	273	211	111	102	94	1227	404	378	373	328
N	Ŋ	N	μ,	N	N	N	N	N	N	N	N	N	N	N	N
D83086	B83398	D41732	856750	AC0821	A35699	AH2432	E71334	S25047	S06612	D89798	T49963	B84745	T49164	E84647	H87535
70		heterogeneous nuc		probable exported	-			Ig heavy chain '	chorion protein	ਨ	hypothetical prote	able RNA-k	zinc transporter-	hypothetical prote	hypothetical prot

ALIGNMENTS

A.Status: preliminary A.Nolecule type: DMA A.Nolecule type: DMA A.Residues: 1-205 <5TO> A.Residues: 1-205 <5TO> A.Cross-references: GB:AE005673; NID:gl3424664; PIDN:AAK24986.1; GSPDB:GN00148 C.Senetics:	R.Mischan, M.C., Feldblyum, T. V.; Paulsen, L.T., Felson, K.E., Eisen, J.; Heidal B.; Labb, M.T.; DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwim, M.L.; Haft, D.H. n. J., Ernolaeva, M., White, O., Salaberg, S.L.; Shapiro, L.; Vencer, J.C., Frae Proc. Natl. Acad. Sci. U.S.A. 88, 4135-4141, 2001 A; Title: Complete Genome Sequence of Caulobacter crescentus. A, Feference number: A87249, MUID:21173698, PMID:11259647 A, Accession: F87636	RESULT 2 P87623 hypothetical protein CC3024 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Sectes: Ca-log-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: P87625	Qy 3 GHGYGS8FDY 12 Db 36 GHGYGS8FFY 45	Query Match 69.4%; Score 50; DB 2 Best Local Similarity 80.0%; Pred. No. 0.84; Matches 8; Conservative 1; Mismatches	A;Molecule type: DNA A;Molecule: 1-172 <sant> A;Assiduse: 1-172 <sant> A;Cross-references: Myds;Alj9i151 A;Cross-references: Myds;Alj9i151 A;Assiduse: 1-172 <antonional assidus<="" assiduse:="" td=""></antonional></sant></sant>
:913424664; PIDN:AAK24986.1; GSPDB:GN	lleen, I.T., Nelson, K.E., Eisen, J.; R.J., Durkin, A.S., Gwinn, M.L., Hatberg, S.L., Shapiro, L., Venter, J.C. Caulobacter crescentus. 73698; PMID:11259647]] - Caulobacter crescentus nn 20-Apr-2001 #text_change 20-Apr-20		ore 50; DB 2; Length 173; ed. No. 0.84; Mismatches 1; Indels 0; Gaps	mbia; BAC clone KlOA8
00148	Heidel t, D.H ; Fras	7		0;	*

65.3**%**;

Score 47; Pred. No.

DB 2;

Length 205;

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R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E.A.; Rose, D.J.; Mau, B.; Shoo, Y. Science 71, 1453-1462, 1997
Science 727, 1453-1462, 1997
A.7tlle: The complete genome sequence of Escherichia coli K-12.
A.Reference number: A64720; MUID:97426617; PMID:9278503
A.Recession: C64757
                                                                               C:Superfamily; conserved hypothetical iron-sulfur protein HP0138; ferredoxin 2[4Fe-48] C:Reywords: $Fe-45; electron transfer; iron-sulfur protein metalloprotein F:312.315,318,372/Binding site: 4Fe-48 cluster (Cys) (covalent) #status predicted F:322,362,365,366/Binding site: 4Fe-48 cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                    A:Crose-references: GB:AB000137, GB:U00096; NID:g2367108; PIDN:AAC73410.1; PID:g1786498
A:Experimental source: etrain K-12, substrain M31655
C)Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probable iron-sulfur procesh y6gF - Escherichia coll (strain K-12)
C.Specias: Escherichia coll (c.Specias: Escherichia coll (strain K-12)
C.Date: 12-Sep-1937 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C.Date:
                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-475 < BLAT>
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A;Experimental source: strain 1021, megaphlasmid pSymal
R;Galibert, P.; Finan, T.M.; Jongs, S.; Parly
B;Galibert, P.; Finan, T.M.; Jongs, S.; Parly
B;Galibert, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fiss
L.; Hyman, R.W.; Jones, T.
L.; Hyman, R.W.; Jones, T.
Seience 293, 668-672, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Authors: Kahn, D., Kahn, M.L., Kalman, S., Keating, D.H., Kiss, E.; Komp, C.; Lelaure, hebault, P., Vandenbol, M., Vorbnier, F.J., Wadner, S., Wells, D.H., Wong, K., Yeh, K., A;Ritle: The composite genome of the legume symbiont Sincrhizobium meliloti.

A;Reference number: As503; MUD:2136624; pMID:1147404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.F.; Balloy-Habler, F.; Bowe, S.; Kallann, S.; Kesting, D.H.; Palm, C.; Peck, M.C.; Surrycki, R.; Wells, D.H.; Yeh, K.C. Poroc, Nat. Acad. Sci. U.S.A. 98, 9883-9886, 2001
A.Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melliot Ap.Reference number: A95262, MUID:21396509; EMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SMa1776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-456 <KUR>
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C.Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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                     Score 44; DB 2;
Pred. No. 21;
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Pred. No. 20;
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N.A.; Fisher, R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   V.; Riley,
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A; Gene: EC$0345
C; Superfamily: conserved hypot
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RESULT 1
A90672
hypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs0345 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs045 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs045 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs045 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs045 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs045 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs045 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs045 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs045 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs045 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs045 [imported] - Escherichia coli (strain O157:H7, subhypothetical protein ECs045 [imported] - Escherichia coli (strain
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R.Hayashi, T., Makino, K., Obnishi, M., Kurokawa, K., Ishii, K., Yokoyama, K., gasawara, N., Yasunaga, T., Khiara, S., Shiba, T., Hattori, M., Shinagawa, H. DNA Res. 8, 11-22, 2001

BY Thile: Complete genome sequence of enterophemoral Escherichia coli 0157:H7

A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: A90672

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-475 < HAY>

A;Cross-references: GB:BA000007; PIDN:BAB33768.1; PID:g13359802; A;Experimental source: strain O157:H7, substrain RIMD 0509952 GSPDB:GN00154

61.1%; 77.8%; hypothetical iron-sulfur protein HP0138; Score 44; DΒ ferredoxin

2 GGHGYGSSF 10

Conservative

1; Mismatches

Indels

0, N

Pred. No.

hypothetical protein Yopf (imported) - Escherichia coli (strain 0157;H7, substr. CiSpecies: Bacherichia coli (strain 0157;H7, substr. CiSpecies: H6-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001 CiAccesion: ESS22

Eiperna, F7, Plumiett III. G.; Burland, V.; Mau. B.; Glasner, J.D.; Rose, D.J. Riperna, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Nature 409, 529-533, 2001

A'Ille: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
A;Beference number: A85480; MUID:21074335; PMID:21206551
A;Accession: BB5222
A;Status: preliminary
A;Moleculo type: DMA.
A;Moleculo type: DMA.
A;Moleculo type: DMA.
A;Cross: references: GB:AB005174; NID:912513108; PIDN:ABG54641.1; GSPDB:A;Cross: references: GB:AB005174; NID:912513108; PIDN:ABG54641.1; GSPDB:AG05474; NID:912513108; PIDN:ABG54641; NID:912513108; NID:912513108; NID:912513108; NID:912513108; NID:912513108; NID:912513108; NID:91251 GSPDB:GN00145;

ferredoxin

61.1%;

Score 44;

2;

Length 475

2 0

Pred. No.

Mismatches BB

0

Gaps

N GCHGYGSSF 10 Conservative

GCHGYGSIY 337

hypothetical protein BH197 [imported] - Bacillus halodurans (strain C-125) C:Species: Bacillus halodurans C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C:Accession: B3924 K; Takaki, Y., Maeno, G.; Sasaki, R.; Masui, N.; FR N., Fuji

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C,Accession: T33380

R,Beck, C., Namaley, P., Keppler, N.

R,Beck, C., Namaley, P., Keppler, N.

R, Description: The sequence of C. elegans cosmid H22K11.

A,Reference number: Z21333

A,Recession: T23380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein DKP2p56650222.1 - human
C:Species: Homo eaplens (man)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-35 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 28, 4317-431, 2000
A,Tilla: Complete genome sequence Of the alkaliphilic Dacterium Bacillus halodurans and
A,Reference number: A3350, MUID:20512582; PMID:11058132
A,Accession: 293824
                                                                                      A;Introns: 35/1; 79/1; 128/1
                                                                                                            A; Map position: X
                                                                                                                              A,Gene: CESP:H22K11.3
                                                                                                                                                                                                  A;Cross-references: EMBL:AF077544; PIDN:AAC64619.1; GSPDB:GN00028; CESP:H22K11.3
                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein HZKK11.3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: adult uterus; clone DKFZp586F0222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AL117395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-215 < KOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z18722
A; Accession: T17207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the Protein Sequence Database, September 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T17207
R;Koehrer, K.; Beyel
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A;Experimental source: strain C-125
                                                                                                                                                                             A;Experimental source: strain Bristol N2; clone H22K11
                                                                                                                                                                                                                    A, Molecule type: DNA
A, Residues: 1-235 < BEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                           Query Match
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nes 7; Conservation
                     Local Similarity
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tes 7; Conserv
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   Conservative
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                     59.7%;
Score 43; DB 2; Length 235;
Pred. No. 15;
2; Mismatches 0; Indels
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Pred. No. 14;
1; Mismatches
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Pred. No. 2.2;
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Gaps
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                  submitted to the EMBL Data Library, January 1996
A,Description: The sequence of C. elegans cosmid C54D1.
A;Reference number: Z20527
                                                                                                                       hypothetical protein C54D1.3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Pate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Peb-2000
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A; Accession: T28808
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                                                                                                        C; Accession:
                                                                                      R;Minx, M.
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Choccession: 702661 R.Kim, C.Y., Theony, S.Y., Cheony, Y.H., Han, C.D., Cho, M.J. submitted to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                        A; Reference number: Z14689
A; Accession: T02661
                                                                                                                                                                                                                                                                                                                                                                       //yeophospholiyaae homolog - rice
C.Specias: OTypa aativa (Lice)
C.pate: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
                                                                                                                                                       A;Gene: LPL1
                                                                                                                                                                             C;Genetics:
                                                                                                                                                                                            A;Cross-references: EMBL:AF039531; NID:g2801535; PID:g2801536
                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-304 < KIM>
                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                              Matches
                                                                                                                 Query Match
                                                                                                 Local
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87 DGVHGYVSSLDH 98
                                     1 DGGHGYGSSFDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGHGYGSSF 10
                                                                                                 Similarity
                                                                              Conservative
                                                                                              59.7%;
                                                                           l; Mismatches
                                                                                              Score 43;
Pred. No.
                                                                                                 20,
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                                                                              3; Indels
                                                                                                                 Length 304;
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                                                                           Gaps
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A;Molecule type: DNA A;Residues: 1-390 <BEV> A;Cross-references: EMBL:AL163814 A; Accession: T48524 C.Rocession: 198524. R.Bevan, M., Hilbert, H., Braum, M., Holzer, B.; Brandt, A.; Duesterhoeft, submitted to the Protein Sequence Database, April 2000) yoophospholiyaas-like protein - Arabidopsis thaliana NyAlsenate namas; protein 72222.40 (19pacias: Arabidopsis thaliana (mouse-ear cresse) (19pacias: Arabidopsis thaliana (mouse-ear-2008) A; Note: T22P22.40 A; Map position: 5 A; Introns: 127/2; 140/2; 164/1; 185/3; 215/3; 246/3 A; Status: preliminary RESULT 12 A; Experimental source: cultivar Columbia; BAC clone T22P22 Matches Query Match Local 169 DGLHGYVPSLDY 180 1 DGGHGYGSSFDY 12 Similarity Conservative 58.3%; Score 42; DB 66.7%; Pred. No. 36; tive 0; Mismatches DB 2; Length 390; 4 ٥,

0

T28808

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A;Residues: 1-142 <DAV>
A;Cross-references: EMBL:M67445
C;Genetics:
                                                                                               A;Crosa-references: EMEL:122015; NID:g1339990; FIDN:AAC04962.1; FID:g349754; MIPS:YAR01 R.Davides, C.J.; Hutchison III, C.A. Muclaic Acids Res. 19, 5731-5738, 1991
A;Tille: A discreted DMA equencing strategy based upon Tn3 transposon mutagenesis: appl. A;Feterence number: S20121, NVID:92051323; PMID:1588741
A;Getession: S20121.
                                                                                                                                                                                                                                                                                                                                                                                                                            97002 protein - yeast (Saccharomyces cerevisiae)
N.Alternate names; protein VARD140
(:Species; Saccharomyces cerevisiae
(:)Date: 13-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 19-Apr-2002
(:Accession; 38090; $3010)
                                               A; Molecula type: DNA
A; Residues: 1-142 < DAV>
                                                                                                                                                                                                                                                                                                                                                                             C.Accession: 940904; S20121
R.Clark, M.H.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.; Zeng, B.; Delaney,
submitted to the EMBL Data Library, November 1993
                                                                                                                                                                                                                                                  A; Residues: 1-702 < CLA>
                                                                                                                                                                                                                                                                                                     A; Accession: S40904
                                                                                                                                                                                                                                                                                                                         A;Description: Sequencing of chromosome I of Saccharomyces cerevisiae: Analysis of the A;Reference number: $40891
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A;Fitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Feterone number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE002093; NID:g3763927; PIDN:AAC64307.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-492 <STO>
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C.Specise: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Feb-2001 Heequance_revision 02-Feb-2001 #text_change 02-Feb-2001
C.Pacession: Ads83
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A, Molecule type: NMA
A, Residuss: 1-1163 AMIN
A, Cross-references: EMBL/U46673; PIDM:AAC48153.1; GSPDB:GN00028; CESP;CS4D1.3
A, EXperimental source: strain Bristol NJ; clone C54D1
C) Genetics:
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Best Local S
Matches 6
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 2;
Pred. No. 1.1e+02;
0; Mismatches 3
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Rivdievezer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 179, 295-207, 1993
Apfille: Antigen-driven B cell differentiation in vivo.
A; Reference number: PH1675; MUID:33301607; PMID:3315385
A; Accession: PH1733
A; McCession: PH1733
A; McCession: PH1735
A; McCession: BH1734
A; McCession: Could be cell
A; McCession: Could be cell
A; McCession: The authors translated the codon ACA for residue 13 as Ala
A; Superismint, immunojoubulin V region; immunoglobulin homology
Search completed: November 
Job time: 4.65407 secs
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C;Species: Mus musculus (house mouse)
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A;Cross-references: SGD:S0000069
A;Map position: 1R
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Best Local :
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

protein ٠ protein search, using sw model

2

Run on:

November 7, 2003, 07:21:18; Search time 0, 855154 Seconds (without alignments) 552.278 willion cell updates/sec

Perfect score: sequence: 1 DGGHGYGSSFDY 12 US-09-661-992B-6 72

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 10 Maximum Match 100% Listing first 45 summaries

Database SwissProt_41:*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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P19192		P42790					P51992		P07183		Q9vqe5	
bacteriopha	homo sapien	pseudomonas	halophilic	bos taurus	plasmodium	Φ		xenopus lae	drosophila	schizosacch	drosophila	

ALIGNMENTS

ULT 1					
YKGF ECOLI	STANDARD;	PRT:	475 AA.		
P77536;	•				
01-NOV-1997 (F	el. 35, Created	_			
01-NOV-1997 (F	01-NOV-1997 (Rel. 35, Last sequence update)	quence u	pdate)		
15-SEP-2003 (R	el. 42, Last an	notation	update)		
Putative elect	Putative electron transport protein ykar.	rotein v	rar.		
YKGF OR B0307.	,	,			
Escherichia coli.	н.				
Bacteria; Prot	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	maproteol	bacteria	1; Enteroba	cteriales:
Enterobacteria	Enterobacteriaceae; Escherichia.	ia.			
NCBI_TaxID=562;	•				
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SEQUENCE FROM N.A.	N.A.				
STRAIN=K12 / MG1655;	G1655;				
MEDLINE=974266	MEDLINE=97426617; PubMed=9278503;	503,			
Blattner F.R.,	Plunkett G. II	I, Bloch	C.A., E	erna N.T.,	Burland V.
Riley M., Coll	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.	lasner J	.D., Roc	le C.K., Ma	vhew G.F.
Gregor J., Dav	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.	trick H.	Goed	en M.A. R	ose D.J.
Mau B., Shao Y.;	٠,				
"The complete	"The complete genome sequence of Escherichia coli K-12.";	of Esch	erichia	coli K-12.	
Science 277:14	Science 277:1453-1474(1997)				

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SEQUENCE FROM N.A. Aranjo R., Aparicio A.M., Chung E., Davis K., Duncan M., Allen B., Aranjo R., Aparicio A.M., Chung E., Davis K., Federspia M., Blunan R., Kalman S., Komp C., Kurdi O., Lee H., Lin Manath A., Oefner P., Roberts D., Stram C., Davis R.W.; Manath A., Oefner P., Roberts D., Bartis M.D. Davis R.W.; Submitted (1907-1905) to the EMEL/CombinA/DOM databases -1-SIMILARITY. THE IRON SULURE CONTERS ARE SIMILAR TO THOSE OF BACTERIAL-TYPE' 4FE-4S FERREDOXINS.

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EMBL; AE000137; AAC73410.1; -. EMBL; U73857; AAB18034.1; -. PIR; C64757; C64757.

Goodene; BG11583; /ycg. InterPro; IPRO1453; Fe.S. Binding. Ffam: PP00071; East; 2: 2. Ending. Ffam: PP00071; East; 2: 2. Ending. PR051TE; P800173; TIGE00273; 1. PR051TE; P800176; AFB4; PEREBIOXIN; 2: 2. Ending. AFB4; PEREB

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IRON-SULFUR 2 (4FE-4S)
IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
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RX MEDIJUNG-2238857, PubMed-1447932.

RA Klausner R.D. Collins F.S. Wagner L. Shemmer C.D.

RA Klausner R.D. Collins F.S. Wagner L. Shemmer C.D.

RA Altechul S. F., Zeeberg B. Buerow K.H. Scheefer C.F. Baht N.K.

RA Hopkins R.F., Jordan H., Moore T., Max S.I. Mang J. Hasch R.

RA Hopkins R.F., Jordan H., Moore T., Max S.I. Mang J. Hasch R.

RA Stapleton M., Soares M.B., Benaldo M.F. Casavant T.L. Scheer T.B.

RA Stapleton M., Soares M.B., Benaldo M.F., Casavant F.D. Mullahy S.J.

RA Richards S., Loquellano N.A., Peters G.J., Abramson B., Mullahy S.J.

RA Richards S., Hoquellano N.A., Peters G.J., Abramson B., Mullahy S.J.

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

RA Palbey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanota A.

RA Martillahon D.K., Mazny D.M., Soderyene B.J., Lu X., Gibbs R.A.,

RA Holting M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,

RA Bandillahon S. W., Vanng A.C., Shevchanko Y., Bouffard G.G.,

RA Martillahon S., Kothelm J.E., Johns S.J.M., Marta M.A.;

RA Molting M., Scheli J. E., Johns S.J.M., Marta M.A.;

RA Schelin J.E., Johns S.J.M., Marta M.A.;

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Best Local :
SEQUENCE OF 94-104 AND 288-298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The hnRNP 2H9 gene, which is involved in multiply spliced gene.";
Biochim. Biophys. Acta 1492:108-119(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning of human 219 heterogeneous nuclear ribonucleopyteins, Relation with splicing and early heat shock-induced splicing arrest.", J. Biol. Chem. 272:1827-1836(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rodil Hunax STANDARI, BPT, 346 AA.
P31942, QOSECI, QONESS, QONESS, CONTA, QONET4, QOS
01. UTL-1993 (Rel. 26, Created)
28-PES-2003 (Rel. 41, Late sequence update)
18-ESE-2003 (Rel. 42, Late amovestion update)
Heesingeneous nuclear ribonuclesprotechi H3 (Inhaye
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Submitted (SEP-1999) to the
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MEDLINE=20461765; PubMed=10858537;
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Fuchs J.-P.;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 137-346 FROM N.A.
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Primates;
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to the EMBL/GenBank/DDBJ databases.
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                           99:16899-16903 (2002)
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Pred. No. 13;
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RON-SULFUR 1 (4FE-4S) (B:
6B2429D387336F72 CRC64;
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ENGL. AF13260; ANAS319, 1;
ENGL. AF13260; ANAS3441
ENGL. AF13260; ANAS3441
ENGL. AF13260; ANAS3441
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ENGL. AF13260; ANAS3461
ENGL. AF13260; ANAS3461
ENGL. AF13260; ANAS3481
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Interry...
Ffam; PP00076; xrm; 4.
PROSITE; P800102; REM; 2.
PROSITE; P800102; REM; RNP J; FALSE NBG.
Nuclear protein; RNA-Binding; Ribonicaleoprotein; Repeat;
Nuclear protein; RNA-Binding; Ribonicaleoprotein; Repeat;
Nuclear protein; Alternative opplicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GK; P31942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:5043; HNRPH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; T17207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ++
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Electrophoresis 13:960-96(1992).

FINCTION: Involved in the splicing process and participates early heat shock-induced splicing arrest. But to their great structural variations the different isoforms may possess difficult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Microsequences of 145 proteins recorded in the two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vandekerckhove J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBOId=F31942-6; Sequence=VSP_005839, VSP_005843, VSP_005844;
IBOId=F31942-5; Sequence=VSP_005841, VSP_005843, VSP_005843;
Namec6; Synonyme=ZHSE;
IBOId=F31942-6; Sequence=VSP_005841, VSP_005842, VSP_005843, VSP_005843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoIdePi1942-1, Sequence=Displayed,
Name=2, Syncopynes2H9A,
Name=2, Syncopynes2H9A,
IsoIdePi1942-2, Sequence=VSP_005840,
Name=3, Syncopynes2H9A,
IsoIdePi1942-3, Sequence=VSP_005838,
IsoIdePi1942-3, Sequence=VSP_005838,
IsoIdePi1942-4, Sequence=VSP_005839,
IsoIdePi1942-4, Sequence=VSP_005839,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1;
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/FTId-VSP 005838.
/FTId-VSP 005838.
Missing (In isoform 4 and j
/FTId-VSP 005839.
Missing (In isoform 2).
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STPAINS-288c / AB972,
MEDLINE-5500315; PubMed-7941740;
MEDLINE-5500315; PubMed-7941740;
Delaney S., Oxel Hette B: T. B. Batton N.B., Kaback D.B., Bussey H.;
"Sequencing of chromosome I of Saccharowyces cerevisiae analysis of
the 42 Mbp SPOT-CBNI-CDCL5 region.";
Teast 10:353-431 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AWG-1992 (Rel. 23, Created)
01-FBE-1995 (Rel. 31, Last sequence update)
22-FBE-0903 (Rel. 41, Last annotation update)
Pypochetical 78.3 kDa proteil in SENN4-ADEL intergenic region.
YAKO14C ON FUNZ.
                                                                                                                                                                                                                                                                                                                                                          This SHISS-PROT entry is copyright. It is produced through a collaboration between the Saiss Institute of Bloidiformatics and the SMIG outstation between the Saiss Institute of Bloidiformatics and the SMIG outstation its the Buropens Bloidiformatics institute. There are no restrictions on its use by mon-position that the said of the said in no way use by money that the statistics and said for commercial entities requires a license agreement (see http://www.iab-sbi.ch/announce/entities requires allowers).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEDILUNE-2051323; PubWed-1559741;
Davies C.J., Hitchison C.A. III;
"A directed DNR sequencing strategy based upon Tn3 transposon mtagenesis: application to the ADE1 locus on Saccharomyces orrevialse chromosome L."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEAST
PROSITE; PS50002; SH3; 1.
Hypothetical protein; SH3 domain
DOMAIN 259 320 SH3
                                                            InterPro; IPR001452; SH3. 
Pfam; PF00018; SH3; 1. 
SMART; SM00326; SH3; 1.
                                                                                                                         GG/ GG:0005935, Cibud neck, IDA.
GG/ GG:0005934; Cibud tcb; IDA.
GG/ GG:0005934; Cibud tcb; IDA ster
GG/ GG:0000131, Crintiplant bud ster
GG/ GG:0000282, Pibud site selection;
GG/ GG:0039447; Prifilamentous growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                             EMBL; L22015; AAC04962.1; -.
EMBL; M67445; AAA34397.1; -.
                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 19:5731-5738(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-142 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YAI4_YEAST
                                                                                                                                                                                                                                 PIR; S40904; S40904.
SGD; S0000069; BUD14.

    -!- SIMILARITY: Contains 1 SH3 domain.

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RR -> HE (IN REF. 4).
F7D14C2947930E9E CRC64;
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Missing (in isoform 5 and isoform 6).
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QHRYIELFLNSTPGGGSG -> RKWCLWHTILFPKREFIK
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RESULT 4
KRHA_RABIT
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                                                                          KRHA SHEEP
                                                                                                    RESULT 5
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Q02957;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This setts-spor entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the Embla outstation - the European Bioinformatics Institute. There are no restrictions on its use by modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.iab-stb.ch/announce/or smid an enalt to license agreement (See http://www.iab-stb.ch/announce/or smid an enalt to licensessib-stb.nh/a
01-JUN-1994 (Rel. 29, Created)
                     KRHA SHEEP
Q02958;
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Fratini A., Powell B.C., Rogers G.E.;
"Sequence, expression, and evolutionary conservation of a gene
encoding a glycine/tyrosine-rich keratin-associated protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vextebrata; Bu
Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryotolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keratin; Multigene family; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; B45466; B45466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUCH AS WOOL AND HAIR CONSISTS OF MICHOPIBRILS EMBEDDED IN A RIGHT MATRIX OF OTHER PROTEINS. I.HE MATRIX PROTEINS INCLUDE THE HIGH-BULLOW AND GLYCINE/TROSHINE-RICH PROTEINS, HAVING MOLECULAR WEIGHTS OF 6-20 Kam WHEERSS HE MICHOPIBRILS COMPAIN THE HANGER, LOW-SULFUR PROTEINS (40-56 kba). DEFERMENTATIVE SHAFE KARP REOTEINS ARE FIRST EXPRESSED IN DIFFERMENTATIVE HAIR SHAFT KERATINACTIES A CONSIDERABLE DISTANCE LASOR THE PROJECTIES AND THE PROJECTION OF THE PROJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE KAP6 GLYCINE/TYROSINE-RICH TYPE II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
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P01772;
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIAUNE-93119467, PubMed-7680040;
Fratini A., Powell B.C., Rogers G.E.;
"Sequence, expression, and evolutionary conservation of a ge
encoding a glycine/tyrosine-rich keratin-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Var-vuw-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Kerattin, glycine/tyrosine-rich of hair.
KAPG-1.
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STRAIN=Merino X Dorset horn;
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NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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   heavy chain V-III region KOL.
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SUCH AS MOOL AND MAIR CONSIST OF MICHOPIERIES REBEIDED IN A RIGID
MARRIX OF OTHER ROTZINS, THE MATRIX PROTEINS INCLUSE THE HIGH-
WEIGHTS OF 6-20 KNA WHEREAS THE MICHOPIERIES CONTAIN THE LANGER,
LOM-SULFUR PROTEINS (40-56 KNA).
DIFFERENTIATION BASES THE MICHOPIERIES CONTAIN THE LANGER,
LOW-SULFUR PROTEINS (40-56 KNA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene family; Repeat; Acetylation.
0 0 0 ACETYLATION.
                                                                                                                                                                                                                                                                            GHGYGSSFDY
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                  (Rel. 01, Created)
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Pred. No.
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SMART; SM00406; IGv; 1.
PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region; 3D-s
                                                                                                                                                                                                                                                                                                                                                                GO; GO;0006955; P:immune response; NAS
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig.MC.
InterPro; IPR003966; Ig.MC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marguart M., Deisenhofer J., Huber R., Palm W.; "Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa; Chordeta; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and 1.0-A resolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=81072295; PubMed=7441755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1- SIMILARITY: Contains 1 immunoglobulin-like domain
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                                                                                                                                                                                                                                                                                                                                                                                                       GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                             2FB4; 12-JUL-89.
2IG2; 12-JUL-89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A02055; G1HUKL.
   Similarity
7; Conser
                                        126 AA;
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99
106
108
1108
                                        13718 MW;
          55.6%;
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Score 40; DB 1;
Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                          IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
                                      E4D71B52B16F8776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen-binding fragment
                    Length 126;
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    NEBULINE-1463050; PubMed-11470798;
Chappell S.A., Owens G.C., Mauro V.P.,
AS 'Leader of Ebma', a cold stress-induced meWh, mediates internal
initiation of translation with increased efficiency under condition
of mild hypothermia.",
of mild hypothermia.",
J. Biol. Chem. 276:36517-36522(2001).
                                                                                                                                                              SEQUENCE FR
STRAIN=ICR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   080086; 080080 (Rel. 38 Created)
15-JUL-1999 (Rel. 38 Last sequence update)
28-PBS-2003 (Rel. 41 Last annotation update)
Putative RNN-binding protein 3 (RNA binding motif protein
                                                                                                                                                                                                                                           Danno S., Matsuda T., Fujita J.;
"Isolation and characterization of mouse rbm3
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D11137; BAA01911.1; -.
EMBL; S56877; AAB25853.1; -.
PIR; T04310; T04310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMED outeration - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutes as long as its content is in way notified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensessb-sib.ch/se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gramene; Q07077;
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"Wolseular cloning and characterization of gravity specific
"Wolseular cloning and characterization of gravity specific
rice (Orycas astiva L.) supponsion callus ",
"J. Genet. 5-1315-481 (1921).

1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALIY IN CALLUS.
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01-OCT-1996 (Rel. 34, Last sequen
01-OCT-1996 (Rel. 34, Last annota
Gravity specific protein GSC 233.
Oryza sativa (Rice)
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007077;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDUCTION: BY GRAVITY STRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     سر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGGHGYGS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
276:36917-36922 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.6%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15563 MW; A1C302F1988AC864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                          efficiency under conditions
                                                                                                                                                                                                                                                                                                                                                                                                     Muridae;
                                                                                                                                                                                                                                                                     CDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                     Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
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SO PTT
                                                                                                                                                                                                                                                                                             Query Match
Best Local &
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WGD; WGI:1099460; Rbm3.
INCEPTO; IPRODSO4; RNA_rec_mot.
Pfam; PF0076; rrm; 1.
PROSITE; PS0076; RRN; 1.
PROSITE; PS00030; RRW; 1.
PROSITE; PS00030; RRW_RNP_1; 1.
                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SHESS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMPLO cutsaboration the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions a long as its concentral is in order to way more than the streement is not sense by and for commercial usege by and this streement is not sense to sense the sense of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB016424; BAA32060.1; -. EMBL; AY052560; AAL10707.1; -. HSSP; P09651; 1HA1.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-binding.

    -!- SIMILARITY: Contains 1 RNA recognition motif (RRM)

                                                                                                                                                                     123
                                                                                                                                                                                                                            ω
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                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                           GYGYGRSRDY 132
                                                                                                                                                                                                                                 GHGYGSSFDY
                                                                                                                                                                                                                                                                                                                                                                                                                     153 AA;
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   886
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                 55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                     16605 MW;
                                                                                                                                                                                                                                                                                        ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA-BINDING (RRM).
GLY-RICH.
                                                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                C54A66A1A9E4FF3D CRC64;
                                                                                                                                                                                                                                                                                   Mismatches
     157
                                                                                                                                                                                                                                                                                                                      DB 1; Length 153;
17;
Ä
                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
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RBM3_HUMAN P98179; 01-OCT-1996 RBM3 OR RNPL. 01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
15-587-2003 (Rel. 42, Last annotation update)
Putative RNA-binding protein 3 (RNA binding motif protein Bukaryota; Metazoa; Chordata; Mammalia; Butheria; Primates; Homo sapiens (Human). Catarrhini; Hominidae; Homo Craniata; Vertebrata; Euteleostomi; 3) (RNPL)

TREAT AA CARA RABARA RA "RBM3, a novel human gene in Xp11.23 with a putative RNA-binding domain."; Meindl A., Blechschmidt K., SEQUENCE FROM N.A. MEDLINE=96177665; PubMed=8634703; NCBI_TaxID=9606; SEQUENCE FROM N.A. Derry J.M., Kerns J.A., Francke U Genet. 4:2307-2311(1995) (OCT-1999) Rosenthal Nyakatura G., Ö the EMBL/GenBank/DDBJ databases Strom T.M., Drescher B., Menzel ٩

SEQUENCE FROM N.A.

SSUE=Placenta;

MEDLINE-2239(5); pubMed-1247932;
Strausberg R. D., Feingold E. A., Groves L. H., Derge J. G.,
Klaunner R. D., Collins F. S., Magner L., Schmenn C. M., Schmier G. D.,
Altechni S. F., Zeeberg B., Bascow K. H., Schmeter C. P., Bhan N. K.,
Hopkins R. F., Jordan H., Moore T., Max S. I., Wang J., Hsieh P.,
Dlatchenko L., Marusina K., Farmer A. A., Rubin G. M., Hong L.,
Scapecon M., Scares M. B., Bonaldo M. F., Casavant T. L., Scheetz T. S.,
Scapecon M., Scares M. B., Bonaldo M. F., Casavant T. L., Scheetz T. S.,
Benghesch M.J., Ugdin T. B., Toshiyuki S., Canninch P., Prange C.,
Behan S. M., Moran D. N., McKeeters G. J., McKennon R. D., Mullady S. J.,
Bonak S. M., McBan D. N., McKeeters G. J., McKeeters G. J.,
Kichards S., McCharley K. C., Malles S., Gurman G., Shaba N., McKeeters G. M., Willallon D. K., Multry D. M., Sodergren E. J., Lu X., Gibbs N., V.,
Villalon D. K., Multry D. M., Sodergren E. J., Lu X., Gibbs N., V.

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                        P_SYNV
RRPP_SYNV
PZ1299;
                                                                                                            STRAIN-ATCC PV-263,
MEDLINE-91021022; PubMed-2219720;
Hillman B.I., Heaton L.A., Hunter
"Structure of the gene encoding t
                                                                                                                                                                                                                                  Sonchus yellow net virus (SYNV).
Viruses; ssRNA negative-strand viruses; Mononegavirales
Rhabdoviridae; Nucleorhabdovirus.
                                                                                                                                                                                                                                                                                                                           01-MAX-1991 (Rel. 18, Created)
01-MAX-1991 (Rel. 10, Last sequence update)
02-EBB-2003 (Rel. 10, Last amockation update)
RNA polymerase alpha subunit (BC 2.7.7.48) (Nonstructural protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SMISS-PROF entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformation and the EMBL outsaforms the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions at since an its content is in our removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send on enail to licensessibs-sib.ch/se
                                                                             Virology 179:201-207(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
SMART; SM00350; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP196969; AAF06803.1; -.
EMBL; BC006825; AAH6825.1; -.
EMBL; G01859; G01859.
HSSP; P09651; 1HA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Milting M., Madan A., Young A.C., Shevblenko Y., Souffard G.G., Blakesley R. W., Touchman J.W., Green E.D., Dickeon M.C., Rodrigues A.C., Grimmood J., Schmutz J., Weyer R. M., Smailus D.E., Schmerch A., Schein J.E., Jones S.J.M., Abarra M.J., Shales U., Smailus D.E., Generation and induse DNA, sequences W., Servick M. J., Scher M. J., Scher M. J., Scher M. J., Shales U., Smailus D.E., Generation and induse DNA, sequences W., Servick M. J., Scher B. J., Weyer R. J., Scher B. J., Sc
                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                      NCBI_TaxID=11307;
                                                                                                                                                                                                                                                                                                               phosphoprotein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 300027; -.
GO; GO:0003723; F:RNA binding activity;
GO; GO:0006396; P:RNA processing; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew, HGNC:9900; RBM3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U28686; AAB17212.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                      PUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE FOLYMERASE. IT MAY EUNCTION IN TEMPLATE BINDING.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 GYGYGRSRDY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GHGYGSSFDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1HA1
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149
17170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.6%;
70.0%;
                                                                                                            encoding the M1 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹
                    nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLY-RICH. (RRM)
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91C12E2A3E32CFA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         286 AA
                                                                                                            protein of sonchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 157;
                                                                                                                           Jackson A.O.;
                                                                                                            yellow net
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                 Query Match
Best Local &
Matches
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Hypothetical SEQUENCE 2:

l protein; Complete proteome. 211 AA; 23888 MW; 91FFE8824C630327 CRC64;

114 GGHGWHTSLDH 124

N Similarity
6; Conserv

GGHGYGSSFDY 12

Conservative

54.2%;

Score 39; DB Pred. No. 34;

DB 1; Length 211;

Mismatches

Indels

0;

Gaps

0

TIGR; TP0359;

EMBL; AE001215; AAC65354.1; -. PIR; E71334; E71334.

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Science 281:375-388(1998).

Venter J.C.;

"Complete genome sequence of Treponema pallidum, the syphilis spirochete.";

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RESULT 11
Y359 TREP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                  083378;
16-0CT-2001
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Oshin M., Hickey E.K., Clayron K., Ketchum K.,
Sodergren E., Bardham J.M., McLood M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
Kodonald L., Artiach P., Bowman C., Octon M.D., Pylii C., Garland S.,
Hetch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                    MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                             Treponema pallidum.
Bacteria; Spirochaetes;
                                                                                                                                                                                                                                                                                                                              Hypothetical protein TP0359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A45350, A45350.
Transferase; RNA-directed RNA polymerase; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L32603; AAA50383.1; -. EMBL; M35689; AAA47897.1; -. PIR; A45350; A45350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SHISS-PROY entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outsu
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                      NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                       16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGGHGYG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 AA; 31775 MW;
                                                                                                                                                                                                                                                                                                                                                                        (Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                     TP0359
                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                         Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6BE6F095788B6C98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
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RESULT 12
SYPH_HUMAN
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P08247;
                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its 
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modified and this statement is not removed. Usage by and for commercial 
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fisher S.E., Ciccodicola A., Tanaka K., Curci A., Desicato S., 
D'Urso M., Craig I.W., Tender and the synappophysin locus 
"Sequence-based exon prediction around the synappophysin locus 
reveals a gene-rich area containing movel genes in human proximal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERQUENCE FROM N.A.
MEDLINE-88067797; PubMed-3120152;
Suedhof T.C., Lottspeich F., Greengard P., Mehl E., Jahn R.;
"The cDNA and derived amino acid sequences for rat and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ogscelk, T., Lafrenlere R.G., Archer B.T. III. Johnston P.A., Willard H.F., Francke U., Suedhof T.C.;
*Synaprophysin: structure of the human gene and assignment to the X chromosome in man and mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; sutele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1988 (Rel. 08, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
OKJ M 21475; -. GO: 003045; C:integral to synaptic vesicle membrane; NAS InterPro; IPR001285; Synaptophysin.
                                                                                  EMBL; X06389; CAA29686.1; -.
EMBL; U93305; AAB92358.1; -.
PIR; A35699; A35699.
                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:11506; SYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98008923; PubMed=9344658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90365048; PubMed=1975480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fomo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synaptophysin (Major synaptic vesicle protein P38)
                                                                                                                                                                                                                                                                                                                                         DOMAIN. THE CALCIUM-BINDING ACTIVITY IS THOUGHT TO BE LOCALIZED IN THE CYTOPLASHIC TAIL OF THE PROTEIN.
SIMILARITY: HIGHLY CONSERVED FROM CALTILAGENOUS FIRST TO HUMANS;
NO HANDLOGY IS GOODN TO OTHER MOYNE CALTUM-SINDING SPOTEINS. THE GUYCINE-RICH DOMAIN SHOME SIMILARITY TO TIPE I AND II CYTOSKELETAL KERALTI AND DOVINE CARTILAGE ALPHA I (II) CHAIN
SIMILARITY: MEMBER OF THE STANFOORHEISIN/SYNAPTOGREVIN CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: CHARACTERISTIC OF A TYPE OF SMALL (30-80 NM) KRUROSECRETORY VESICLES, INCLUDING PRESYNAPTIC VESICLES, BYT ALSO VESICLES OF TWANDLES UNDOENDOCKINE CELLS OF BOTH NEURONAL AND EPITHELIAL PHENOTYPE.
                                                                                                                                                                                                                                                                                                                             PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLASMA MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acids Res. 15:9607-9607(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMOHEXAMER OR HOMOTETRAMER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47:551-561(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 AA
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Query Match Best Local

Similarity

60.0%;

Conservative

1; Mismatches Pred. No. 63; Score 39,

Indels

0 Gaps

0

DB 1; Length 384;

Matches

1 DGGHGYGSSF 10

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RESULT 13
VPAP_PRVKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                 use by non-profit institutions as long as its content is in no way modified a settlement is not removed. Usage by and for commercial entities regulates a license agreement (See http://www.iab-sib.ch/announce/or send an email to licensesiab-sib.ch).
Pfam; PF02282; UL42; 2.
DNA-binding; DNA replication.
SEQUENCE 384 AA; 40305 MW;
                                                                                                                                                                                                                    This SHISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMSL outstation the Suropean Bioinformatics institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                            "Cloning, sequencing, and functional characterization of the two submaits of the pseudorables virus DNA polymerase holoenzyme: evidence for specificity of interaction.";
J. Virol. 69:2811-2818 (1959).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudorabies virus (strain Kaplan) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPAP PRVKA
P36702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0220; SYNAPTOPHYSN.
PROSITE; PS00604; SYNAPTOP; 1.
Calcium-binding; Synapse; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01284; MARVEL; 1.
                                                                                            EMBL; M94355; AAA74384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epstein A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berthomme H., Monahan S.J., Parris D.S., Jacquemont B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95222727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=33703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alphaherpesvirinae; Varicellovirus.
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                                                                    InterPro; IPR003202; UL42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                          PUNCTION: ACCESSORY SUBUNIT OF THE DNA POLYMERASE THAT ACTS TO INCHEASE THE PROCESSITUTY OF POLYMERICANITON (BY SIMILARITY). SIMILARITY: TO OTHER HERPESVIRUSES POLYMERASE ACCESSORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymerase processivity factor (Polymerase
) (UL42 homolog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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107
131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=7707503;
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130
137
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      40305 MW;
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Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEATS, GLY-RICH.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVILLEDA
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POTENTIAL.
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592289C43B12EFA7 CRC64;
          FFAC3EF0C1984936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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RESULT 15
DMP1 BOVII
ID DMP1
AC Q9513
DT 30-M3
DT 30-M3
DT 30-M3
DE Denti
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Matches 6
DMP1_BOWIN STANDARD; PKI; Jivan.

Q95120;

30-MAY-2000 (Rel. 39, Lest sequence update)

30-MAY-2000 (Rel. 39, Last sequence update)

30-MAY-2000 (Rel. 39, Last amoctation update)

Depth.maptix acidio phosphoprotein 1 precursor (Dentin matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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RB27_DROME
P48809;
01-FEB-1996
                                                                                                                      BOVIN
                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50102; RRM; 2.
PROSITE; PS00010; RRM; RNP 1; 2.
RNN-binding; Nuclear protein; Ribonucleoprotein; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Coll Biol. 116:257-269 (1992).

J. COLD Biol. 116:257-269 (1992).

HENCHION: THIS PROTEIN IS A COMPONENT OF RIBONUCLEOSOMES. COULD INSERT OF A DORBALIZING MORPHOGEN (DM) ORIGITATING IN THE GENERAL VESICLE.

J. SUBCELULLAN LOCATION: MUCLEAR AND/OR CYPOFLASMIC.

-1- SUBCELULLAN LOCATION: MUCLEAR AND/OR CYPOFLASMIC.
                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00076; rrm; 2.
SMART; SM00360; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005654; C:nucleoplasm; IDA.
GO; GO:0030529; C:ribonucleoprotein complex; IDA.
InterPro; IPR00504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X62639; CAA44505.1; -. PIR; D41732; D41732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Canton-S; TISSUE=Embryo;
MEDLINE=92112968; PubMed=1730754;
Matunis E.L., Matunis M.J., Dreyfuss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly)
Bukaryuta; Metacoa, Arthopoda; Javapoda; Insecta; Pterygota;
Meoptera, Endopterygota; Diptera; Bachycera; Miscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0004838; Hrb27C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P09651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heterogeneous nuclear ribonucleoprotein 27C (hnRNP 48) (HRP48.1).
HRB27C OR HRP48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of the major hnRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                  340
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                                                                                                                                                                                                                                            f; Conserv
                                                                                                                                                                                  GYGSGYDY 347
                                                                                                                                                                                                                GYGSSFDY 12
                                                                                                                                                                                                                                                                                                             96
385 AA;
                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                          88 RNA-BINDING (RRM) 1.
173 RNA-BINDING (RRM) 2.
41030 MW; 7543E50FA96C9D4E CRC64;
                                                                                                                                                                                                                                                           54.2%;
                                                                                                                                                                                                                                              Score 39; DB
Pred. No. 63;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.
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                                                                                                                                                                                                                                                                          Length 385;
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Query Match
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Matches
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WEDLINE-97(8)952, PubMed-9109824;

WEDLINE-97(8)952, PubMed-9109824;

WEDLINE-97(8)959, PubMed-9109824;

WEDLINE-97(8)959, PubMed-9109824;

WITCH K.L., Laberaki-O'Comnor K., Young M.F., Dixon M.J.;

WITCH G. A., WEDLING                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBU outcaction the Buropean Bioinformatics Institute. There are no restrictions in the Buropean Bioinformatics institute. There are no restrictions on the Buropean Bioinformatics institutions as long as its content is in one way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send on email to licenses@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U47636; AAB09412.1; -. Extracellular matrix; Signal
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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Mammalia; Butheria; Cetartiodacryla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovine; Bos.
NCBL_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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N-LINKED (GLCNAC. .) (POTENTIAL)
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N-LINKED (GLCNAC. .) (POTENTIAL)
CELL ATTACHMENT SITE (POTENTIAL)
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Database
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1: sp_archea:*
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Matches
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Niarman M.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Melson K.E.,
Eisen J., Heidelberg J.F., Ally M.R.K., Ohm. M. Meddon J.R.,
Potocka I., Melson M.C., Derton A., Stephens C., Phadke N.D., Ely B.,
Debey R.T., Dodden R.J., Durkin A.S., Oskin M.L., Estetty V., Berry K.,
Kolonay J.F., Smit J. Crewen M.B., Douril M., Shetty V., Berry K.,
Witherbock T., Tran K., Molf A., Vanathevan J., Emolkeva M., White O.,
Salzberg S.L., Venter J.C., Shapirun Prasen C.M.,
"Complete Genome sequence of Caulobacter Crescentus.",
Proc. Natl Aband. Sci. URS. 89:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nealpel F., Albrecht J.C., Fleckenstein B.; Weipel F., Albrecht J.C., Fleckenstein B.; was sociated rhadinovirus human herpesvirus 8: determinants of its pathogenicity?";
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Viruses; deDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinas; Rhadinovirus.
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01-JUN-2001
01-MAR-2002
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Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
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A; 153463 MW;
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63.6%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B.;
8 cloned from Kaposi's sarcoma.";
                                                                                                                                                                                                                             F10B59E380745A49 CRC64;
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                                                                                                                                            DB 12;
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                                                            2
                                                                                                                                      Length 1376;
                                                            Indels
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Matches
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Best Local
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Q98139;
01-FEB-1997
01-FEB-1997 (FrEMELICA) 02, Created)
01-FEB-1997 (FREMELICA) 02, Last sequence update)
01-MAR-2003 (FREMELICA) 23, Last amnotation update)
Major capsid procesin-1, 23, Last amnotation update)
Majorai's sarcoma-associated herpesvirus (KSHV) (Human Viruses, danmiterpesviridae; Radionovirus.
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InterPro; IPR003006; Ig_MHC.
Pfam; PF03122; Herpes MCP; 1.
PRAINTS; PR00235; HSVCReSIDMCP.
PROSITE; PS00239; IG MHC; 1.
SEQUENCE 1376 AA; 153419 MW;
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Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.,
Submitted (MAY-1997) to the RMBL/GenBank/DDBJ databases.
RMBL, U75698; AAC57106.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Russo J.J., Bolersty R.A., Chien M.-C., Chen J., Yan M., Maddalen Farry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S., "Nucleotide sequence of the Kaposi Sarcoma-associated herpesvirus (HHVS).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINES-97094384; PubMed=8939871;
MOODE P.S., Boshoff C., Weiss R.A., (
"Molecular mimicry of human cytokine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaposi's saxcoma-associated herpesvirus (KSHV) (Human herpesvirus
Viruses; deNDM viruses, Do ENA stage; Herpesviridae;
Gammaherpesvirinee, Rhadinovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A.
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J. Virol. 70:549-558(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORF 25
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01-MAY-1997
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7 (TrEMBLrel.
3 (TrEMBLrel.
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03, Last sequence update)
23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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Pred. No.
                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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E., McGeoch D.J., Chang Y.,
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                                                                            herpesvirus
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RESULT Q9GP019

ID G99019

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Best Local S
Matches 7
                                                                                                                                                                                                                                                  Olsophoj.

Ol-MAR-2001 (TrEMBLrel. 16, Created)
Ol-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Ol-ON-2002 (TrEMBLrel. 22, Last amnotation update)
Hypothetical 37, 6 kDa protein.
Txodes ricinus (castor bean tick),
Entaryota, Metazora, Hrchropoda; Chelicerata, Arachnida, Acari;
Paramitiformes; Ixodida; Ixodidae; Ixodes.
                                          TISSUE=Salivary gland,
Leboulle G., Rochez C.,
Godfroid E., Bollen A.,
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=34613;
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Submitteed (NOV-1995) to the EMBL/GenBank/DDBJ databases
EMBL; U40377, AAB08392.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-86099469; pubMed=8523568;

MODER P.S., Gao S.J., Dominguez G., Cesarman E., Lungu O.,

Knowles D.M., Carber R., Pellett P.E., WoGooch D.J., Chang Y.;

Knowles D.M., Carber R., Pellett P.E., Wo
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                  'Isolation of Ixodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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J. Virol. 70:549-558(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of herpesvirus-like DNA sequences in Kaposi's sarcoma
patients with and without HTV infection.";
N. Engl. J. Med. 33:1181-1185(1995).
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Knowles D.M., Moore P.S.;
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7; Conservative
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      ricinus salivary gland
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                                                                                    Louahed J.,
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Pred. No. 63;
2; Mismatches
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                                                                                    Rutti B.,
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Oryza satiwa (Rice), and
Oryza satiwa (Japonica cultivar-group).
Bukaryona yididhalatas, Etreptophyta, En
Spermatophyta, Magnoliophyta, Elilopeida;
Enthartoideae, Oryzeae, Oryza,
Chromatophyta, Status, Stat

Embryophyta; Tracheophyta; a; Poales; Poaceae;

NCBI_TaxID=4530,

SEQUENCE FROM N.A. SPECIES=O.sativa; STRAIN=Nipponbare; MCCombie W.R., de la Bastide M., Spiegel L.,

Nascimento

L., Balija V.,

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Ol-UN-2002 (TrEMBLrel. 21, I
Probable penicillin-binding p
CPE2140.
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ENGI, AP001393; ENBS1846.ij.
InterPro; IP8005111; PBP dimer;
InterPro; IP8001460; TramSpeptdse.

Pfam; PP003177; PBP_dimer; I.
Pfam; PP00905; TramSpeptidse; 1.
Pfam; PP00905; TramSpeptidse; 1.
Complete proteome;
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08665120 (Tremence). 21, Created)
01-UNR-2002 (Tremence). 22, Last sequence update)
01-OUT-2002 (Tremence). 22, Last sequence update)
01-OUT-2002 (Tremence). 22, Last annocation update)
Phypothetical protein.
050NBA0004A10.17 OR OSUMANO053D03.17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shinhzu 7., Ohteni K., Hirakawa H., Ohhihma K., Yamachita A.,
Shiha T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-sater.")
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Bacteria; Firmicutes; C
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RESULT OF REAL            RESULT 10
Q93WZ6
Q93WZ
ID Q93WZ
AC Q93WZ
DT 01-AH
DT 01-AH
OS Prunn
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Best Local S
Matches 7
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Best Local s
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Q925H2;
Q1-DEC-2001
           039W26 PRELIMINARY; PRT; 193 AA.
039W26.
01-DEC-2001 (TYEMBLYel. 19, Created)
01-DEC-2001 (TYEMBLYel. 19, Last sequence update)
01-OFC-2002 (TYEMBLYel. 22, Last smoothation update)
Abscisic stress ripening-like protein.
Prunus persica (Feach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-3118977; pubWed-11200294; TRatchenhoo A.V., Visconti, R.P., Shang L., Papenbrook T., Fruett N.D., Too T., Ogawa M., Awgulawitsch A.; "Overexpression of Hoxcall in differentiating bezutinocytes results in domineulation of a novel hair kerstin gene cluster and alopecia."; perelogment 118-1181-1198 (2001). Berelogment 118-1197.198 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (fremmire). 19, Created)
01-DEC-2001 (fremmire). 19, Last sequence update)
01-OCT-2002 (fremmire). 12, Last amnotation update)
Keratin-associated protein 16.9,
KETNP16-9 OR KETNP16.9.
Mus musculus (Mouse).
Mushayocat, Mesasou, Chordata, Craniata, Vertebrata, Mushayocat, Mesasou, Chordata, Craniata, Vertebrata, Mushayota, St., Mesasou, Chordata, Caniata, Caniata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SERCIES-O-sativa (jagonica cultivar-group);
Ming R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Sat
Currie J., Collutz K.,
"Rice Genomic Sequence.";
Submitted (SEP-2002) to the BMBL/GenBank/DDBJ databases
BMBL, AC191662; AMM01513.1; -.
BMBL, AC191662; AMM01513.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 348 AA; 35920 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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7; Conserv
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7, Conserv
                                                                                                                                                                                                                                                                           GGYGYGSSY 65
                                                                                                                                                                                                                                                                                                                              GGHGYGSSF 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 AA;
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8849 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    61.1%;
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Cunnius D.M., Katzenberger F., Muller S.,
g C., Dike S., O'Shaughnessy A., Palmer L.,
                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB
Pred. No. 7.9;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93936AD6E6177369 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                       11; Length 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Indels
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Q8IQE1
ID Q8IQE
AC Q8IQE
DT 01-MA
DT 01-MA
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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Q8IQE1;
Q8IQE1;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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050000 PRELIMINARY, PRT; 200 AA.
050000 OL-UN-198 (TERBILFAL 06. Created)
01-UN-199 (TERBILFAL 06. Created)
01-UN-199 (TERBILFAL 1. 22. Last amnotation update)
01-0CT-2002 (TERBILFAL 22. Last annotation update)
01-0CT-2002 (TERBILFAL 23. Cast annotation update)
                                                                                                                                                                                                                                                                                                   STRAIN-Bergieroni, TISSIE-Mescoarp, and Exocarp, Moguic-A-Mosgie D., Gomez R.-M., Fills-Lycaon B., Wholenike-A-Mosgie D., Gomez R.-M., Fills-Lycaon B., Wholenike-Cloning and Mucheckide Sequence of an Abscist Streese., Ripening-Induced (ARR)-Like Froetin From Apricot (Accession No. 193164). Gene Expression Durking Fruit Ripening-Lycaon No. 193164).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abacisic strees ripening protein homolog.
Prunus armeniaca (Apricor)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Agnoliophyta, eadicoryledons; core eudicots; Kosidae;
eurosida I, Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIM-Ov. Suncrest; TISSUE-FDAIL;
Callahan A.M., Morgens P.H., Coben R.A., Scorza R.;
Ragulation of peach gene expression in a peach/almond hybrid.";
Submitted (CCT-2000) to the RMEL/GenBank/DDBJ databases.
BRMI, AR137062; AALE6889.1;
InterPro, IIROJA456; ABA, MDS.
Pfam: PRO2496; ABA, MDS.
Pfam: PRO2496; ABA, MDS.
D00C20DB062D719F CRC64;
                                                                                                                                                                                InterPro; IPR003496; ABA WDS.
Pfam; PF02496; ABA WDS; 1.
                                                                                                                                                                                                                                    Plant Physiol. 115:1288-1288(1997)
EMBL; U93164; AAB97140.1; -.
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Callahan A.M., Morgens P.H., Coben R.A.,
"Isolation and initial characterization
during peach fruit development.";
J. Am. Soc. Hortic. Sci. 118:531-537(19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Vizidiplantae, Streptophyta, Embryophyta, Tracheobhyta, 
Spermatophyta, Magnoliophyta, eudicotyledoma; orce eudicots, Rosidae; 
eurosida I, Rosales, Rosaceae, Amygdaloideae; Prunus.
MCBL_TAXTD-3760 J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=36596;
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                                                          Similarity
8; Conserv
GGHGYGSSFDY 12
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                                                          Conservative
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                                                                                                                                                         ABA_WDS, I.
AA, 21240 MW;
                                                                              61.1%;
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Pred. No.
                                                                              Score 44; DB
Pred. No. 21;
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                                                                                                                                                         C145BAASE94C2D62 CRC64;
                                                          Mismatches
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                                                                                                      Length 200;
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(TrEMBLrel. 23, (TrEMBLrel. 23, PRELIMINARY,

Created)
Last sequence update)

PRT;

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Madhami M.D. Celiniker S.E. Holt R.A., Evens C.A., Goreyne d.D.,
RA Madhami M.B. P.G., Scherer S.E., L.E. P.M., Rockins R.A., Galle R.P.
RA Gescrye R.A., Lawis S.E., Richards S., Ashburner W., Henderson S.M.,
RA Gescrye R.A., Lawis S.E., Richards S., Ashburner W., Henderson S.M.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Enany G., Chen L.X.
RA Battandon R.C., Rogers W.H., Blace S.G., Chanpe M., Presifers M.B.
Ra Battandon R.C., Rogers W.H., Blace S.G., Chanpe M., Presifers M.
RA Battandon R.C., Rogers W.H., Blace S.G., Chanpe M., Presifers M.
RA Battandon R.C., Rogers W.H., Blace S.G., Chanpe M., Presifers M.
RA Battandon R.C., Rogers M. R., Bouck J., Brokest M., P., Fottier P.,
RA Battandon R.C., Basan D.A., Butler H., Cadise B., Center A., Chandra I.,
RA Battandon R., Doug L.E., Donne B., Battandor D., Bolchakov S.
RA Bottova D., Bocchan M.R., Bouck J., Brokestin P., Fottier P.,
RA Bottis K.C., Basan D.A., Butler H., Cadise B., Center A., Chandra I.,
RA Horlis M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Bottis K., Cabridian A.R., Garder H., Cadise B., Center A., Chandra I.,
RA Harris M.L., Harvey D., Heinan T.J., Hernandoz J.R., Houck J.,
RA Harris M.L., Harvey D., Heinan T.J., Hernandoz J.R., Houck J.,
RA Harris M.L., Harvey D., Heinan T.J., Hernandoz J.R., Houck J.,
RA Harris M.L., Harvey D., Heinan T.J., Hernandoz J.R., Houck J.,
RA Harris M.L., Harvey D., Heinan T.J., Hernandoz J.R., Houck J.,
RA Harris M.L., Harvey D., Heinan T.J., Hernandoz J.R., Houck J.,
RA Harris M.L., Harvey D., Marris M.B., Walson D.L.,
RA Harris M.L., Harvey D., Heinan T.J., Hernandoz J.R., Houck J.,
RA Harris M.L., Harvey D., Marris M.B., Walson D.L.,
RA Harris M.L., Harvey D., Marris M.B., Walson D.L.,
RA Harris M.L., Harvey D., Marris M.B., Walson D.L.,
RA Harris M.L., Harvey D., Marris M.B., Walson D.L.,
RA Harris M.L., Harvey D., Marris M.B., Walson D.L.,
RA Harris M.L., Harvey D., Marris M.B., Walson D.L.,
RA Harris M.L., Harvey D., Marris M.B., Walson D.L.,
RA Harris M.L., Harvey D., Marris M.B., Walson D.L.,

                                                                                                                                      M. Calliker S.E., Adams M.D., Krommiller B., Wan K.H., Holt E.A.,

N. Erana C.A., Gocayne J.D., Ananatides P.G., Baradon R.C., Rogers Y.

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorgett W., Doup L.E., Doyle C., Dreamek D., Farfan D.,

Breticha S., Fries E., Galle R.F., Gorg W.S., George K.A.,

Gonzalez M., Houch J., Backing R.J., Howelth D., Bowland T.J.,

Bregnan T., C. Jaki M. Munche B. M., Hoeth D., Bowland T.J.,

M. M. Carlson J.W., Munch B. M., Marken G. W., Namo J.

M. Machelo J., Paragon V., Park S., Patel. S., Pieter B.A., Namo J.

M. Pichaels J., Paragon V., Park S., Patel. S., Richards S., Sobelear F.,

M. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

M. Hillams S.M., Zavori J.S., Smith H.O., Veater J.C., Rabin G.M.,

"Sequencing of Drosophila melanogaster genome.",

u. Spintted (Mork-2001) To the SHE/Centalar/Doyl databases.
                Misra S. Croshy M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Hradecky P., Handa Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Barman B., Carlson J.W., Cellniker S.B.,
Clamp M., Dryddle R., Barmert D., Frabe B., do Groy A., Hartis N.,
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Bebydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Celniker S.E., Adams M.D.,
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                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 23, Last annotation update)
   B., Millburn G., Richter J., Russo S.,
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Best Local
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Q92YA4;
                                   01-UN-2001 (TEMBLYel. 17, Created)
01-UN-2001 (TEMBLYel. 17, Last sequence update)
01-MAR-2003 (TEMBLYel. 23, Last annotation update)
                                                                                                                     Q9CJY4
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                                                                                                                                                                                                                                                        4 HGYGSSFD 11
                                                                                                                                                                                                                                                                                                      7; Conserv
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                     PRELIMINARY;
                   protein
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61.1%; 87.5%;

Score 44; DB Pred. No. 55;

DB 16; Length 456;

1;

Mismatches

Indels

0

Gaps

0

PM1854

467 AA.

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RREAR RETAR
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01-DEC-2001 (TrEMELrel. 19, Last sequence update)
01-DEC-2001 (TrEMELrel. 19, Last amount update)
11-DEC-2001 (TrEMELREL. 20, Last amount update)
13-DEC-2001 (TrEMELREL. 20, Last amount update)
14-DEC-2001 (TrEMELREL. 20, Last amount update)
15-DEC-2001 (TrEMELREL. 20, Last amount
                                                                                                                                                                                                               REDITES-21395809, PubMed-11481432;
Barnett M.J. Fisher R.F. Jones T., Komp C., Abola A.D.,
Barnett M.J. Fisher R.F. Bowger L., Capala D., Galibbert R. Gouy J.,
Gurjal M., Honga A., Butast L., Hyman R.M., Kahn D., Kahn M.L.,
Yalman S., Keating D.H., Balm C., Beck M.C., Surryck, R.-C., Pevils R.M., Bederspiel N.A., Long S.R.;
Wallbertide sequence and predicted functions of the entire
Wallbertide sequence and predicted functions of the entire
Sincorhizoblum mebiloci psymb megaplasmid. 7.
Proc. Matl. Acad. Sci. U. S.A. 98:8803-9886 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium meliloti (Sinorhizobium meliloti)
Plasmid pSymA (megaplasmid 1)
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Submitted (MAR-2000)
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InterPro, IPR000379; Ser_estrs_eite
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 456 AA; 49502 MW; B8A67515B59DAOA CRC64;
                                                                                                                                                                      EMBL; AE007284; AAK65638.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2002)
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Pred. No. 41;
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RESULT 15
QANGE 7
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                           A& HAyashi T. Makino K. Obnishi M. Kurokawa K., Ishi K. Yubowaa K.,
A& Hida T., Tahaka M. Tabaka T., Tahaka M., Tabowaa K.,
A& Iida T., Takami H., Honda T., Sasakawa C., Ossawara M., Yasunnga T.,
A& Kihara S., Sihba T., Hattori M., Shinagowa H.,
Terodishe genome sequence of entoxohemorrhagic Bacherichia coli
T. C157;HJ and genomic comparison with a laboratoxy strain K-12.";
DNN Res. 8:11-22(2001).
TRE EMEL, JABO2501, BAB33768 J., -.
TREMEL, JABO2501, BAB33768 J., -.
THACEPTO, IPROUASO1, Ped'S ferredoxin.
THACEPTO, IPROUASO1, Ped'S ferredoxin.
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THERENE, TOROUTO1, Fed'S. THEODOXIN. 2.
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Best Local !
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MEDLINE=21156231; PubMed=11258796;
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YKGF OR Z0385 OR ECS0345.
Escherichia coli O157:H7.
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OleMAR-2002 (TrEMBLrel. 20, Created)

01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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"Complete genotic sequence of Estcurella multocida Pm70.";
Proc. Nat. Acad. Sci. U.S.A. 98:3460-3465 (2001).
BMBL, ABC06231, AAX09381.;
LinceProc. JER001450; 4Fe4S ferredoxin.
LinceProc. JER001450; 4Fe4S Estradoxin.
Pfam. EPF00177: Erst; 1.—
DIGENOVA PROMOTO TIGEO0273. 1.
TIGEO0273. TIGEO0273. 1.
PROSITES. P800198. 4Fe4S ERREBOXIN; 2.
BROSTES. P800198. 4Fe4S ERREBOXIN; 2.
BROST
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Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8X6E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
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7; Conserv
proteome
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77.8%;
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Pred. No. 56;
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                                     Query Match

Best Local Similarity

Matches 7; Conserv
                                                                           SEQUENCE
329 GGHGYGSIY 337
                   N
                  GGHGYGSSF 10
                                                                           475 AA;
                                     Conservative
                                                                           53000 MW;
                                             61.1%;
77.8%;
                                     1; Mismatches
                                              Score 44; DB
Pred. No. 57;
                                                                         F81B64DD6A1C1B0E CRC64;
                                                       DB
                                                       16; Length 475.
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Search Job tim rch completed: November time : 6.05728 secs 7, 2003, 07:34:29

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Database
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Maximum Match 10
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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A Geneseq 19Jnn03;
A Geneseq 19Jnn03;
A Geneseq 19geneseq/geneseqp-embl/AA1990.DAT;
A Geneseqp-embl/AA1992.DAT;
A Geneseqp-embl/AA1993.DAT;
A Geneseqp-
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475
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                     100%
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AAB20434
AAR97835
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Anti-PIX/FIXa anti
Anti-PIX/FIXa anti
Kaposi's sarcoma a
Kaposi's sarcoma a
E. coli growth and
Novel human diagno
Human polypeptide
Novel human diagno
Human ovarian tumo
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21	23	18	22	24	24	22	22	22	19	15	15	22	21	21	15	19	19	14	13	5	19	H	23	22	22	21	23	21	21	22	21	22	24	23	23
AAG42281	ABG67265	AAW28314	ABG02460	ABJ25324	ABJ25306	ABB63930	ABB60518	ABB68139	AAW26799	AAR56233	AAR56234	ABG19363	AAB58292	AAG09148	AAR52062	AAW58489	AAW73527	AAR38613	AAR28746	AAR52047	AAW26796	AAR05980	ABB92093	ABB71029	ABB67899	AAG10768	ABB93436	AAG10769	AAG10770	ABG02073	AAY70222	AAG78409	ABU65034		AAE27023
	Discosoma 2 fluore	~	el human d	isolate	SAC isolated antib			a melanc	Anti-gp54 MAb 48-1	125/h13		humai	Lung cancer associ	goog		Human KOL antibody	Humanised OKT3 var	chain.	cha	Heavy Chain variab	~	Somatic immunoglob	Herbicidally activ	Drosophila melanog	Drosophila melanog	,	<		idopsis		RNA-a	acid seq	secreted	gene 18 enc	Human gene 18 enco

ALIGNMENTS

RESULT 1 AAB20389

AAB20389;

21-JUN-2001 (first entry)

AAB20389 standard; Peptide; 12 AA.

Anti-FIX/FIXa antibody 193/K2 CDR3.	
Factor IX; FIX; Factor IXa; FIXa; antibody:	procoa
Factor VIII cofactor; blood coagulation disorder; haemonhilia A	rder:
haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse	tic: t
complementarity determining region, CDR.	1
Mus musculus.	
W0200119992-A2.	
22-MAR-2001.	
13-SEP-2000; 2000WO-EP08936.	
14-SEP-1999; 99AT-0001576.	
(BAXT) BAXTER AG.	
Scheiflinger F, Kerschbaumer R, Falkner F,	Dorner F;

New factor IX/factor IXa antibodies and their derivatives useful for

WPI; 2001-290358/30.

Result No.

increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis

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ARRESULT 2
ARRESULT 2
ARREADAS4
ARREADAS5
ARRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ce The present sequence is that of complementarity determining region (2) (ORM3) of the heavy chain of an antibody expressed by mouse hypothemical patch of the present of the present of the present of the invention. Such antibodies and such antibodies of the invention. Such antibodies and their derivatives (Individual chose that comprise the present CDS) activating lateral trivition (FYR) and the present CDS activating lateral trivition (FYR) and the present of the complement of the present of the complement of the complement of the present of the complement of the complement of the present of the complement                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 12; Conserv
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                                   Scheiflinger F,
                                                                                                                                                                                                                  14-SEP-1999;
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                                                                                                                              (BAXT ) BAXTER AG.
                                                                                                                                                                                                                                                                                                13-SEP-2000; 2000WO-EP08936
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                                                                                                                                                                                                                  99AT-0001576
                                   Kerschbaumer R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= VL
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Pred. No. 0.00013;
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                                   Falkner F,
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Co The present sequence is that of a single chain PV (serV) derivative of antiboly 193/EZ, comparising the heavy (WH) and light (W) chain (W variable regions of 193/EZ comparising the heavy (WH) and light (W) chain (PV) and the regions and the single regions and cloning single regions are sent and cloning single regions are such as the sent of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaposi's sarcoma associated herpesvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaposi's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New factor IX/factor IXs antibodies and their derivatives useful for increasing anidolytic activity of factor IXs, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic disthesis
                                                                                                                                                                                                                                                                                                                                                                              W09615779-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaposi's sarcoma; gamma-2 herpesvirus; KSHV; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR97835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR97835 standard; Protein; 1376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Fig 15; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-290358/30.
N-PSDB; AAF30724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diathesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 DGGHGYGSSFDY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sarcoma associated herpesvirus ORF25 product
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Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1024..1030
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Ig and MHC protein signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 72; DB 22;
Pred. No. 0.0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Herpes virus associated with Kaposi's sarcoma - also definitive DNA

WPI; 1996-268320/27

(UYCO) UNIV COLUMBIA NEW YORK

Moore PS;

21-NOV-1994; 11-APR-1995; 21-NOV-1995; 30-MAY-1996.

95US-0420235. 94US-0343101. 95WO-US15138

N-PSDB; AAT30687 Chang Y,

sequences,

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Best Local
Kaposi's sarcoma associated herpes vitus (EGNY) clone ESS (AMT16806), obdd. from a KS Lesion genomic library; includes IS complete ORFs (AMT16807-2)) named according to their herpesvirus saintri postitional homologues. The major ceptal protein (hAMP3607) the the product of ORFS (AMT16807-2) KSHV proteins and peptides may be obtd. by incorporating encoding sequences into a vector and expression in host cells. They are useful averaged to relate the second artibodies of singer the useful averaged to relate the vectors and expression artibodies of singer the useful average of the singer than the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1994;
21-NOV-1994;
11-APR-1995;
                                                                                                                                                                                                                                                                                               Claim 17; Page 188-193; 305pp; English
                                                                                                                                                                                                                                                                                                                                                            Herpes: virus DNA associated with Kaposi's sarcoma - also associated vectors and proteins, used in detection and vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT16807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-151362/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYCO ) UNIV COLUMBIA NEW YORK (GRAN/) GRANT D E. (VIEL/) VIELE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09606159-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaposi's sarcoma associated herpesvirus major capsid protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
13-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lambda chone KS5 (AMT30681) is a fragment of a newly identified gamma-2 horpewitus espociated with Kaposi's sarcoma (KS). KS5 17 open reading frames (AMT30682-9), 15 of which are complete, including ORF25 (AMT30687). The protein produces (AME97830-44, respectively) of the 17 ORF8 can be expressed in subaryotic or bacterial host cells for use as vaccines, for KS diagnosis, or i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaposi's sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                capsid protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moore PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , useful for of Kaposi's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 175-180; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0292365.
94US-0343101.
95US-0420235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US10194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSHV; lymphoma; AIDS; vaccine; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 1376 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis of and to develop prods. for sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viele L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                              Novel nucleic acids that inhibit Escherichia coli proliferation, useful for screening for homologous genes and for designing expression vectors
                                                                                                                                                                                                                   Claim 19; Page 467-468; 522pp; English
                                                                                                                                                                                                                                                                                 N-PSDB; AAH84604.
                                                                                                                                                                                                                                                                                          WPI; 2001-335933/35
                                                                                                                                                                                                                                                                                                               Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                   09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                      09-NOV-2000; 2000WO-US30950
                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli; growth; proliferation; microbial; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli growth and proliferation related protein sequence SEQ ID NO:403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 DĞĞHĞYĞLRYE 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
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                                                                                                                                                                                                                                                                                                             Ohlsen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     microorganism.
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                                                                                                                                                                                                                                                                                                             Zyskind J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475
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Pred. No.
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: Pred. No. 99; 1; Mismatches

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GCHGYGSSF

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RESULTA 6

ABG27993

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Matches 7; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID No 58352; 103pp; English
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23-AUG-2000; 2000US-0649167
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77.8%;
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Score 43; DB
Pred. No. 24;
1; Mismatches
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                                                                                   22;
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Conservative

Indels

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Query Match Best Local Similarity

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                                                                                                                                         The invention relates to an isolated polymocleotie (1) comprising a muleotide sequence selected from any 6.94 sequences (REZILIS-MEZIZO66) or their nature protein ording portion, active domain coding protein or complementary sequences. The polymocent human genome for identifying expressed genee or for physical mapping as mean genome. The encoded polymoperides (REMESISO) or mapping as many genome. The encoded polymoperides (REMESISO) or mapping and active the second of the second sequences of the sequences of the second sequences of the sequences of the second sequences of the sequences of the second
                                                                parasitic), arthritis, etc.

Note: The sequence data for this patent did not form
specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; SEQ ID NO 1685; 1012pp + Sequence Listing; English
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                                      ftp.wipo.int/pub/published_pct_sequences.
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Yang Y, Ma
T, Wang J,
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Y, Yamazaki V, Chen R,
Wang D, Drmanac RT;
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R, Wang Z,
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directly from WIPO
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diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity
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23-AUG-2000; 2000US-0649167.
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                                                                                                                               139 AA;
                                          Conservative
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                                                            59.7%;
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Pred. No.
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AAE27023
ID AAE27
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                                                                                                                                                                                                                                                                                                                               or This invention describes movel nucleic acid (cmbh) sequence (h) which the have anticancer activity and are highly expressed in overing tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (h) are used (i) for recombinant expression of polypeptides (b) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of (in its antibotics of the antipotics of the activity for treating this form of tancers of the activity and the activity of the activity for treatment of a particular antibotics (a) see sharply vectors) and (iii) for generation of specific antibotics (a) see sharply vectors) and (iii) for generation of specific antibotics (a) see sharply vectors) and (iii) for generation of specific antibotics (a) see sharply vectors) and (iii) for generation of specific antibotics as specificantly longer fragment of the same unknown gene, discorring the estimated frequency of this chart of the same unknown gene, discorring the estimated frequency of the same unknown gene, discorring the estimated frequency of the same unknown gene, discorring the estimated frequency of the same unknown gene, discorring the estimated frequency of the same unknown gene, discorring the estimated frequency of the same unknown gene, discorring the estimated frequency of the same unknown gene, discorring the estimated frequency of the same unknown gene, discorring the estimated frequency of the same than the same and the same unknown gene, discorring the section of the same unknown gene, discorring the section of the same and                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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Best Local Similarity
AAE27023 standard; Protein; 223 AA
                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mucleic acid sequences expressed in ovarian, and some other, cancer
tissues, and derived polymeptides, for treatment of ovarian cancer and
identification of therapeutic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed sequence tag; EST; human; ovarian tumor; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ovarian tumor EST fragment encoded protein 134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-2000
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                                                                                                                                                        2 GGHGYGSSFD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 GGYGYGSGF 60
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                                                                                                                                                                                                                                                                                               220
                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                        59.7%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinzmann B,
                                                                                                                                                                                                                        Score 43;
Pred. No.

    Mismatches

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                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                   2
                                                                                                                                                                                                                                          Length 220
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pilarsky C,
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Gaps 0

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Comparing the state of the stat
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(ROSE/) ROSEN C A.
(LIYY/) LI Y.
(ZENG/) EXAG Z.
(KXAM/) KYAM H.
(FISC/) FISCHER C L.
(LIHH/) LI H.
(LSOPP/) SOPET D R.
(GENT/) GENTZ R L.
(WEIY/) WEI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted polypeptides and polymoclectides for diagnosing, preventing, treating immune, hyperproliferative, cardiovascular, neurological, reproductive disorders and identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM,
Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immunodeficiency, X-linked agammaglobulinamia, septic shock; autoimmune disorder; rheumenoid arthritis multiple scloods; concer, carvers disease; disbetes mellitus, haematopoiete disorder; artoker; respiratory disorder; attemna allegy, gastroimeattual disorder; respiratory disorder; attemna allegy, gastroimeattual disorder; Parkinsor's disease; alterodegomerative disorder; mindide; particular disorder; productis; respiratory disorder; productis; respiratory disorder; particular disorder; proproductis consiliation; respiratory disorder; patter glosenlorephritis; consiliation; endocrine disorder; addisorder; ante glosenlorephritis; consiliation; endocrine disorder; addisorder; disorder; reproductive system disorder; endocrine disorder; delisorder; disorder; confidence di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 205-206; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cherapeutic use
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Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry
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, Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kyaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fischer CL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection; oorneal infection; skin sqing; food additive; preservative; tissue regeneration; tissue regeneration; immunouppressive, antiproliterative; processatic; oardiant; vasotropic; nauroprotective; nootropic; nauroprotective; antipactorial; vinoide; funglaide; ophthalmological; gene therapy; antipactorial; vinoide; funglaide; ophthalmological; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, secreted protein, autoimmine disease, hyperproliferative disorder; theumatold arthitis; neoplasm, cerebrovascular disorder; napigenesis; carebral ischaemia, cardiovascular disorder; nervous system disorder; cardiac, attention of disorder; carebral ischaemia, cardiovascular disorder; nervous system disorder; cardiac, attention of disorder disorder; cardiac, attention of disorder disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-FEB-2001; 2001US-265583P
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                                                                                                                                                                                                                                 (WEIY/
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                                                                                                                                                                                                                                                                                                                                                          KYAW/)
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                                                                                                                            MOORE P A.
YOUNG P E.
GREENE J M.
FERRIE A M.
                                                                                                                                                                                                                             LIY.
) ZENG Z.
) ZENG Z.
) XYAW H.
) FISCHER C L.
LI H.
SOMPET D R.
GENTZ R L.
) WEI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                  RUBEN S
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Pred. No.
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Ruben SM, Soppet DR, Ferrie AM;

Rosen CA, Gentz RL,

Hei Y,

Zeng Z, Ky, , Moore PA,

Kyaw H,

Young PE, Fischer CL,

er CL, Li Greene JM;

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RESULT 12
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CCC ANZ7135 Abhylásí rapresent human secreted protein fragments. The genes
CC ANZ7135 AbZ7164 rapresent human secreted protein fragments. The genes
CC ANZ7135 AbZ7164 rapresent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for gene
CC the trapy. Secreted protein sequences of the inventum are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (s.g.
CC the breast or liver), cerebrovascular disorders (e.g. carciac arrest), narvous
CC the breast or liver), cerebrovascular disorders (e.g. carciac arrest), narvous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and coular disorders (e.g. cornela infection). The
CC bolypeptides can also be used to aid wound healing and epithelial cell
CC polypeptides can also be used to aid wound healing and epithelial cell
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CC polypeptides can also be used to aid cell
CC polypeptides can also be
                                                                                                                                                                                                                                                                                            Socreted protein; immunodeficioncy; multiple sclerosis; severe combined immunodeficioncy; severe combined immunodeficioncy; replanatory controler; rheumatory condition; septic shock; inflammatory condition; septic shock; inflammatory bowal disease; corbin's disease; period shock; inflammatory bowal disease; satisfactory disorder; asthma; allergy; stroke; gastrointestinal disorder; central nervous system disorder; stellared isorder; disease; lachamic brain hijury; neurodegenerative disorder; brainfactorie; disease; cardiovasoular disorder; brainfactorie; sease; cardiovasoular disorder; brainfactorie; sease; cardiovasoular disorder; renal disorder; hyperpoliterative disorder; acute glamanionsphritis; addispris disease; paradioritis; disorder; recoller, infectious disease; paradioriticis disorder; recoller.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                          11-MAY-2001; 2001US-0852797.
                                                                               21-NOV-2002
                                                                                                                                     US2002172994-A1
                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein gene 18, protein #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU65034 standard; Protein; 223 AA
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les 7; Conserv
                                                                                                                                                                                                                                                    height; hair colour; human
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                                                                                                                                                                                                                                                                          repair; anglogenesis;
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Pred. No.
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Ferrie AM;
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05-SEP-1997
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                                                                                                                                                                              Ruben SM,
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YOUNG P E.
GREENE J M.
FERRIE A M.
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LI Y.
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                                                                                                                                                                                                         SOPPET D R.
GENTZ R L.
                                                                                                                                                                                                                     FISCHER C L
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                                                                                                                                                                                                                              ZENG Z.
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97US-048100P.
97US-048189P.
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                                                                                                                                                                             Zeng Z,
                                                                                                                                                                          Moore PA,
                                                                                                                                                                              Kyaw H,
                                                                                                                                                                         Young PE,
                                                                                                                                                                               Fischer CL,
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Greene JM; н,

Disclosure; Page 13; 209pp; English.

therapeutic use

WPI; 2003-310989/30

New human secreted polypeptides and polymucleotides for diagnosing, prognosing, preventing and treating immune, hyperproliferative, likkiney, reproductive disporders and for identifying modulators of

liver,

disorders (e.g. systemic exyphomatosus, rhousatoid arthritis, multiple oclerosis, subcimmums haemolytic ansenda, concerns a uncommume therodytic, autoimmume haemolytic ansenda, concerns expectations expected in the control of the c The invention relates to an isolated polypoptide comprising an amino acid sequence at least 934 identical to sequence of 28 bimman secreted protesins, their fragment, polypoptide domain, spitope, secreted form, variant, allalic variant, or species homologue, or the encoded sequence included in ATCC 97921 and 97922. Also included are the encoding mucheic acids, recombinant vectors, host calls, mathodise, and genes. The protesins and nucleic acids are useful for diagnosing, preventing, treating, proposing or meliorating a medical condition e.g. treating, proposing or meliorating a medical condition e.g. acids immunoceficiencies (e.g. X-linked agammaglobulinemia, B cell immunoceficiencies, severe combined numanicoeficiencies), autolimurie are useful to enhance or inhibit complement mediated cell lysis, TOT

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This invention relates to an antibody or an antigan binding associated regarders. The applications of the art Hespo antibodies include tingal contraints of the art Hespo antibodies include tingal contraints of the art Hespo antibodies include tingal contraints of a diagnostic kit for contraints of a contraint of a diagnostic kit for contraints of a contraint of a diagnostic kit for contraints of a contraint of a diagnostic kit for contraints of a contraint of a diagnostic kit for contraints of a contraint of a diagnostic kit for contraints of a contraint of a diagnostic kit for contraints of a contraint of a diagnostic kit for contraints of a contraint of a diagnostic kit for contraints of a contraint of a diagnostic kit for contraints of a contraint of a contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition useful in a composition for the treatment of infections comprises antibody comprising specified sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          estimulating wound and tissue repair, angiogenesis, and the repair of vascular or lymphatic diseases or disorders. They are also useful to prevent hair loss, to medulate mammalian characteristics such as body height, weight, hair colour, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamiae, milmerals, coffectors or other muritional components. The proteins are also useful for identifying binding partners. The present sequence represents a secreese protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NEUT-) NEUTEC PHARMA PLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of anti HSP90 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG78409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Page 46-47; SOpp; English
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the anti HSP90 antibody.
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Claim 1; Page 81; 123pp; English

Human RNA-associated proteins useful in diagnosing, treating and preventing cell proliferative, autoimmune, inflammatory and infectious

WPI; 2000-237651/20. N-PSDB; AAZ51252.

Shih Hillman JL,

Patterson

Yang

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DAM

ď Corley NC,

Bandman

Ó Guegler KJ,), Reddy R,

Gorgone GA, Azimzai Y;

Yue H, Yue H, Tang YT, Baughn MR, Lal 21-AUG-1998; 12-JAN-1999; 20-AUG-1999;

99US-0115639 98US-0097550 99WO-US19361 WO200011171-A2

(INCY-) INCYTE PHARM INC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepatitis; myelofibrosis; primary thrombocythemia; psoriasis; cancer; mixed connective tissue disease; MCTD, HIV; uveitis; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human RNA-associated protein-3 (RNAAP-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA-associated protein; RNAAP; human; clone 2263514; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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Pred. No.
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Commune tissue, it has considered as the human NMA-associated processing thinkary. It is expressed in Incyte clone 265341, derived from UTERROYDO COMMANDERS, it is expressed in Incyte clone 265341, derived from UTERROYDO COMMANDERS as expressed in Incyte clone 2654514, derived from UTERROYDO COMMANDERS as expressed in Incyte clone and infinitely and interest control of the expression of the expression of activity of RNAAD. It is used to treat cell provided and anti-microbial activity commanders in Infectious disorders, like activity of RNAAD. It is used to treat cell provided the expression or activity of RNAAD. It is used to treat cell provided the expression of activity of RNAAD. It is used to treat cell provided the expression of activity of RNAAD. It is used to treat cell to treat the expression provided the expression of activity of RNAAD. It is used to treat cell to treat the expression of activity of RNAAD. It is used to treat cell to treat the expression of activity of RNAAD. It is used to treat cell to treat the expression of activity of RNAAD. It is used to treat cell to treat cell to treat the expression of activity of RNAAD. It is used to treat cell to treat the expression of activity of RNAAD. It is used to treat cell to treat the expression of the expressi
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Matches 7; Conserv
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The invention relates to isolated polypuchectide (I) and polypeptide (II) sequences (II) is useful as hybridisation probes, polymerase chain reaction (PCN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production for (II). The polypuchectides are also used in diagnostice as expressed sequence tags for identifying expressed spaces, (II) is useful in gene therapy techniques (II) or to treat disease states involving (II) is useful for generating or the production of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polymiclectide and encoded polypoptides, useful in diagnostics, forensics, gene mapping, identification dustations responsible for generic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 32432; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #2064.
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Pred. No.
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                                                                                                                                  quantitating a polypoptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypoptide and polymocleotide sequences have applications in diagnostics, forenskie, pene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and assume cald sequences. Associolo-Associ77 represent novel human actic sequences of the invention.
Sequence
                                            Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Matches
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seq length: 2000000000
Published Applications An:

1 'ogn2 & forcodate // Dubpas/USO7 PUBCOMB. pep. *

2 'ogn2 & forcodate // Dubpas/USO7 MEW FUB .pep. *

3 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

4 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

5 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

5 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

6 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

8 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

10 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

11 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

12 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

13 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

14 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

15 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

16 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

17 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

18 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

19 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

10 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

11 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

12 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

13 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

14 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

15 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *

16 'ogn2 & forcodate // Dubpas/USO6 & FUBCOMB. pep. *
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(Without alignments)
195.799 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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55 55 55 55 55 55 55 55 55 55 55 55 55	Query Match
102 475 223 223 223 248 126 126 126 126 126 126 126 126 126 126	% Query Match Length DB
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US-10-023-386-22277 US-10-023-386-22277 US-10-023-38-21-116 US-09-03-31-116 US-09-03-31-116 US-09-03-10-116	ID
Sequence 28237, A Sequence 116, App Sequence 126, App Sequence 12, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 16, Appli S	Description

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37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37.5	36	38	38	138	38	38	38	8	38.5	9	9	39	39
51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	52.1	52.8	52.8	52.8	52.8	52.8	52.8	52.8				54.2		54.2
519	511	459	446	432	432	338	313	279	267	246	229	195	10	10	10	286	1239	620	582	558	491	428	382	307	348	657	657	657	657
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US-09-815-242-11388	US-10-227-629-5	US-10-102-806-469	-10-156-	US-09-315-355-18	US-09-919-172-9	US-10-425-586-4	US-10-425-586-3	US-10-204-887-138	US-10-425-586-7		-10-425	US-10-425-586-5	US-09-572-404B-2874	US-09-572-404B-2864	US-09-572-404B-1872	US-10-374-534-2	US-09-871-388-2	-10-156-	-10-156	US-09-770-517C-2	US-10-156-761-14939	-062-	US-10-029-180-56	US-09-036-613-7	US-10-156-761-8089	US-10-401-436-2	-10-402-067-	-402-312-	US-10-401-437-2
113		46		Sequence 18, Appl					7	σ.	B. Apr	ر.	2874	2864	18		N	Sequence 7979, Ap	μ.		1493	372	S.		80	N	N	Sequence 2, Appli	•

ALIGNMENTS

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RESULT 2
US-10-287-274-403
US-10-287-287-403
US-10-287-287-403
US-10-287-287-403
US-10-287-287-403
US-10-287-287-403
US-10-287-287-403
US-10-287-287-403
US-10-287-407-403
US-10-287-407-407
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US-10-287-407
US-10-287-4
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Publication & US/0029364

Publication & US/00294704A

APPLICANT: Penn Sharron G.

APPLICANT: Penn Sharron G.

APPLICANT: Panth, David R.

APPLICANT: Panth C.

TITLE OF INVESTICN: HUMAN GENOMS-DERIVED SINGLE EXON NUCLEIC ACID PROBES USERV

TITLE OF INVESTICN: WINDOWS ANALYSIS INO

FILE REFERENCE: ADDOICANT-2
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US-10-029-386-28297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 28297
LENGTH: 102
TYPE: PRT
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Best Local :
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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; ORGANISM: Homo sapiens
US-09-853-161-116
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US-10-287-274-403
   Query Match 59.7%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                     SEQ ID NO 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 116, Application US/09853161
Patent No. US20020076756A1
GENERAL INFORMATION:
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PRIOR APPLICATION INMER: US 09/111164
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 403
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Best Local Similarity
                                                                                                                                                                                                           SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765
PRIOT: FILING DATE: 1997-09-05
                                                                                                                                                                                                                                PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
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CURRENT FILING DATE: 2001-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
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PRIOR FILING DATE: 1998-03-12
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PRIOR APPLICATION NUMBER: 09/152,060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
                                                                                                                                           LENGTH: 2
TYPE: PRT
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PRIOR APPLICATION NUMBER: 60/048,100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/287,274
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/164415
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TILE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETY
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                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/068,368
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/048,970
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/050,934
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FILING DATE: 1997-03-14
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77.8%;
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   Score 43; DB 9; Length 223;
Pred. No. 54;
1; Mismatches 2; Indels
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Pred. No.
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Gaps
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US-09-852-797-116
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Best Local Similarity
7; Conserve
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US-09-852-659A-116
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                                                                                  APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 116
                                                                                                                                                                            Sequence 116, Application US/09852797
Patent No. US20020172994A1
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Patent No. US20020077287A1
FILE REFERENCE: PZ003P2
                                         TITLE OF INVENTION: 28 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/040,710
PRIOR ELLIMG DATE: 1997-03-14
PRIOR ELLIMG DATE: 1997-05-30
PRIOR ETLING DATE: 1997-05-30
PRIOR ETLING DATE: 1997-05-30
PRIOR ETLING DATE: 1997-05-30
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PRIOR ELICHIO DATE: 1998-09-11
PRIOR EPILATION NUMBER: PC//US98/04858
PRIOR ETLING DATE: 1998-03-12
PRIOR ETLING DATE: 1997-03-14
PRIOR ETLING DATE: 1997-03-14
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CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
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TITLE OF INVENTION: 28 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 223
TYPE: PRT
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OR FILING DATE: 1,997-06-3
OR FILING DATE: 1,997-06-3
OR FILING DATE: 1,997-05-3
OR FILING DATE: 1,997-05-3
OR FILING DATE: 1,997-05-06
OR FILING DATE: 1,997-06-06

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Pred No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ed. No. 54;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 223;
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Gaps 0;

CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT FILING DATE: 2001-05-11
FRIOR APPLICATION NUMBER: 60/265,583
FRIOR FILING DATE: 2001-02-02
FRIOR FILING DATE: 2001-02-05
FRIOR FILING DATE: 1001-09/152,060
FRIOR FILING DATE: 1098-09-11
FRIOR FILING DATE: 1098-09-11
FRIOR FILING DATE: 1098-03-12
FRIOR FILING DATE: 1098-03-12

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US-10-240-819-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR PRINCIPTION INNMESS. 66()-50,934
PRIOR PILLYG LARGE. 1940-50-304
PRIOR PRINCIPTION INNMESS. 62()-408.100
PRIOR PRINCIPTION INNMESS. 62()-408.357
PRIOR PRINCIPTION INNMESS. 62()-408.357
PRIOR PRINCIPTION INNMESS. 62()-408.359
PRIOR PRINCIPTION INNMESS. 62()-408.359
PRIOR PRINCIPTION INNMESS. 62()-408.370
PRIOR PRINCIPTION INNMESS. 62()-408.370
PRIOR PRINCIPTION INNMESS. 62()-608.368
PRIOR PRINCIPTION INNMESS. 62()-608.368
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SEQ ID NO 116
LENGTH: 223
                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10240819
Publication No. US20030180285A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                             Matches
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: GB 0008305.5
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/240,819
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION UNMEER: PCT/GB01/01195
PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANY: BURNIE, JAMES ERTER THE POLYENE OR BETA GLICAN TITLE OF INVENTION: TEXTREMENT OF FUNGAL INFECTIONS WITH FOLIENT OR STATE OF INVENTION: SYNCHESES INFINITOR NATI-FUNGALS COMMINED WITH ANTI HEPPO TITLE OF INVENTION: ANTIBODIES FILE REPERENCE: 060885/029613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION UMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Synthetic modified OTHER INFORMATION: hsp90 antibody
                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                        FEATURE:
                                                                  Local Similarity 63.6%; tes 7; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 GGHGYGGAGD 171
102 GGRDFGDSFDY 112
                                      2 GGHGYGSSFDY 12
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    Mismatches

                                                                                                      Pred. No. 60;
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                                                                                Mismatches
                                                                                                                           DB 12; Length 248;
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RESULT 7 US-09-253-794-7

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US-09-229-200A-8
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                                                                                                                                                                                Sequence 8, Application US/09229200A
Patent No. US/002009919A1
GENERAL INFORMATION:
GENERAL INFORMATION: CDA Specific Recombinant Antibody
ITILE OF INFERTION: CDA Specific Recombinant Antibody
NUMBER OF BOILDINESS: 28
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
MEDIAN OF STREET COME Oblineon & Johnson
STREET COME Schingon & Johnson Plaza
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Patent No. US20020018750A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZITY 20007-5109
COMPUTER READABLE SORM:
WEDTUM TYPE: Ploppy disk
COMPUTER: IDM COMPUTER: DESCRIPTION OF PROPERTY OF PLOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT PAPELACHION DER. 13/09/253,794
FILLE ADELICATION NUMBER: US 08/318/157
PRIOR APPLICATION NUMBER: US 08/318/157
FILLE ADELICATION NUMBER: US 08/318/157
FILLE ADELICATION MAMBER: 23.665
ATTORREY/AGRET INFORMATION:
MAMBE: SANE, Bornhard D.
MSGISTRATION MAMBER: 23.665
MSGISTRATION MAMBER: 18-665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 56
CONRESSPONDENCE ADDRESS;
ADDRESSEE: FOley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARMOUR, KAEDEYN L.
TITLE OF INVENTION: CEDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
                       ZIP. 0893-7903
COMPUTER READABLE FORM:
REDIUM TYPES: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
TELEPHONE: (202)672-5300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 DGGHGFCSS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DGGRGYGSS 9
                                                                                                                                          CITY: New Brunswick
STATE: NJ
OPERATING SYSTEM: PC-DOS
                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                      USA
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77.8%;
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Pred. No. 86;
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Query Match
Best Lccal Similarity
Matches 7; Conserve
                                                                                                             ; TYPE: amino acid TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 18: US-09-229-200A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/09229200A
Patent No. US/002099179A:
GREERAL INFORMATION:
GREERAL INFORMATION: CP4 Specific Recombinant Antibody
TITLE OF INVESTICH: CP4 Specific Recombinant Antibody
NUMBER OF SQUENCES: 28
CORRESPONDENCE ADDRESSE: JOHNSON & JOHNSON
ADDRESSE: JOHNSON & JOHNSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 126
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APPLICATION NUMBER: 18/19/229,200A
PILING DATE: 11-181-1999
CLASSIFICATION: Unbromm
ATTORNEY ARENT INFORMATION:
NAME: John N. Hallen; III
REGISTRATION NUMBER: 05/403
REFERENCE/DOCKST NUMBER: 067-948
TELECOMMOTICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                OPERATION SYSTEM: PC-DOS
OPERATION SYSTEM: PC-DOS
OPERATION SYSTEM: PC-DOS
OPERATION SYSTEM: PC-DOS
CURRENT APPLICATION NUMBER: US/09/229,200A
PPLIANO DATE: 13-JBn-1999
PILING DATE: 13-JBn-1999
                                                                                                                                                                                                                                                                           CLASSIFICATION: «ÜNKOMI)
ATTORNY/AGENT INFORMATION:
NAWE: JOHN W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET MUMBER: ORT-948
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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7; Conserv
DGGHGYGSS 9
                                                                                                                                                                                                                                                               TELEPHONE: (858) 784-3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 08933-7003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New Brunswick
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Johnson & Johnson Plaza
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TELEFAX: (908) 524-2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                   Conservative
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                                                  55.6%;
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                                Score 40; DB 9;
Pred. No. 86;
1; Mismatches

    Mismatches

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Pred. No. 86;
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US-10-422-09-10
Sequence 10 Application US/10422049
Publication No. US2003019967981
GENERAL INFORMATION:
APPLICANT: Addit, John Robert
APPLICANT: Addit, John Robert
APPLICANT: Bentage, John Spencer
TITRE BENTAGE FILING DATE: 199-00-12
PRIOR APPLICANTION NUMBER: US/09/267, 281
PRIOR APPLICANTION NUMBER: 08/456, 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-795-515-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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Best Local Similarity
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Publication No. US20030039645A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (215) 568-343
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DOTECN YATKO
REGISTRATION MUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TREFERENCE/LOCKET OF ALTON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC TOOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION MOMBER: US/09/795,515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS;
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645Alris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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Pred. No.
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Mismatches
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RESULT 13
US-09-925-302-630
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US-10-422-049-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-267-286A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-267-286A-11
                                                                                                                                      Sequence 630, Application US/09925302 Fatent No. US20020044941A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10267286A Publication No. US20030108548A1 GENERAL INFORMATION:
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LENGTH: 126
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LENGTH: 126
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APPLICANT: Rosen et al.
TITLE DG INVERTION: Nucleic Acids, Probeins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001.08-10.
FRIOR APPLICATION NUMBER: DCT/USON/05918
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REPRENCE: **CD17*:004USCI
CURRENT REFLICATION NUMBER: US/10/267,286A
CURRENT RILINO MATE: 2003-01-28
PRIOR REPLICATION NUMBER: 08/557,050
PRIOR RILING DATE: 139-10-07/854/06198
PRIOR REPLICATION MOMBER: E07/854/06198
PRIOR REPLICATION MOMBER: E07/854/06198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BUTVIN, BOERT A.
APPLICANT: BUTVIN, BOERT A.
APPLICANT: BUTVIN, BOERT A.
APPLICANT: OLIVIFE, LINDA K.
APPLICANT: OLIVIFE, LINDA K.
TITLE OF INVENTION: MOTHOUS AND MATERIALS FOR MODULATION OF THE
TITLE OF INVENTION: IMMISSIEPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
TITLE OF INVENTION: ANTIBOLIES
TITLE OF INVENTION: ANTIBOLIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICE FILING DATE: 1995-06-01
PRICE RPILCHON NUMBER: 08/373,882
PRICE FILING DATE: 1995-01-17
PRICE APPLICHICAN NUMBER: 07/920,378
PRICE FILING DATE: 1992-09-28
PRICE FILING DATE: 1992-09-28
OPTWARE: PACHATIN Vo.S: 20
OPTWARE: 1982-011 Vo.S: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 08/070,116
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                           99 DGGHGFCSS 107
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                                                                                                                                                                                                                                                                                                                                                     1 DGGHGYGSS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DOGHGYGSS 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%;
Similarity 77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        77.8%;

    Mismatches

    Mismatches

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Pred. No. 86;
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Pred. No. 86;
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                                                                                                                                                                                                                                                                                                                                                                                                  0;
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PILE REFERENCE

CHEENT APELICATION NUMBER: US/09/738,626

CHEENT APELICATION NUMBER: US/99/37484

PRIOR PILLAN DAME: 2000.12-18

PRIOR PILLAN DAME: 109/13/7484

PRIOR PILLAN DAME: 109/13/7484

PRIOR PILLAN DAME: 109/13/7484

PRIOR PILLAN DAME: 109/13/7484

PRIOR PILLAN DAME: 2000.4-07

PRIOR PILLAN DAME: 2000.04-07

PRIOR PILLAN DAME: 2000.
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US-09-925-302-630
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PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ 1D NOS: 895
SOFTWARE: Patentin Ver. 2.0
SEQ 1D NO 630
LEMETE: 5
                                                                                                                                            Matches
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Publication No. US20020197605A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                       ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 295
282 DĞĞDĞĞĞFDFDF 293
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                                                                      1 DGGHGYGSSFDY 12
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YOKOI, HARUHIKO
TATBISHI, NAOKO
SENCH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIZOGUCHI,
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                                                                                                                                       Conservative
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                                                                                                                                       1; Mismatches
                                                                                                                                                                                Score 39; DB 10; Length 295;
Pred. No. 2.8e+02;
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Pred. No. 1.1e+02;
                                                                                                                                            4.
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Sequence 1. Application US/0950368

Patent No. US/020061580A1

APPLICANT Genemor International, Inc.
TITUS OF INVENTION: Alpha/beta Hydrolase-Fold Enzymes
FILE REFERENCE: GS:11-FCT
CURRENT APPLICATION (MORBER: US/09/950,368
CURRENT FILING DATE: 2001.09-10
PRIOR APPLICATION (MORBER: 09/35),666

RESULT 15 US-09-950-368-1

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PRIOR FILING DATE: 1999-07-20

NUMBER OF SEX LN UNG: 1999-07

SEQ LN UNG: 1999-07

SEQ TO NO. 1

LENGTH: 657

TYPE: PRI

ORGANISM: Bacillus

US-09-960-368-1

Query Match Similarity 66.7%; Pred. No. 6e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 469 GRIGGESF 10

DB 469 GRIGGESF 17

Search completed: November 7, 2003, 08:16:50
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Scoring table: Sequence:

BLOSUM62

Title: Perfect score:

US-09-661-992B-6 72

ş

protein

Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 20, Appl Sequence 20, Appl Sequence 2, Appl Sequence 2, Appl Sequence 10, Appl Sequence 2, Appl Sequence 3, Appl Sequence 3, Appl Sequence 10, Appl Sequence 11, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein search, using sw model
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1 /ggn2 6/ptcdate/l/iaa/5h. COMB.psp;
2 /ggn2 6/ptcdate/l/iaa/5h.COMB.psp;
3 /ggn2 6/ptcdate/l/iaa/5h.COMB.psp;
4 /ggn2 6/ptcdate/l/iaa/6h.COMB.psp;
5 /ggn2 6/ptcdate/l/iaa/6h.COMB.psp;
5 /ggn2 6/ptcdate/l/iaa/bCTUS.COMB.psp;
6 /ggn2 6/ptcdate/l/iaa/bCTUS.COMB.psp;
7 /ggn2 6/ptcdate/l/iaa/bCTUS.COMB.psp;
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                        US-08-33-101A-18
US-09-13-68-18
US-09-13-68-18
US-09-19-68-18
US-08-573-624-3
US-08-73-624-3
US-08-73-634-3
US-08-73-634-3
US-08-73-634-3
US-08-73-634-3
US-08-73-74-11
US-08-622-538-50
US-08-73-631-74-11
US-08-622-538-70
US-08-73-631-74-18
US-08-73-74-18
US-
                                                                                              US-09-252-991A-24590
                                                                    Sequence 18, Appl
Sequence 18, Appl
Sequence 3, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 19, App
Sequence
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Patent No. S880759

GENERAL INFORMATION:
APPLICANT: Moore, Patrick S.
APPLICANT: Moore, Patrick S.
APPLICANT: Moore, Thique Associated Kaposi's Sarcoma APPLICANT SERVICOS UNIQUE Associated Kaposi's Sarcoma APPLICANT SERVICOS UNIQUE ASSOCIATED APPLICANT SERVICOS UNIQUE NO APPLICANT SERVICOS UNIQ
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US-08-343-101A-18
        Query Match
Best Local Similarity
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SEQUENCE CHARGE SEQ 1D NO.
SEQUENCE CHARGERERISTICS.
LENGTH: 861 emils acide
TYPE: emino acide
STRANDENDENSS: esngle
FORDOGY: The threat
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CLASSIFICATION: 514
ATTONNEY/AGRIT INFORMATION:
NAME: White Bed, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION INFORMATION:
TELEPROME: 21,212-78-9400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
ZIP: 10036
COMPUTER REALDANGE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
OMERATING SYSTEM: PC-DOS/MS-DOS
OMERATING SYSTEM: PC-DOS/MS-DOS
OMERATING SYSTEM: PC-DOS/MS-DOS
OMERATING SYSTEM: DC-DOS/MS-DOS
OMERATING SYSTEM: DC-DOS
OMERATING
OMERATING SYSTEM: DC-DOS
OMERATING SYSTE
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ANTI-SENSE: N
FEATURE:
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ADDRESSEE: Cooper &
                                                                                                                                                                                                                     NAME/KEY: Peptide
LOCATION: 1.861
OTHER INFORMATION:
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CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 861 amino acids
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1185 Avenue of the Americas
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US-08-733-674-29
US-08-733-674-29
US-09-525-2911-2096
US-09-525-2911-2096
US-09-515-61-474-10
US-09-515-61-474-20
US-09-517-310-2
US-09-517-312-2
US-09-517-312-2
US-09-517-315-2
US-09-517-315-2
US-09-518-35A-2
US-09-518-35A-2
US-09-594-922A-10
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Matches

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US-09-519-489-18
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                      ; Sequence 18, Application US/09519489; Patent No. 6500663; GENERAL INFORMATION:
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US-09-183-688-18
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TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036
COMPUTER READABLE FORM.
MEDIUM TYPES: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SISTEM: PC-1005/NS-1008
SOFTWARE: FarculIN Release #1.24
CURRENT APPL/CATION DATA
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           APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 861 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chang, Yuan
APPLICANT: Moore, Patrick S.
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                                                                                                                                                                                Local Similarity 
hes 7; Conserv
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1185 A
                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
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Y: U.S.A.
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1185 Avenue of the Americas
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Pred. No. 32;
2; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Sequence 3, Application US/08420235B
Patent No. 5801042
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CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/09/519,489
FILIGO DATE:
                                                                                                                                                                                                GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 861 amino acids
                                                                    MERAL INFOGUENCE:
APPLICANT: Chang Yuan
APPLICANT: MOOTE, PERLICK S.
TITLE OF INVESTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVESTION: SEQUENCES AND USES THEREOF

THE OF INVESTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P
REGISTRATION NUMBER: 28,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CITY: New York
STATE: New York
COUNTRY: U.S.A.
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TELEPHONE: 212-278-0400
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TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma
TITLE OF INVENTION: VII: Sequences And Uses Thereof
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
mes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1.861
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Peptide
LOCATION: 1.861
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468 DGGHGYGLRYB 478
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                                                      E: Cooper & Dunham LLP
1185 Avenue of the Americas
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1185 Avenue of the Americas
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Pred. No. 32;
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; LENGTH, 1376
; TYPE: PRT
; OTCHEN TENT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-08-793-624-3
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Sequence 3. Application PC/TUS9510194
GENERAL INCOMPATION.
APPLICANT: The Trustees of Columbia University in the City of APPLICANT: City.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THERROP
NUMBER OF SEQUENCES. 4.
CORRESPONDENCE ADDRESS:
ADDRESSES: Cooper & Dunham Lip
STEERT: 115 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPHICANT: (Chang. Yuan
APPLICANT: Norse: Patrick 8.
TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma Virus Sequences And
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 45185-C-PCT-18/JFFM
CURRENT APPLICATION HOMSER: US/08/793,624C
CURRENT FILING DATE: 1997-02-18
SUPPRINE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.25 CURRENT APPLICATION DATA:
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45
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Local Similarity 63.6%;
nes 7; Conservative
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GY: linear
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                                                                                                                                                       The Trustees of Columbia University in the City of New York
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Pred. No. 50;
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Pred. No. 50;
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JS-09-152-060-116
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US-09-152-060-116
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                                               SOPTWARE: PatentIn Ver.
SEQ ID NO 116
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6448230
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CURRENT APPLICATION UNMERS: US/09/152,060
CURRENT FILING DATE: 1998.09-11
ENALIER APPLICATION UNMERS: PCT/US98/04858
ENALIER FILING DATE: 1998-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 7; Conserv
                                                                                                               NUMBER OF SEQ ID NOS: 118
                                                                                                                               BRATLER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION WIMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER FILING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
            ORGANISM: Homo sapiens
                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/057,765
EARLIER FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/040,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                         SARLIER FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/050,934
                                                                                                                                                                                                                                                                                                                                     ARLIER FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                        ARLIER APPLICATION NUMBER: 60/048,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-C-PCT/JEW/MSC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/10194 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476 DGGHGYGLRYE 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09152060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.3%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Query Match
Best Local Similarity
Watches 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-19311
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GENERAL IMPORMATION;

GENERAL INFORMATION;

MADELICANT: MARC J; Rubenfield et all

TITLE OF INVENTION HOLERIC ACID AND ANIXO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: ADVIS 1.52

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

FRIOR APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US/09/252,991A

PRIOR FILING ANTE: 1995-02-18

PRIOR FILING ANTE: 1995-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GUILD,
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                         COMPUTER READABLE FORM:
WEDLIM TYPE: PLOPPY disk
COMPUTER: HE 900/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
FCASSIFICATION: 53
FCLECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 293-7860
TELEFAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephe
APPLICANT: REES, Anthor
APPLICANT: ROGUSKA, Michae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States
ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2100 Pens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pensylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 DGGQGHGVGFD 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DGGHGYGSSFD 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 63. 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michael A.
Braydon C.
SURFACE RESIDUE VENEERING OF RODENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.3%;
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anthony R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 4; Length 328;
Pred. No. 65;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 4; Length 223;
Pred. No. 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                         / MOLECULE TYPE: peptide
US-07-942-245-33
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US-07-942-245-33
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                                                                           Query Match 55.6%; Score 40; DB Best Local Similarity 77.8%; Pred. No. 49;
                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 77.1
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 563964
                                                                                                                                                                                                TELEX: 6491103
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROGUSKA,
APPLICANT: GUILL,
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 6491103
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                           CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 293-7060
TELECAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2100 Pens
CITY: Washington
                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                  LENGTH: 125 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sughrue, Mion, Zinn, I
STREET: 2100 Pensylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33,
99 DGGHGFCSS 107
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                               1 DGGHGYGSS 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D.C.
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROGUSKA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEDERSEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stephen M.J.
Stephen M.J.
Anthony R.
Michael A.
Braydon C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SURFACE RESIDUE VENEERING OF RODENT ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18:

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zinn, Macpeak & Seas
Avenue, N.W.
                                                                                       DB 1; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 117;
                                                          0;
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                                                          Gaps
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; Sequence 8, Application US/08107669D ; Patent No. 5766886 ; GENERAL INFORMATION:

US-08-107-669D-8

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RESULT 12
US-08-472-788A-8
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Best Local Similarity
Thes 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) MOLECULE TYPE: protein US-08-107-669D-8
                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08472788A Patent No. 5770196
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Studni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
        COMPUTER READRAGE FORM:
WEDITH TYPE: Floppy disk
COMPUTER: IBM PO compatible
COMPUTER: IBM PO compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Rolease #1.0, Version #1.25
CUREARY APPLICATION DATA
APPLICATION INDEER: US/06/472,788A
FILIAR DATE: U7-JWM-1956
FILIAR DATE: U7-JWM-1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
TOPOLOGY: lin-
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202/371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                STREET: 1100 New
CITY: Washington
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/01
FILING DATE: 13-AUG-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Michele A. Cimbala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                    E: Sterne, Kessler, Goldstein and Fox P.L.L.C.
1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                  USA
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1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                         Studnicka, Gary M.
VENTION: Modified Antibody Variable Domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 49;
1; Mismatches
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RESULT 13
US-08-477-531B-8
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Matches 7; Conserv
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,
                                                                              FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 13-DEC-1991
                                                                                                                                      APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
                                                                                                                                                                                                          CLASSIFICATION: 436
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 14-DEC-
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CITY: Washington
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TOPOLOGY:
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REFERENCE/DOCKET NUMBER: 0610.1000003
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REGISTRATION NUMBER: 33,
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1100 New York Ave., N.W., Suite 600
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77.8%;
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                 0610.1000004/MAC
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Pred. No. 49;
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RESULT 15
US-08-08-842A-8
US-08-08-842A-8
Sequence 6, Application US/08082842A
Ratent No. 5869619
Fatent No. 5876100:
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TOPOLECULE TYPE: protein
US-08-477-531B-8
                                                                                                                                                                                                                                                                 US-08-303-569B-10
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: . US/08/303,569B
FILING DATE: 07-SEP-1994
CLASSIFICATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION: NAME: Trujillo botton fatko
REGISTRATION NUMBER: . 15,719
REGERRACE/DOCKET NUMBER: . CARP-0032
TRLCOMMUTICATION INFORMATION: TRUBERS . 1212:35 66-3100
TRUBERS . 1212:35 66-3100
TRUBERS . 100, 200 100; 101:
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Best Local Similarity
Matches 7; Conserv
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COMPTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: MEDIUM TYPE: MEDIUM TYPE:
CURRENT APPICAL TOWN MUNBER: US/08/303,569B
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                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Adair, John R.
APPLICANT: Abrai, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: humaised Antibodies
HOMBER OF SEQUENCES: 31
CORRESTONDENCE ADDRESS: BALLETTY PROBLEM (ATT Machiewicz & No. 5859205ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
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99 DGGHGFCSS 107
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amino acid
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Pred. No. 49;
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Pred. No.
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Search completed: November 7, 2003, 07:30:06 Job time: 2.76235 secs

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US-08-082-842A-8
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Best Local
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RECOR ADPLICATION AND CONTROL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
NOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
LENGTH: 126 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20005-3934

COMPUTER READMALE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIN PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOPTHABE: PC-EDCS/MS-DCS
SOPTHABE: PC-EDCS/MS-DCS
SOPTHABE: PS-EDCS/MS-DCS
APPLICATION NOMESE: US/08/082,842A
PILIMO DATE: JS-UN-1938
CIACUTE PARTS: JS-UN-1938
CIACUTE PARTS: JS-UN-1938
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TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202/371-2540
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STATE: D.C.
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99 DGGHGFCSS 107
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7; Conserv
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77.8%;
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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439	445.5	446.5	152	459	466	469.5	472	481	484	487.5	492.5	492.5	500.5	504	504.5	504.5	508	508.5	511	514	522	523.5	525.5	529	533	535	543.5	543.5	
68.0	69.0		70.0	71.1	72.1	72.7	73.1	74.5	74.9		76.2			78.0	78.1	78.1	78.6	78.7	79.1		80.8		81.3			82.8	84.1		
105	93	120	99	105	114	101	105	119	105	114	118	114	120	119	139	115	124	115	117	113	136	109	118	117	118	119	146	120	
ν	N	N	N	N	N	N	N	N	ν	N	N	N	N	Ν	N	Ν	N	N	N	2	N	2	N	ы	N	N	4	N	:
S24763	C24672	S26789	\$26326	\$24766	PL0256	D24672	824764	B32530	\$24765	C32967	A32530	D32967	S19963	H45722	PH1225	\$19965	PH1404	819968	S32187	B36259	\$35759	826325	S37204	S32190	S19967	A53285	\$33905	B42848	***************************************
Ig	d .	d,	ď	Ę,	ij,	ij,	ij,	ğ	Ę,	Į,	i,	ij,	ij	ant	ų,	H.	ğ	ij	ij	Ĭġ	뫔	ğ	ğ	ij	ij	ij	Į.	91	;
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45	44	43	42	41	40	39	8	37	36	35	34	33	32	31	30
367	367	367.5	370.5	377	382	382.5	386.5	390	393	396	400	411	423	433	435
56.8	56.8	56.9	57.4	58.4	59.1	59.2	59.8	60.4	60.8	61.3	61.9	63′.6	65.5	67.0	67.3
126	119	136	469	122	98	118	135	160	98	98	117	102	134	142	131
ю	N	N	N	N	N	N	Ŋ	N	N	N	N	N	N	N	N
144151	\$20640	S31600	S37483	S36271	H34964	S36265	S49530	PL0105	\$46460	A49051	S18554	C32530	S21916	S19245	S26792
Ig heavy	Ig heavy	heavy	gamma	heavy	heavy	heavy			Ig heavy	Ig heavy	Ig heavy	Ig heavy	Ig heavy	Ig heavy	Ig heavy
chain V r	chain V r	chain V r	-2a chain	chain V r	chain V-I	chain V x	ntibody V	erythrocy	chain V r	chain V7	chain V r	chain V r	chain V r	chain pre	chain V r

ALIGNMENTS

RESULT 1 B42848

Lis mub heavy chain V region - mouse (fragmont)
ClSpecies: Mus musculus (Douse mouse)
ClDate: 27-Apr.1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
ClAccesion: B42848; 33390;
KFell, H.F.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Narken, J.S.,
U. Biol. Chem. 27, 15525-1558, 1992
A.Fitle: Chimeric & anti-tumor antibody. Genomic construction, expression, and callectence number: A2648; MUID:92348410, PMID:1639794
A.Faccession: B42848

PID:g195066 NCBIP:109961)

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RESULT 2
833905

13 heavy hain precursor V region - synthetic
C;Beels: synthetic
C;Beels: 13-Jan-1998 Heavt_change 20-Oct-2000
C;Dete: 13-Jan-1998 Heavt_change 20-Oct-2000
C;Dete: 13-Jan-1998 Heavt_change 20-Oct-2000
C;Dete: 13-Jan-1998 Heavt_change 20-Oct-2000
E;Decession: 333905 R. J. Hollsterom, K.B.; Murray Jr., E.D.; Chang, C.P.; Hell
Froc Nath. Acad. Set. U.S.A. 64, 3359-349, 1987
Froc Nath. Acad. Set. U.S.A. 64, 3359-349, 1987
A;Title: Chimark compuse humbar 1001 and thody that can mediate lysis of cancer cells
A;Title: Chimark compuse humbar 1001 and thody that can mediate lysis of cancer cells
A;Title: Chimark compuse humbar 2001 and thody that
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A;Cross-references: RMBI;M90691
C;Superfamily; immunoglobulin V region; immunoglobulin homology
F;15-99/Domain: immunoglobulin homology <IVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type; DMA
A;Cross-references; GB:M900590; NID:g195065; PIDN:AAA33146.1;
A;Cross-references; GB:M900590; NID:g195065; PIDN:AAA33146.1;
A;Molecule type; MAAA
A;Molecule type; MAAA
A;Molecule type; MAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QIQLVQSGPELKKPGETVXISCKASGYTFTNYGMNWVKQAPGKGLKMMGWINTYTGQPTY
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RESULT 1

AS2385

13 pheny chain V and J regions, monoclonal antibody SCET.M8.1 - mouse (fragment)
Classcies; Was musculius (house mouse)
Clate: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
Clacesion.453186
Research.J. Minuseva. 6: Ferro. T.; Naito, M.; Kurosewa, Y.
MOL. Immurol. 28, 1063-1072, 1991
MOL. Immurol. 28, 1063-1072, 1991
MOL. Thereofore the review of monoclonal anti-steroid antibodies: prime
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A;Reference number: A5285; MVID:92017897; PMID:1922102
A;Recession: A5286
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-119 <83M9
A;Conss-references: GB:D12736; NID:g220595; PIDN:BAA02228.1; PID:g220596
A;Cross-references: GB:D12736; NID:g220596; PIDN:BAA02228.1; PID:g220596
A;Cross-references: GB:D12736; NID:g220596; PIDN:BAA02228.1; PID:g220596
A;Cross-references: GB:D12736; PID:g220596; PIDN:BAA02228.1; PID:g220596
A;Cross-references: GB:D12736; PIDN:g220596
A;Cross-references: GB:D12736; PIDN:g220596
A;Cross-references: GB:D12736; PIDN:g22059
A;Cross-veferences: BWBL:X65090
C;Saperfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;12-95/Domain: immunoglobulin homology <1Mel>
                                                                                                                                                                                                                                               RiWeissenhorn, W.; Biethnueller, G.; Weiss, E.M.; Rieber, E.P. submitted to the BML Data Library, March 1992.
A. Description: Structural characterization of CD4 mab.
A. Pederence number: 81963
A. Pederence number: 81963
                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-118 < WEI>
                                                                                                                                                                                                              A;Status: preliminary
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C:Speciae: Nw musculiat (house mouse)
C:Date: 06-789-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: 51967)
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A; Residues: 1-146 <LIU>
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C;Superfamily: immunoglobulin V-region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IM40
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A; Accession: $37204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 99
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119 60

QIQLVQSGPELKKPGETVKISCKASGYTFIDYSMHWVKQVPGKGLKWMGWINTETGEAKY EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 99;

Conservative

7,

Mismatches

Similarity

81.3%; 83.2%;

Score 525.5; DB 2 Pred. No. 6.7e-39;

DB 2;

Length 118;

1

Gaps

1-118 <FIS>

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Ig heavy chain V region - mouse
CiBpace: 19-Mar-1997 #Bequence_revision 19-Mar-1997 #text_change 20-Jun-2000
CiDaces 19-Mar-1999 #Bequence_revision 19-Mar-1997 #text_change 20-Jun-2000
CiDacession 537204
Riffscher, R.; Voss, A.; Hunziker, M.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1999.
A.;Description, Production and cloning of TMV-specific monoclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Readduag: 1-117 -1721.
A;Cross-references: EMEL:770098; NID:9288258; PIDN:CAA49702.1; PID:9288259
A;Cross-references: EMEL:770098; NID:9288258; PIDN:CAA49702.1; PID:9288259
C;Super:Emily: immunoglobulin tomology
F;15-98/Domain: immunoglobulin homology <17945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig beavy chain V region - mouse (fragment)
C:Species: Mas musculus (house mouse)
C:Date: 06-Peb-1995 #sequence_revision 06-Peb-1995 #text_change 21-Jan-2000
C;Accession: 832190
R;Azui, 8.
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                                                                                                                                                                                            RESULT 6
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A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, February 1993
A;Reference number: S32185
A;Accession: S32190
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                               97;
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                                                                                                                                                                                                                                                         ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCARWITT--AFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                    QIQLVQSGPELKKPGETVKISCKASGYTFTTYGMSWMKQAPGKGLKWMGWINTYSGVPTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKGRFAFSLETSASAFLLINNLKNEDTATÝFĆTRAFÝDYDGAWFPÝWGQGTLÝTVSA 118
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Pred. No. 3.3e-39
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Pred. No. 1.5e-39;
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RESULT 9
     Ig heavy chain V region C; Species: Mus musculus
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Al,Cross-references: BMDLX72796; NID:9312496; PIDM:CNA51316.1; PID:9312497
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology (FMO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the BMBL Data Library, May A.Reference number: S35759 A.Retesion: S35759 A.Retaus: pprintininary A.Rolecule type: mRNA Nolecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BHI9D10 protein - mouse (fragment)
C.Species: Mas musculus (house mouse)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C.Paccession: 835759
R.Froyen, G.F.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W. Exp. Med. 174, 611-624, 1991
W. Tarp. Med. 174, 611-624, 1991
A.FRICHE: Antibodies that are specific for a single amino acid interchange in a protein
A.FRICHESSION: 286309; MUID:91341421; PMID:1908510
A.FRICHESSION: 286328
A.FRICHE: PREINIANY
A.FRICHESSION: AREA
A.FRICHESSION: AREA
A.FRICHESSION: AREA
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C.Superfamily. immunoglobulin v.region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lg heavy chain V region - mouse
C:Species: Was musculus (bouse mouse)
C:Pate: 11-7an-1995 #sequence_revision 13-7an-1995 #text_change 20-7un-2000
C:Pate: 13-7an-1995 #sequence_revision 13-7an-1995 #text_change 20-7un-2000
C:Pate:8sion: 2815215
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Best Local S
Matches 98
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Best Local :
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                                                                                                                                                   118
                                                                                                              135
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                                                                                                              SS
                                                                                                                                                   SA 119
                                                                                                                                                                               VDDFKGRFVFSLETSASAAYLQINNLKNEDTATYFCA----RRGFYAMDYWGQGTSVTV
                                                                                                                                                                                                                                                   QIQLVQSGPELKKPGETVKISCKASGYTFTDYGMMVKQAPGQGLKWMGWINTYTGESTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKKPGETYKISCKASGYTFTNYGMMWYKQAPGKGLKMMGWINTYTGEFTYADDFKGRFAF
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                                                                                                                 136
                                                                                                                                                                                                                                                                                                                               Conservative
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        (house mouse
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88.5%;
                                                                                                                                                                                                                                                                                                                                              80.3%;
                      mouse
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                                                                                                                                                                                                                                                                                                                                              Score 522; DB 2; Length 136;
Pred. No. 1.6e-38;
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Pred. No. 9.3e-39;
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           A;Accession: S19968
A;Status: preliminary
A;Molecule type: mRNA
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S32187
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A;Residues: 1-115 <WEI;
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Cipate: 18-dan-1991 #sequence_revision 13-dan-1993 #text_change 21-; Cipacession B36259 R; Allber, B; Scherf, T; Levitt, M; Anglister, J. Biochamistry 29, 1003-21004, 1990 A; Title: NRR-derived model for a peptide-antibody complex. A; Title: NRR-derived model for a peptide-antibody complex. A; Accession: B36259 MID: 91104915; PMID: 2271636 A; Accession: B36259 A; Biolegale type: m8XA A; Molegale type: m8XA A; Malegale type: m8XA A; Molegale type: m8XA A; 
                                                                                                                                                                                                    Ig heavy chain V region (M-T408) - mouse (fragment) C;Spectes: Mus muscullus (house mouse) C:Date: 06-reb-1995 #sequence_ravision 06-reb-1995 #text_change C;Accession: $19968
A;Description: Structural characterization of CD4 mab
A;Reference number: S19963
                                                                                              R; Weissenhorn, W.; Riethmueller, G.; Weiss, B.M.; Rieber, submitted to the EMBL Data Library, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)(Cross-references: EWBL:X70091; NID:9288251; PIDN:CAA49696.1; PID:9288252
C:SupertEmily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin bomology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Date Library, February 1993
A.Reference number: $32185
A.Jaccession: $33187
A.Jaccession: $33187
A.Status: preliminary
A.Status: preliminary
A.Molecule type: mRVA.
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C:Species (Man musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: 832187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ADDEKGREAPSLETSASTAYLQINNLKNEDTATYPCALYGNSPKGPAYWGQGTLVTVSA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVKLVESGFELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVKLVESGPELKKPGETVKISCKASGYIFINYGMWVKQAPGKGLKWMGWINTYTGEPTY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDFKGRFAFSLETSASIVYLQINNLKNEDTATYFCASWRN--YGFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSFKGFAYWGQGTLVTVSA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.1%; Score 511; DB 2; ilarity 79.8%; Pred. No. 1.2e-37; Conservative 10; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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78.2%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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A, Status; preliminary
A, Molecule type; mWAA
A, Molecule type; mWAA
A, Residuse; 1-115 - 40EI-
A), Cross-references: BMBL:X65088
C, Supert/anily; immunojolobulin V region; immunoglobulin homology
C, Monyords: heterocerrame; immunojolobulin
C, Monyords: heterocerrame; immunojolobulin
F, 6-91, Flomain; immunojolobulin homology <-IMM>
                                                                                                                                                                                                                                                                                                                                                                                      Stages that V region (M-T321) - mouse (fragment) Claspecies Mus musculus (house mouse) Claspecies (Gramman Musculus M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin C;Superfamily: immunoglobulin homology <IMM>
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c;Superfamily: immunoglobulin region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;10-93/Domain: immunoglobulin homology <1M4>
                                                                                                                                                                                                                                                                                                 A;Reference number: S19963
A;Accession: S19965
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A; Residues: 1-124 <SHI>
A; Accession: PH1406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYW 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDFKGRFAFSLETSASTAYLQINNLKNEDMATYFCA-----RGFPWY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GREAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPK----GFAYWGQGTLVTVSA 119
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80.5%;
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Pred. No. 2.3e-37;
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Pred. No. 2e-37;
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                                                                                                                                                                                                                                                                          anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 109) Cipate: 22-Sep-1999 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000 Cipacession: 145722 #text_change 21-Jan-2000 Cipacession: 145722 #text_change 21-Jan-2000 Cipacession: 145722 #text_change 21-Jan-2000 M. Sidingson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M. J. Virol. 67, 489-196, 1993 #text_change is that distinguish three antigenic size that distinguish three antigenic size factories mumber: A45722; MUID:93100433; PMID:7677958 M.; Accession: H45722 #text_change is the conceptual translation A; Molecule type: modelc acid is the conceptual translation A; Molecule type: modelc acid is the seasons and the conceptual translation A; Molecule type: modelc acid
                                                                                                                                        A;Note: sequence extracted from NCBI backbone C;Superfamily: immunoglobulin V region; immuno C;Reywords: glycoprotein C;Reywords: glycoprotein F;15-99/Domain: immunoglobulin homology <IMM>
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                                  Local Similarity
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78.0%;

Score 504; DB 2 Pred. No. 5e-37; 9; Mismatches

10,

8,

Gaps

DB 2; Length 119;

ckbone (NCBIP:120597) immunoglobulin homol

3. S Site

78.0%;

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Cispecies hus musculus (house mouse)
Cibace: 17-Apr.1993 #sequence_revision 17-Apr.1993 #text_change 21-Jan.2000
CiAccession: PH1225
R.Weissenborn, W.; Schwarz, W.; Kaliza, B.; Schwirzke, M.; Reiter, C.; Flieger, I.
Gene 121, 271-278, 1992
A.Fills: Combinatoxial functions of two chimeric antibodies directed to human CDA
A.Feciscence number: PH1224; WUID:93077041; PWID:1446824
A.Accession: PH1225
A.Molecula type: mRNA
A.Feciscences: 1-139 «RSI»
A.Fec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;20-139/Broduct: Ig heavy chain v region whom P;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain precursor V region (M-T151) - mouse C:Species: Mus musculus (house mouse)
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Best Local S
Matches 95
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137 VSS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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Pred. No. 4.4e-37;
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Page 5

Search completed: November 7, 2003, 07:36:18 Job time: 15:5112 secs

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                                                              P01772 homo sapien
P01765 homo sapien
P01803 mus musculu
P01742 homo sapien
P01811 mus musculu
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P01763 homo sapien
P01808 mus musculu
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TATID=10999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-82152818; PubMed-6801765;
Safas J., Fabbitts T.H., Betess P., Slaughter C., Tucker P.W.,
Cagna J.D.,
                                        P01769
P80421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 53.9%; Score 348; DB 1; Length 140; Similarity 54.1%; Pred, No. 1.3e-28; 66; Conservative 24; Mismatches 28; Indels
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science 218:309-311(1982);
-: SIMILARITY: Contains 1 immunoglobulin-like domain.
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PRE, A94154; HNMSCO ...

INCEPTO : IRRODOTIO, IG-11ke.

INCEPTO : IRRODOSIOS [4] WHC.

INCEPTO : IRRODOSIOS [4] WHC.

INCEPTO : IRRODOSIOS [4] WHC.

FRAME, SHOOON | 104, 1.

PROSTIFE SPROSING; ICO, I.

IRROMATI, SHOOON | 104, 1.

IRROMANDOSION | 104, 1.

IRRODOSION 
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22-JUL-1986 (Rel. 01, Lafer Sequence update)
15-889-2003 (Rel. 42, Lafe annocation update)
15 heavy offain V region 9307 precursor.
Mus musculus (Nouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 140 AA.
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HV3D_HUMAN
HV34_MOUSE
                                                                                                                                     HV41 MOUSE
HV50 MOUSE
HV50 MOUSE
HV14 MOUSE
                                            AV3H HUMAN
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core greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                        (without alignments)
652.278 Million cell updates/sec
                                                                                                                                                                  November 7, 2003, 07:21:18 ; Search time 8.57944 Seconds
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                          127863 segs, 47026705 residues
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HV1C HUMAN
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Maximum DB seg length: 200000000
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Match Length DB
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Result No.

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61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLVT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMAWVKQAPGKGLKWMGWINTYTGEPTY
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N. Vegion determinant (idiotope) expressed at high frequency in B. Imphoryees is encoded by a large set of antibody structural genes."; PRR 800 J. 317-523 (1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Gaps
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Mammalia, Eutebreia, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI Taria,1009),
                                                                                                                                                                                                              iehman D.M., Putham F.M.;
Panthon of a human mu chain:
Panthon of a possible of the variable region of a human mu chain:
Proc. NAET, Acad. 56: U.S.A. 773239-3241(1980).
PROC. PROC. PROS. PROM. PROM. PROM. THE PLASHA OF

-- MISCELLARBOUS: THIS MY CHAIN WAS ISCULATED FROM THE PLASHA OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATIENT WITH MACROGLOBULINEMIA.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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SRAFI, SNOGOGE, 1GOV; 1.
Immunoglobulin V region; Pyrcolidom carboxylic acid.
DOMIN 1 112
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MESSP, POLT77, ZEPE

CO) CO:0005321 F: santigen binding activity, NAS.

CO) CO:0005321 F: santigen binding activity, NAS.

CO) CO:0005525 F: santimen response; NAS.

INCEPTO: IRROGOROG, IQ-NAC.

INCEPTO: IRROGOROG, IQ-NAC.
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Mus musculus (Mouse).
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                                                                                                                                                                   AEDLINE=81013859; PubMed=6774332;
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SMART, SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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InterPro, IPR007110; Ig-like.
InterPro, IPR03506; Ig_MHC.
InterPro, IPR005596; Ig_V.
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P06330;
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NON_TER
SEQUENCE
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HV51 MOUSE
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SO NEKFKGKITILIVDKSSSTAYMQLRSLISEDSAVYFCARSHYYGGS-YDFDYWGGGTPLIV 138
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15.58F-2003 [Rel] 42, Last sequence update)
15.58F-2003 (Rel] 42, Last ammotation update)
16.88F-2003 (Rel] 42, Last ammotation update)
17 Dheavy chain / region 36.55.
18 memorius (Mouse).
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15.-200.-1986 (Rel. 0), Lata sapelence update)
15.-282-2036 (Rel. 42, Lata amoration update)
19.-282-2036 (Rel. 42, Lata amorati
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53.7%; Pred. No. 2.9e-28;
ive 24; Mismatches 28; Indels
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1859; pd1789; 1MCP.
INCOCTO: IPROGNIIO 1g-like.
INCOCTO: IPROGNIIO 1g-like.
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SMARY: SM00405; IGv. 1.
PROSITE; PE06035; IG LIKE; 1.
Immunoglobulin V region; Hybridoma.
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Best Local Similarity 53.7%
Matches 65; Conservative
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                                                                                                                                                                   SA 119
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P01768;
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ID HV03 MOUSE
AC P01747;
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HV3G HUMAN
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51.2%; Score 330.5; DB 1; Length 118; 53.3%; Pred. No. 6.7e-27; ive 21; Mismatches 32; Indels 3;

64; Conservative

Matches

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Query Match Best Local Similarity

115 AA.

STANDARD;

HV32 MOUSE P01801;

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99 104 D. SEGNERIT. 105 118 J. SEGNERIT. 12 96 BY SIMILARITY. 118 AA, 12934 MM, 9479ERE4C762A018 CRC64,

DOMAIN DISULFID NON TER SEQUENCE

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DOMAIN

V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.

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issi WHISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatica and the REBLO dutestrion - the Bropens Bioinformatica Institute. There are no restrictions on its use Byropens Bioinformatica in a long as its content in in no way madified and this stransment is not removed. Usage by and for commercial entities requires a license agreement (see http://www.lab-eib.ch/announce/or entry and meal to license@lab-eib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 NEKFKSKAILIVDKPSSIAYMQLSSIASEDSAVYYCARYDYYGSS--YFDYWGQGTTLIV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLQQPGABLVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGSTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         History chain variable region contribution to the NRP family of cell 24(65-57)(1901).

Cell 24(65-57)(1901).

MAKING ANTIBODIES: THE B1-8 NW CHAIN WAS CLONED FROM A PHYROLOGY.

MAKING MATIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL.

(VIPB ANTIBODIES).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Gaps
                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION B1-8/186-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.4%; Score 325.5; DB 1; Length 139; 50.0%; Pred. No. 2.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Conservative 28; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15419 MW; 1B57DD4FD0C9F465 CRC64;
PRT, 139 AA. POLTS, PRT, 139 AA. POLTS, POLT
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SMARY, SMO406; 1g; 1, 1
FROSITE; PS50835; 1G LIKE; 1
Immunoglobulin V region; Signal; 3D-structure.
                                                                                                                                                                                                 Ig heavy chain V region B1-8/186-2 precursor
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D SEGMENT.
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PDB; LAGO, Z-YAKY-98.
PDB; LAGW, 15-70L-98.
INTERPEYO; PRRO0710; IG-11ke.
InterPeyo; IPR003306; IG-MHC.
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                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 EPTYADDFKGRPAPSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGPAYMGQGTLVT 116
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-1- MIEGELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                      1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
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                                                                                                                                                                                                                                                                                  Gaps
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MEDLINES-209351, PubMed=6798111,
OCHBRON N., Slankard J., Paul L., Hood L.,
The complete V domain amino acid sequences of two myeloma inulin-
```

12;

ch 51.1%; Score 330; DB 1; Length 115; Similarity 54.5%; Precd. No. 7.38-2; Tonger 15; Mismatches 28; Indels 75; Conservative 15; Mismatches 28; Indels

Local Similarity

Matches

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115 115 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

IG-LIKE. BY SIMILARITY.

DISULFID NON TER SEQUENCE Query Match

Pfan, Proto47; 19; 1.
SMART, SM00406; 1G; 1.
SMART, SM00406; 1G; 1.
Immunoglobulin V region.
DOMAIN

Henry Synthy.

1. SIMILARITY. Contains 1 immunoglobulin-like domain.
PRS. POLYSA INCO.
INGENED PROFINE.
INGENED PROFINE.
INGENED IRROGING 19-like.
INGENED IRROGING 19-like.
INGENED IRROGING 19-like.

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RASULTS
HV13 MOUS
ID HV131
AC P011
AC P017
DT 21---
DT 21---
DT 15--
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DT 05--
DT 15--
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Best Local S
Matches 64
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P01756;
21-JUL-1986
SEQUENCE.
MEDLINE=80078170, PubMed=6765983,
Schilling J., Clevinger B., Davie J.M.,
                                                                                                                                                                        21-JUL-1996 (Rel. 01, Created)
21-JUL-1996 (Rel. 02, Last aequence update)
21-JUL-1996 (Rel. 42, Last amotation update)
15-SEP-2003 (Rel. 42, Last amotation update)
19-bary chain v region JSSB
19-ba
                                                                                                                                                                                                                                                                                                                                                                                                                          HV13 MOUSE
                                                                                                                                                   NCRI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A02039; MHMS4E.
HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN HAS ALSO BEEN DETERMINED.

- MISCELLAMEOUS: THIS PROTEIN BINDS DEXTRAN.

- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heavy chain constant region domains.";
Biochemistry 21:5415-5424 (1982).
-i- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hood
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Kehry M.R., Fuhrman J.S., Schilli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986
15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete amino acid sequence of a mouse mu chain: homology among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region MOPC 104E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDYDWY-----
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 325; DB 1;
Pred. No. 2.4e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                     Hood L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 117;
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HER PAG542; Purson.
HER PAG
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Best Local S
Matches 64
IntesPro 18700110, 19-1ke.

IntesPro 187001006; 19-WC.

IntesPro 187001006; 19-WC.

Pfam; PF00017; 19: 10-Y

PROSITE; PS00955; IG_LIKE; 1.

IMMUNOJOBOSI; IG_LIKE; 1.

IMMUNOJOBOSI; IG_LIKE; 1.

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P01759;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SSP-2003 (Rel. 42, Last amochation
15-Bary Chain V-III region ABE-47N.
Mis muoculus (Mouse).
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 PIR; A90400; AVMSB7.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 16:1170-1175(1977)

- MISCELLANGOUS: THIS CHAIN WAS ISOLATED FROM A MYELONA BIDES INULIN.

-- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=77134726; PubMed=402936;
Vrana M., Rudikoff S., Potter M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostoni,
Mammalla, Buhteria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCPI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Maino acid sequence of homogeneous antibodies to dextran rearrangements in heavy chain V-region gene segments.";
Rature 283:35-40(1980).

1-1 MISCELLANSOUS: THE SEQUENCES OF A HYBRIDONA, PROTEINS BIND DEXTREAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MILCH OCCUR IN THE D AND J SEGMENTS DEXTRAN.

1-1 MISCELLANSOUS: THIS PROTEIN SINDS DEXTRAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Heavy-chain variable-region sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 VSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NOKFKGKATLITVDKSSSTAYMQLNSLTSEDSAVYYCARDRYWY-----FDVWGAGTTVT
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Last annotation update)
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Pred. No. 2.4e-26;
                                              IG-LIKE.
BY SIMILARITY.
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BY SIMILARITY
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InterPro; IPR003006, Ig_MHC.
InterPro; IPR003566, Ig_V.
Pram; PP000477, Ig; 1.
PMART; SM00465, IGv; 1.
PMCSITE; ES50835, IG_LIKE; 1.
ImmunOglobultat V region.
                       HV01 MOUSE
P01745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
NON_TER
SEQUENCE
21-JUL-1986 (Rel. 01, Created)
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P01807; 1956 (Rel. 01, Created)
21-UU-1956 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last amoreation update)
15-bary chain V-III region H3082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Immunol, 128:302-307(1982).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=82099361; PubMed=6798111;
Johnson N., Slankard J., Paul L.,
"The complete V domain amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01810; 2FBJ
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                                                                                                                                                                                                                   119 Å 119
                                                                                                                                                                                                                                                          61 HYAESVKGRFTISRDDSKSSVYLRMMNLRPEDTGIYYCT----TGFAYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                    59 TYADDFKGRFAFSLETSASTAYLQINNLKNBDTATYFCALYGNSPKGFAYWGQGTLVTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                     BVKLVESGÞBLKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWI--NTYTGEP
                                                                                                                                                                                                                                                                                                                                                          EVKLEESGGGLVQPGGSMKLSCVASGFTFSNYWRNWVRQSPEKGLEWVAEIRLKSHNYAT
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                                                                                                                                                                         115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 AA;
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                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 323; DB 1;
Pred. No. 3.8e-26;
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9B4517648C121C5A CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 115;
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Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYL5 MOUSES STANDARD; PRT; 136 AA. POL759; St. Juli-1996 (Rel. Ol. Created) 21-UL-1996 (Rel. Ol. Late sequence update) 21-UL-1996 (Rel. Ol. Late sequence update) 15-SEP-2003 (Rel. 42 Late amortation up
                                                                                                                                                                                                                                              MEDLINE=82222262; Pubm
Knapp M.R., Liu C.-P.,
Blattner F.R.;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and sequence of the cDNA corresponding region of immunoglobulin heavy chain MPCl1."; mucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-VUI-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MPC 11.
Mus musculus (Mouse).
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    -I- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MENNA ISOLATED
FROM A MYELOMA THAT SECRETES IGG2B.

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Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zakut R., Cohen J., Givol D.;
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MEDITINE=81053741; PubMed=6253904;
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                                                                                                                                                                                                                                                                       PubMed=6806821; .-P., Newell N., Ward R.B., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8:4839-4840(1980)
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51.2%; Pred. No. 6.4e-26;
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by two adjacent CH genes."; Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982). -!- SIMILARITY: Contains 1 immunoglobulin-like domain

"Simultaneous expression of immunoglobulin by a cloud B-cell lymphoma: a single copy

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and delta heavy chains the VH gene is shared

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Best Local S
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    DOMAIN
DOMAIN
                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Sign
                                                                                                                                                                                                                                              (1)
SEQUENCE FROM N.A.
MEDLINE-84248078; PubMed=6429663;
MEDLINE-8-8-64248078; Richards J.E.,
                                                                     SIGNAL
                                                                                                                                InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                          PIR; A02033; HVMST7.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                      Proc.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                            P0930.
23-0CT-1986 (Rel. 02, Created)
23-0CT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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                                                                                                                                                                                                                             Illegitimate recombination generates a class switch
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                                                                                                                                                                                                    in an IgD-secreting plasmacytoma.";
Natl. Acad. Sci. U.S.A. 81:4164-4168(1984)
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IPR003006; Ig_MHC.
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IG HEAVY CHAIN V REGION TEPC 1017. FRANEWOCK-1.
COMPLEMENTARITY-DETERMINING-1.
FRANEWOCK-2.
COMPLEMENTARITY-DETERMINING-2.
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Pred. No.
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Matches 59
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PDB; 11GC; 03-JUN-95.

InterPro; IER007110; Ig-like.

InterPro; IPR003006; Ig-MHC.

InterPro; IPR003596; Ig-v.
CONFLICT
CONFLICT
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21-JUL-1986
21-JUL-1986
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                         MEDIINE=77100368; PubMed=401950;
Adetugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
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                                                               CHAIN
                                                                             Immunoglobulin
NON TER
SIGNAL <
                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                    region;
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127
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115
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                                    IG HEAVY CHAIN V REGION MOPC D SEGMENT.
JH4 SEGMENT.
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Pred. No. 7.4e-26
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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I (IN REF. V REF. 2).
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                                                                                                                                                                                                                                                                                                   RESULT 15
HY27_MOUSE STANDARD; PRT, 113 AA.
AC P01796 (Rel. 01, Created)
D7 21_UUL_1986 (Rel. 01, Created)
D7 21_UUL_1986 (Rel. 01, Last sequence update)
D7 21_UUL_1986 (Rel. 42, Last amnotation update)
D8 21_UUL_1986 (Rel. 42, Last amnotation update)
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                                                                                                                                                                                                                 Query March 49.4%; Score 319; DB 1; Length 113; Best Local Similarity 42.4%; Pred. No. 9.4e-26; Marches 63; Conservative 18; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                              IntesPro; IPB007110, 1g-1kke.
IntesPro; IPB003006; 1g MC.
IntesPro; IPB003506; 1g V.
Pfam; PP00047; 1g; 1.
Pfam; PP00047; 1g; 1.
PR00517B; PS008085; IGLIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                             DISULFID
NON TER
SEQUENCE
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CONFLICT
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SEQUENCE
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-- SINLIARITY: Contains 1 immunoglobulin-like domain.
BER, A03818, AWNSAB.
BSSP, P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEDILINE-70150406; PubMed=117344;
Vrana M., Rudikoff S., Porter M.;
"Sequence variation among heavy chains from inulin-binding myeloma
procefus: 1, Acad. Sci. U.S.A. 75:1957-1961(1978).
TO MISCILLANGUS: THIS CHAIN HAS ISOLATED FROM A MIELOMA PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                61 HYAESVKGRFTIŠRDDSKSSVYLOMINIRABDTGIYYCT----TGFAYWGQGTLVTV 113
                                                                                                59 TYADDEKGREAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 ADTYKGRFTISRDNEKNTLEIQMTSLRSBDTAMYYCARMGNYPYYAMDYMOQGTSVTVSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSD-KGFAYMGQGTLVTVSA 119
                                                                                                                                                             1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWI--NTYTGEP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 DVQLVESGGGLVQPGGSRXLSCAASGFTFSSFGMHWVRQAPEKGLBWVAYISSGSSTLHY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWWGWINTYTGEPTY 60
                                                                                                                                        EVKLEESGGGLVQPGGSMKLSCVASGFTFSNYWWWWVRQSPEKGLEWVAEIRLKSHNYAT 60
                                                                                                                                                                                                                                                                                          22 98 BY SIMILARITY.
113 113
113 AA; 12675 MW; 76658C121C598285 CRC64;
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BY SIMILARITY.
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Y -> W (IN REF. 2).
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                             Database :
                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
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646
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                                                                                SPTREMBL_23:*
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sp archea:*
sp bacteria:*
sp fungi:*
sp human:*
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11: sp_rcdent:*
12: sp_vtnus:*
13: sp_vertebrate:*
14: sp_unclases(fied:*)
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
17: sp_archeap:*
17: sp_archeap:*
18: sp_archeap:*
19: sp_archeap:*
10: sp_archeap:

sp invertebrate:*
sp mammal:*
sp mhc:*
sp organelle:*
sp phage:*
sp phage:*

SUMMARIES

Result Score NO. Score 1 545.5 2 486.5 3 486.5 6 377 7 376.5	Query Match 76.6 75.3 71.4 61.1	Length DB 241 1 484 1 218 1 102 1 119 4 119 4	B ID 11 Q921A6 11 Q992A6 11 Q992A6 11 Q992A6 11 Q992B6 11 Q992B6 4 Q90194	Description 0921a6 ma 0921a6 ma 0921a6 ma 0921a7 ma 0920a7 ma 0920a7 ma 0920a7 homo 092134 homo 092136 ma
1 545.5	10			
495	76.6		•	
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9 362	56.0		11 Q9D8	09/814
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12 354	54.8			08wv24 h
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16 344	53.3			0925.43
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Q9UL89 Q924Q2 Q9JL83	Q8WU38 Q924Q3 Q8VCX4	Q924P9 Q9Y298 Q924Q1 Q924Q7	Q966A6 Q8R3V9 Q9UL93 Q924P5 Q924R1	Q90L90 Q9JL75 Q9UL91 Q9UL91 Q924R8 Q92LC4	Q9GYZ2 Q8VCV5 Q91WT1 Q96BB9 Q96Z4R5 Q90XF0 Q8VDC9
Q91183 mus musculu Q91183 mms musculu	Q8w136 homo sapien Q924q3 mus musculu Q8vcx4 mus musculu	Q924pp mus musculu Q924pp mus musculu Q9y298 homo sapien Q924q1 mus musculu Q924q7 mus musculu			m

ALIGNMENTS

RESULT 1 10921A6: 10 0921A6: 20 01-DEC-2001 (TYENGLIVEL 19, Created) 20 01-DEC-2001 (TYENGLIVEL 19, Created) 20 01-DEC-2001 (TYENGLIVEL 19, Last sequence update) 21 01-DEC-2001 (TYENGLIVEL 19, Last sequence update) 22 01-DEC-2001 (TYENGLIVEL 19, Last sequence update) 23 Last Last Annotation update) 24 01-DEC-2001 (TYENGLIVEL 19, Last sequence update) 25 Last Last Last Last Last Last Last Last
221A6
Murinae, Mus. Murinae, Mus. , Lee S.D., nd VL of a with NCA-95 and 4; ength 241; dels 1; Gaps

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Best Local S
Matches 93
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Shmitted (PER-001) to the BM
ENBL, BC003495, ANH03495.1;

HSSP, D01801, 2253,

InterPro, IRR007110, 7g_Hike.

InterPro, IRR007110, 7g_Hike.

InterPro, IRR00710, 7g_Hike.

InterPro, IRR00710, 7g_Hike.

InterPro, IRR00710, 7g_Hike.

IRR05171, PER0037, 7g_Hike.

IRR05171, PER0037, 7g_Hike.

IRR05171, PER00370, 7g_Hike.

IRR051717, PER00370, 7g_Hike.

IRR051
                                                                                                                                                                                                                              MRP5 (Fragment).
Mus musculus (Mouse).
Bukaryota; Metazoa; Ch
Mammalia; Butheria; Rc
                                                                                                                                                                                                                                                                                                                      01-DEC-2001
01-DEC-2001
01-MAR-2003
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Q99LA6;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                  Q92581
Q92581
**Medianism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice."; World J. Gastroenterol. 6;709-717(2000).
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Mus musculus (Mouse).
Bukaryota; Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                         PubMed=11819679;
                                                                                                                                                    STRAIN-BALB/c;
                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                     Zeng G., Yan X.,
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(TrEMBLrel. 19,
(TrEMBLrel. 23,
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Rodentia;
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                                                                                                                                                                                                                                                                                                                  , Created)
Last seq
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Pred. No. 3.8e-41;
9; Mismatches 17;
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                               sequence update)
annotation update)
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thi; Muridae; Murinae; Mus
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Best Local S
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Best Local S
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01-OCT-2000
01-MAR-2003
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interru, 19; 2.

Pfam; PF00047; 19; 2.

SWART; SW00406; IGv; 1.

SWORTE; PS50835; IG LIKE; 1.

PROSITE; PS50835; IG LIKE; 1.
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A.CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the same strain.";
Int. J. Radiat. Biol. Relat.
EMBL; AF240168; AAK43733 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cui D., Zeng G., Yan X., Li X., Su ("Cloning of mouse genes related to of the irradiated mice by treatment
                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                        16
     76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                         89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
ASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                  M00406; IGV; 1.
PS50835; IG_LIKE;
                                                            ETVKISCKASGYTFTDYSMHWVKQAPGKGLKWMGWINTETGEPTYADDFKGRFAFSLETS
                                                                                                         ETVKISCKASGYIFINYGMNWVKQAPGKGLKWMGWINTYTGEPTYADDFKGRFAFSLETS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABBEKGRFAFSLETSASTAYLQISNLKNEDTATYFCWRW-DYDGGFAYWGQGTTVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
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                                                                                                                                                                                                                                                                                                             102
102 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 AA;
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                             71.4%;
                                                                                                                                                                                                                                                                                                                  11543 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23013 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.3%;
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                                                                                                                                                                                                                  Score 461; DB 11;
Pred. No. 1.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 486.5;
Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stud.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata, Vertebrata,
Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                  E590C292093F6711 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527E4FA8F7982817 CRC64;
                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repairing
t with the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Med. 19:71-80(2001).
                                                                                                                                                                                                                                           Length
                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epitope of 
is cross-reactive
                                                                                                                                                                                                                                                102;
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                                                                                                                                                                                    Gaps
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102

Q920E8; Q920E8; 01-DEC-2001 01-DEC-2001

PRELIMINARY;

PRT;

120

PAREUTA

PAR

SEQUENCE FROM N.A.

Eukaryota; Metazoa; Mammalia; Eutheria; (Fragment).
Mus musculus (Mouse)

Chordata; Rodentia;

Akkin Jp., Jage A., Jennings I.G., Boratiss O., Votton "Definition of the Idiotope of Pterin-Mimicking Antibodi In Mammalian cells "12000" to the EMBL/GenBank/DDBJ databases EMBL, AS307356, AAL09420.11 IncerPro; IPR0073107 Ig-11ke.
IncerPro; IPR0073107 Ig-11ke.
IncerPro; IPR0073065 Ig-MEG.
IncerPro; IPR0033065 Ig-W.

60

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"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MDEC-2003 (TrEMBLrel. 23, Last amoteation update)
PLerin-mimicking anti-idiotope heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOKFKGKATLTVDKSSSTAYMOLKSLTSEDSAVYYCAVIYYGNSPAWFAYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVKLVESGPBLKKPGETVKISCKASGXIFTNYGMWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRKGREAFSLETSASTAYLQINNLKNEDTATYFCAL--YGNSPKGFAYWGQGTLVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVOLOOSGPELEKPGASVKISCKASGYSFTGYNMWVKOSNGKSLEWIGNIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.1%; SCORE 395; DB 11; Length 120;
Llarity 60.8%; Pred. No. 6.9e-32;
Conservative 21; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jennings I.G., Horaitis O., Cotton R.O
Niotope of Pterin-Mimicking Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPB003006; JG_MHC.
InterPro; IPB003506; IG_v.
Pfam, PB00040; JGy 1.
SWART; SW00406; JGy; 1.
PROSIIE; PS00833; IG_LIKE; 1.
MOM_TER 124 114
NOW_TER 124 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 1.
SMART; SM00406; iGv; 1.
PROSITE; PS5083; IG II.
NON TER 119 119
SEQUENCE 119 AA; 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OSUILG2 PERLIMINARY, PRT; 124 AA.

OSUILG2; PRELIMINARY, Created)
01-MAY-2000 (TERMELTel. 13, Created)
01-MAY-2000 (TERMELTel. 13, Last sequence update)
01-MAY-2000 (TERMELTel. 23, Last samceation update)
MOSIAN-resective immunos/cobulin beavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035022; AAD56258.1; -
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1]
sEQUENCE FROM N.A.
MEDULINE=98277139; PubMed=9614934;
MEDULINE=98277139; PubMed=9514934;
MEDULINE=98277139; PubMed=9514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                    116
                                                                                                                                   121 TVSS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                          ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA--LYGNSFKGFA---YWGQGTLV
                                                                                                                                                                                TVSA 119
                                                                                                                                                                                                                             AQKEQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGLYVVVPAAFSRFDYWGQGTLV
                                                                                                                                                                                                                                                                                                                                    EVQLVESGAEVKKPGASVKVSCKASGYIFSSYIMHWVRQAPGQGLEWMGIINPSGGSTSY
                                                                                                                                                                                                                                                                                                                                                                                     EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQKFQGKVTWTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLWFDPWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDEKGREAESLETSASTAYLQINNLKNEDTATYEÇALYGNSEKGEAYWGQGTLVTVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AA;
    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Buteleostomi; Primates; Catarrhini; Hominidae; Homo.
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57.1%; Pred. No. 4.3e-30;
tive 22; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13205 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 376.5; DB 4; Pred. No. 5.1e-30; Pred. No. 5.1e-30; Indels
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13E64F5345F4A16E CRC64
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125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 124;
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RESULT 6 Q9UL94

Q9UL94

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61 61 Query Match Best Local Similarity Matches 73; Conserv

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DC4834AB1DE56F3C CRC64;

Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
NON TER

DR RILL RAY BANGOR DRAWN
NCBI_TaxID=9606; Homo sapiens (Human). (Fragment).

SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N.,

Berney

Young D.C.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae;

Homo

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Clin. Immunol, Imminopathol. 8:
EMBL; AF035020; AAD56256.1; -.
HSSP; PO1810; 2EBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR00716; Ig-MCC.
InterPro; IPR003596; Ig-WC.

87:184-192(1998)

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Best Local S
Matches 66
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PR00047; ig; 1.
SMART; SMO0406; IGV; I.
PROSITE; PS50815; IG_LIKE; 1.
MEDILINE-2108(56), Pubweel-11277851,

Kawat J. Shilagawa M. Shibata K., Yoshino M., Itoh M., Itoh M., Arakawa T., Hara N., Pukuda S.,

Arakawa T., Hara N., Pukunishi K., Kiyosawa H., Kondo S., Yananaka I.,

Aitawa K., Izawa M., Mishi K., Kiyosawa H., Kondo S., Yananaka I.,

Sakto T., Okasaki Y., Gojobori T., Bono H., Kashkawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

Zashohanam W., Gasarberland T., Glasi C., King B., Kochiwa H.,

Zashohanam W., Gasarberland T., Glasi C., King B., Kochiwa H.,

Shini J., Walka S., Macsuo Y., Nikaldo I., Pasol G., Ohachenbush J.,

Schrini J., Walka S., Macsuo Y., Nikaldo I., Pasol G., Ohachenbush J.,

Schrini J., Walka G., Walka R., Tonika M., Hagner L., Mashio T.,

Sahai K., Okido T., Rumo M., Aono H., Baldarelli R., Bath G.,
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01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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HSSP; P01810; 2FBJ.
InterPro; IPR007110;
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Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin-reactive (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPK-----GFAYWGQGTL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVKLVESGPELKKPGETVKISCKASGYIFTNYGWWYKQAPGKGLKWWGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTVSA 119
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(TYEMBLrel. 13, Last sequence update)
(TYEMBLrel. 23, Last sequence update)
:Ive immunoglobulin heavy chain variable region
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Primates;
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Last sequence update)
Last annotation update
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Pred. No. 9
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InterPro, IRPO07710.1G_MHC.

InterPro, IRPO03896.TG_WHC.

InterPro, IRPO03896.TG_W-1.

SMART, SMOORT 1GY-1.

PROSITE: P8558815.TG_IIXE; 4.

PROSITE: P8052805.TG_MHC.1.

SEQUENCE: A3 AA, SEGS9 WW, 5
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Brownstein M.J., Bult C., Platcher C., Fujita M.,
Gartiboldi M.,
Brownstein M.J., Bult C., Platcher C., Fujita M.,
Lyone P., Marchionni L., Mashina J., Manazarelli J., Mombasets P.,
Lyone P., Marlonni L., Mashina J., Marzarelli J., Mombasets P.,
Mordone P., Kling B., Ringwald M., Kodriguez I., Sakanco N.,
Sasaki H., Sato K., Schembach C., Seya T., Shibata N., Scotch K.-F.,
Sasaki H., Sato K., Schembach C., Seya T., Shibata N., Storch K.-F.,
Sanaki H., Sato, N., Yoshida K., Mang K.H., Weitz C., Whittaker C., Whimis S.,
Hyndaks-Bort B., Yoshida K., Mang K.H., Weitz G., Whittaker C., Whimis S.,
Hyndaks-Bort B., Yoshida K., Mang S., Walley H., Mohrell H., Mohrell H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK007918; BAB25349.1; -. HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.; "Function of a full-length mouse cDNA collection.";
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                                       61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                                                            1 EVKLVESGPELKKEGETVKISCKASGYIFTNYGMMVKQAPGKGLKMMGWINTYTGEPTY
                                                                                                                                                                                       Similarity
NEKFKGKATUTADKSSSTAYNQLSSLTSEDSAVYFCARSGYDYDWFAYWGQGTLVTVSA
                                                                                 QVQLKQSGAELVKPGASVKISCKASGYTFTDYXINWVKQRPGQGLEWIGKIGPGSGSTYY
                                                                                                                                                                   Conservative
                                                                                                                                                                                    56.0%; Score 362; DB 11; 57.1%; Pred. No. 7.1e-28;
                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                  9DED57A514475FBB CRC64;
                                                                                                                                                                                                       DB 11;
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RESULT 10 Q96Q80 Q10 Q96Q80 AC Q96Q8 Q96QS0; Q96QS0; 01-DEC-2001 Putative matrix cell adhesion molecule-3. Homo sepiens (Human). Eukaryota; Metaoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metaoa; Chordata; Craniata; Ventebrata; Euteleostomi; Mammalia, Butheria; Primates; Catarrhini; Hominidae; Homo. 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) SEQUENCE FROM N.A. NCBI_TaxID=9606; PRELIMINARY; PRT; 159 AA

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61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA-----LYGNSPKGFAY-----W

QVQLVQSGABVKKPGASVKVSCKASGYTFSNYXNWVRQAPGQGPEWMCVINPSGGSARY

79 109

EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTY

Query Match Best Local S Matches 68

Similarity

55.2%; Score 356.5; DB 4 52.3%; Pred. No. 6.8e-28; tive 22; Mismatches 29

5D29537E881FAF02 CRC64;

DB 4;

159; 11;

Indels Length

Gaps

Conservative

submitted (JUNS-2001) to the EMBL/GenBank/DDBJ da
EMBL, A003025; AM826561;
InterPro; IPR00110; Ig-like.
InterPro; IPR001065; Ig-WC.
InterPro; IPR001065; Ig-WC.
Pfam; PP0047; Ig-1, Ig-V.
Pfam; PP0047; Ig-1, Ig-V.
PASSITE; BN06465; IG-LIKE; I.
PR051TE; BN06465; IG-LIKE; I.
PR051TE; BN06465; IG-LIKE; I.
PR051TE; BN06465; IG-LIKE; I.

"Homo sapiens putative microfibrillar protein with Ig-like mXNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";

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Lison M.D.;

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REP SECOND
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Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                           O8WY24

O8WY24;

O1-MAR-2002 (TrEMBLrel. 20,

O1-MAR-2002 (TrEMBLrel. 20,

O1-MAR-2003 (TrEMBLrel. 23,
SEQUENCE FROM N.A.

SIEGN S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

"Identification and characterization of SNC66, a Ig-like
down-regulated in colorectal cancer.";
                                                                                                                                                                                                                                                                                                SNC66 protein.
Homo sapiens (Human).
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"Differences in V kappa gene utilization and VT CDR3 sequence among anti-DNA from C3H-Dpr nice and lupus mice with nephritis.",
must be sequenced by the control of the control 
                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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MEDLINE=96409289; PubMed=8814271;
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Mammalia; Eutheria;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 22, Last annotation update)
Apti-DNA heavy chain (Fragment).
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSS0835; IG_LIKE; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDEKGREAESLETSASTAYIQINNLKNEDTATYECA---LYGNSPKG-FAYWGQGTLVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIQLQQSGTELVKPGASVKISCKASGYSFTGYNMWVKQSHGKSLEWVGDINPYYGGTRY
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123 AA;
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Last annotation update)
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Pred. No. 7e-28;
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Sciurognathi; Muridae; Murinae; Mus
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RESULT 14 Q91WR1

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61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSFKGFAYWGQGTLVTVSA 119

PDSVKGRFTISRDNAKNTLYLQNSSLKSEDTAMYYCARHGDYDVGFAYWGQGTLVTVSA

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Best Local !
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InterPro; IPB003006; Ig MC.
InterPro; IPB003506; Ig W.
Pfam; PP00477; Ig 4.
SMART; SM00406; IOv; 1.
PROSITE; ES00250; IG LIKE; 4.
EROUSENCE 497 AB; ES665 MM;
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Q920E7;
01-DEC-2001
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE;
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Mammalia; Eutheria; Rodentia;
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01-MAR-2003 (TEMBLIFE). 33, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 DFKGRFAPSLETSASTAYLQINNLKNEDTATYFCALYGN--SPKGFAY-----WGCGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 QLEQSGAEVTKPGASVKVSCKASGYTFIAYDINWVRQAPGQGLEWMGWMNPQTGNTEFAQ
                                                                                                                                                              65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KLVESGÞELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTYAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
                                                                      EVKLVESGPELKKPGETVKISCKASGYIFTNYGMMVKQAPGKGLKMMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVSS
                                                                                                                                                                                                                                                                                                           119 AA;
                                                                                                                                             54.6%; Score 353; DB 11; ilarity 54.6%; Pred. No. 1.1e-27; Conservative 24; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                     13025 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 354; DB 4;
Pred. No. 4.7e-27
21; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                     F6B904044381CA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F24D08DFA5A663E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                               DB 11;
                                                                                                                                                        30;
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RESULT 15 (0802)
AC (110)
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Best Local Similarity
Matches 67; Conserv
BMBL, BG093188 ANIZ9488.1;
InterPro; IPR003599 [3 Like.
InterPro; IPR003191] [3 Like.
InterPro; IPR003196; Ig_4MC.
InterPro; IPR003196; Ig_4MC.
InterPro; IPR003196; Ig_7MC.
SMART; SM00407; IG_1; 3.
SMART; SM00407; IG_1; 3.
SMART; SM00407; IG_1; 3.
SMART; SM00407; IG_1; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ambaryota; Metazoa; Chordata; Craniata; Verrebrata; Euceleostoni;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2002 [TERMEL.el. 22, Created]
01-0CT-2002 [TERMEL.el. 22, Last sequence update]
01-MAR-2003 [TERMEL.el. 23, Last amnotation update)
$inilar to expressed sequence A183385.
Mis musculus [Wouse].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Breast tumor;
Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassberg R. Strassber
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EMBL, EC01353, AAN1353, 1.

MDD; MG1:96486; IQh-VU558.

InterPro; IRR00306; IQ-HEC.

InterPro; IRR00306; IQ-HEC.

InterPro; IRR00306; IQ-WC.

InterPro; IRR0030596; IQ-W.

STAM; PROQUAT; IQ-W.

STAM; PROQUAT; IQ-W.

SMART; SMO4067; IG-W.

SMART; SMO4067; IG-W.

MAST; SMO406
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091WH2.201 (TrEMBLIFE1. 19, Created)
01-DBC-2001 (TrEMBLIFE1. 19, Last sequence update)
01-DBC-2001 (TrEMBLIFE1. 23, Last annotation update)
Hypothetical 5.30 kDa protein.
1081-VJSSB 08 A189358.
Mus muscullus (Mouse).
Mus muscullus (Mouse). (Chordata, Craniata, Vertebrata, Euteleostomi, Mus muscullus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00290; IG_MHC; 2.
SEQUENCE 480 AA; 51645 MW;
80 NEXTRIGADESSITATION STATEMENT STA
                                                                                                                                                                                                                                                                                                                                                          20
                                                                                         61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYMGQGTLYTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 53.7%; Score 347; DB 11;
Similarity 52.9%; Pred. No. 2.3e-26;
63; Conservative 26; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                QVQLQQSGPELVKDGALVKISCKASGYTTTSFDISWMKQRDGQGPEWIGWISPGDGSSEY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8690A63C669CDBED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
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Search completed: November Job time: 42.343 secs ,7 2003, 07:34:32

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OM protein - protein search, using sw model
                                                                     Copyright
                                                                 GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Run on:	November 7, 2003, 07:21:17; Search time 51:3178 Seconds (without alignments) 368.069 Million cell updates/sec
Title: US-0	US-09-661-992B-82_COPY_1_119
Sequence:	1 EVKLVESGPELKKPGETVKIGNSPKGFAYWGQGTLVTVSA 119
coring table. Broomes	DT COMMCC

1 1107863 seqs, 158726573 residues Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1107863

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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A Genescy Jahund?*

1 (SIDSI) gendets/ genescy/genescy-emb1/Ahl 901 DAT:
2 (SIDSI) gendets/ genescy/genescy-emb1/Ahl 901 DAT:
3 (SIDSI) gendets/ genescy/genescy-emb1/Ahl 901 DAT:
4 (SIDSI) gendets/ genescy/genescy-emb1/Ahl 901 DAT:
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28 (SIDSI) gendets/ genescy-genescy-emb1/Ahl 901 DAT:
29 (SIDSI) gendets/ genescy-genescy-emb1/Ahl 901 DAT:
21 (SIDSI) gendets/ genescy-genescy-emb1/Ahl 901 DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

9	8	7	6	S	4	ω	N	-سو ،	Result
548.5	552	552	552	552	552	552	559.5	646	Score
84.9	85.4	85.4	85.4	85.4	85.4	85.4	86.6	100.0	Query
139	250	250	250	250	250	250	137	242	Query Match Length DB
11	20	19	19	18	18	17	23	22	DB
AAR09428	AAW80422	AAW47012	AAW53168	AAW22400	AAW29261	AAW02278	AAE29158	AAB20433	ID
KM10 Heavy Chain V	Anti-c-erbs-2 spv	Single chain bindi	741F8 anti-c-erbs-	Single chain antib	Anti-c-erbB-2 sing	741F8 anti-c-erbB-	Chimeric 31.1 anti	Anti-FIX/FIXa anti	Description

Variable region of		117	82.5	533	5
Human/murine IL-1	15 AAR47205		82.6	533.5	-
Antibody variable	22 AAB35101		83.0	536	ű
Humanised 323/A3 (83.2	537.5	Ñ
Anti-cancer antibo	20 AAW89536		83.2	537.5	μ
Murine protein #1.			83.2	537.5	ō
region of			83.4	538.5	9
pipiens			83.5	539.5	8
R. pipiens recombi	18 AAW35131			539.5	7
of 741 s			83.6	540	6
Sequence encoded b			83.6	540	5
Human NKG2D polype			84.1	543	4
3B10xP5-23 bispeci			84.1	543	ü
3B10xP5-2 bispecif			84.1	543	2
3B10xP4-14 bispeci			84.1	543	F
L6 sFv protein. U			84.1	543.5	8
			84.1	543.5	29
cDNA clone			84.1	543.5	8
5			84.1		27
2			84.1	543.5	6
Mouse L6 antibody	19 AAW47511	183	84.1	543.5	25
Variable region of			84.1	543.5	24
L6 antibody VH req			84.1	543.5	3
n of the			84.1	543.5	22
region			84.1	543.5	22
Variable region of	9 AAP82938		84.1	543.5	8
region	×		84.1	543.5	6
protein			84.1	543.5	18
		æ	84.1	543.5	7
eqion			84.1	543.5	6
Mouse 4C10 anti-id			٠	544	5
MHC-II MAD L243 he			84.5	546	4
243			84.5	546	ü
antib	24 ABU58898	139	84.9	48.	12
se KM1	Ţ		84.9	548.5	F
MAD KM10 heavy cha	18 AAW06217		84.9	548.5	6

ALIGNMENTS

AAB20433 standard; Protein; 242 AA.

AAB20433;

21-JUN-2001 (first entry

Anti-FIX/FIXa antibody 193/AD3 scFv.

Factor IX, FIX, Pactor IXa, FIXa, sefv, antibody, proceamiant, Factor VIII offsetor, blood cosmination disorder, hemophilia A, haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

Chimeric - Mus musculus. Chimeric - Synthetic.

ΙŽ	CHARLET - SYNCHECTO	Hecic.
Ħ	Key	Location/Oualifiers
₽Ţ	Protein	1119
Ţ		/label= VH
FT	Region	
H		/label= CDR3
PT	Peptide	
FT		/label= Linker
T	Protein	135242
4		/label= VL
FT	Region	
F		/label= CDR3
×		
N	WOZ00119992-A2.	
3		
3	- X-MAX X-	

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Query Match
Best Local Sim
Matches 119;
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                                                             15-MAR-2001; 2001US-276284P
                                                                                                                                      15-MAR-2002, 2002WO-US09193
                                                                                                                                                                                                                                                                                          WO200274251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.1 antibody; pancreatic cancer; pancreatic carcinoma; antibody therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric 31.1 antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE29158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE29158 standard; Protein; 137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New factor IX/factor IXa antibodies and their derivatives useful for
increasing emidolytic activity of factor IXA, and for treating blood
coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Fig 14; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-290358/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BAXT ) BAXTER AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLYTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVKLVESGPELKKPGETVKISCKASGYIFTNYGMMWVKQAPGKGLKMMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 646; DB 22;
Pred. No. 3.4e-46;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 242,
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ANNO2278
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Best Local S
Matches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
29-OCT-1996
                                    07-OCT-1993;
06-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7418; anti-c-erbB-2; monoclonal antibody; single chain Fv; sFv; construct; polypeptide linker; c-terminal amino acid sequence; in vivo imaging; drug targetting experiment; homodimer; increased; binding avidity; tissue retention time.
                                                                                                                                                   07-OCT-1993;
                                                                                                                                                                                                                                   09-JUL-1996
                                                                                                                                                                                                                                                                                                                  US5534254-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     741F8 anti-c-erbB-2 two single chain Fv construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW02278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-759857/82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (updated)
(first entry)
                                    93US-0133804
92US-0831967
                                                                                                                                                   93US-0133804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246..250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 note=
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"claimed C-terminal tail to facilitate crosslinking of two sFv polypeptides"

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The present invention relates to movel mucleic acid sequences encoding light and heavy chain variable regions of the antibody 31.1 Sequences of the invention are useful in expressing chimerised 31.1 antibodies, which can be used for treating pancreatic cancer or for diagnosing pancreatic action carctinems. They are also used in antibody herzpy. The presequence is characteric 31.1 antibody heavy chain variable region.
AAW02278 standard; Protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding light and heavy chain variable regions of antibody 31.1, useful for expressing chimerized 31.1 antibodies for treating pancreatic cancer or for diagnosing pancreatic carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Fig 4; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ITBI-) INT BIOIMMUNE SYSTEMS INC
                                                                                                                                                                                                 61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFC--ALYGNSPKGFAYWGQGTLVTVS
                                                                                                                                                                        80 ADDEKGREAFSLETSASTAYLQINNLKNEDTATYECARAYYG---KYEDYWGQGTTLTVS 136
                                                                                                                                                                                                                                                     20 QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                           1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGWWWXQAPGKGLKWMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                    86.6%;
                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                    Score 559.5; DE
Pred. No. 3e-39;
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                    DB 23;
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                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                       137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 The variable heavy (FR) and variable light (FL) genes of the 74F8 and it-created 2 monoclonal antibody (Mab), were isolated from the 2 CDNA of the parental 74F8 hybridoma line. A two single chain Fy (Mary of the was constructed by connecting the FR and 19 chain Fy (Mary of the was constructed by connecting the FR and the Parental DNA deplex (Mary of the Mary of the Parental DNA deplex (Mary 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                              Ademovirus; ElA; transactivator; transcription activator; stimulate; expression vector; single-chain binding protein; VAI; enhance; PCR; translation; production; immortal; eukaxyotic cell; seFv; primer; single-chain antibody fragment; imaging; tumour; breat cancer; single-chain antibody fragment; imaging; tumour; breat cancer;
                        19-AUG-1997
                                                        US5658763-A
                                                                                                                         ovarian cancer;
                                                                                                                                                                                                                                                                                                                                                AAW29261
                                                                                                                                                                                                                          Anti-c-erbB-2 single chain antibody 741F8.
                                                                                                                                                                                                                                                                                25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; Columns 27-28; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compans. contg. antigen-targetting antibody fragment constructs comprising dimer of single-chain Fv fragments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CREA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 VSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 AEEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                    VSA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNYGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVKLVESGPELKKPGETVKISCKASGYIFTNYGMMVKQAPGKGLKMMGWINTYTGEPTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                          (updated)
(first entry)
                                                                                                                   c-erbB-2 antigen; digoxin intoxication.
                                                                                                                                                                                                                                                                                                                                                Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oppermann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 552; DB 17;
Pred. No. 2.3e-38;
5; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GFANWGQGTLVT
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                                                                                                                                                 25-MAR-2003
09-OCT-1997
                                                                                                                                                                                                 AAW22400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                        119 VSA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 AA;
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Producing single chain binding protein in immortalised eukaryotic cells - which comprise protein coding sequences, a transcription activator and translation promotion sequences, provides high expression at low copy number
Example 2; Column 29-32; 24pp; English.
                                                                                                                                                                                                                           WPI; 1997-424235/39.
                                                                                                                                                                                                                                                                              Dorai H, Oppermann H,
                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-1993;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                           (CREA-) CREATIVE BIOMOLECULES INC
                                                                                                                                                                                                                                                                                                                                                                                              93US-0143498
95US-0463675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0463675
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CO This sequence is a simple chain anti-o-cable-2 anti-body (asray) (constituted to the constitute of ncoxication on 25-MAR-2003 to correct PF field.)

117 VSA 119 63 AEEFKGREAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG---61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLVT 1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY Similarity EIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNTGEPTY Conservative 85.4%; 5. Score 552; DB 18; Pred. No. 2.3e-38; Mismatches Length 250; Indels 8, Gaps 116 62

AAW22400 standard; Protein; 250 AA.

(updated) (first entry)

Single chain antibody 741F8 protein sequence.

Production; single-chain; binding protein; antibody; eukaryote; virus; transcription activator; promoter; expression; adenovirus; ElA, PCR; polymerase chain reaction, amplification; primer; herpes simplex virus thymidine kinase; vector; enhancer; translation; heterologous.

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RESULT 6
RAMS3168
ID RAWS
XX PARMS
AC RAMS
AC RAMS
DT 16-C
XX T6-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to methods of increasing production of a considerabil hinding protein, especially a simple chain antibody, can generating hinding protein, especially a simple chain antibody. Considerability of the protein that are not and stimulates can viral transcription activator protein that are no and stimulates can viral promoter controlling the expression of but an end of the protein can consider the end of the sequence ALT78873, or an ENA sequence able to promote the adenoviral Val gene (ALT78875).

Constructed by the sequence ALT788761. The coding sequence of the sequence presented here is the amino acid sequence of the sequence presented here is the amino acid sequence of the sequence by sequence of the sequence and the protein from the memolional antibody 52005 (ALT78880) or from Paci (ALT78881).

Constructed by sequence and sequence of the memolional antibody 52005 (ALT78880) or from Paci (ALT78881).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 105; Conserv
    Synthetic
                                                                Artigen imaging; single chain Fv; sFv; linker; dimeric; cancer; c-erb8-2; tumour; diagnosis.
                                                                                                                                                    741F8 anti-c-exbB-2 sFv' dimeric construct protein sequence.
                                                                                                                                                                                                                         16-JUL-1998
                                                                                                                                                                                                                                                                                     AAW53168
                                                                                                                                                                                                                                                                                                                                           AAW53168 standard, Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1993;
05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG----GFANWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIQLVQSGPELXKPGETVKISCKASGYTFTNYGMNWVXQAPGKGLKHMGWINTNTGEPTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 AA;
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                                                                                                                                                                                                                         (first entry)
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95US-0461184.
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Pred. No. 2.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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RESULT 7
AAW47012
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Best Local
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06-FEB-1992;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This represents the protein sequence of a 7418 eDv (single chain Pv) C-tentual Gly-type posterior. This was constructed by consecuring the Vh and VI genes with a DN securit. This was constructed by EDPPLIES in the Table of the State of the
                 13-JUL-1998
                                                           AAW47012;
                                                                                                      AAW47012 standard; Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fv fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-311318/27
N-PSDB; AAV21796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Imaging of antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houston LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP.
(CREA-) CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                               119 VSA 121
                                                                                                                                                                                                                                                          117 VSA 119
                                                                                                                                                                                                                                                                                                 63 AEBFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG----GFANWGQGTLVT
                                                                                                                                                                                                                                                                                                                                61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                            EIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huston JS,
              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0133804.
92US-0831967.
95US-0461838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0461838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
122..135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246..250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in vivo - using dimers of single-chain antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Gly4-Cys C-terminal tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oppermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 552; DB 19;
Pred. No. 2.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ħ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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RESULT 8
AAM80422
ID AAW80
XX AAW8
AC AAW8
XX AAW8
DT 28-J
XX Anti
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                             Anti-c-erbB-2 sFv'; c-erbB-2; antigen; tumour cell; antibody 741F8; targeted delivery; antigen-expressing cell.
                                                                                                                                                                                            28-JAN-1999
                                                                                                                                                                                                                                              AAW80422;
                                                                                                                                                                                                                                                                                         AAW80422 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents single chain binding site molecula (aPv). The sequence was expressed to exemplify the invention, which is an enthold entaryout or an expressed of poorly expressed general manimum and expressed entarial manufactures of executive to the property of the product of the contains transferred but sequences operatively transferred into its genome. The transferred but sequences monothe a viral transferription promoter in the promoter is extinated and a single-chain binding protein. The promoter is extinated by a viral transferription entire transferred by the promoter is extinated by a viral transferription entire transferred by the promoter is extinated by a viral conservation of the production of t
                                                                                                                                              Anti-c-erbB-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Columns 31-32; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immortalised eukaryotic cell comprising transfected DNa sequences useful for enhanced production of proteins encoded by non native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-229831/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dorai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5733782-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single chain binding site molecule 7414F8; sFv 741F8; large scale; transactivating transcription activator; viral transcription promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CREA-) CREATIVE BIOMOLECULES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    119 VSA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 VSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG----GFANWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIQLVQSGPELKKPGETVKISCKASGYTFTNYGMMVKQAPGKGLKMMGWINTNTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production; non-native gene; hard to express gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oppermann H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                        (first entry)
                                                                                                                                              SFV'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0464589.
                                                                                                                                          protein sequence
                                                                                                                                                                                                                                                                                         Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        site molecule (sFv) 741F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 552; DB 19;
Pred. No. 2.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
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                                                                                                                                                                                                                                                  RESULT 9
AAR09428
ID AAR(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-OCT-1993;
06-FEB-1992;
05-JUN-1995;
                   Monoclonal antibody; chimera; light; heavy; chain; constant;
                                                                                                                               25-MAR-2003
04-MAR-1993
variable; antigen; diagnosis; cancer; tumour.
                                                                             KM10 Heavy
                                                                                                                                                                                                        AAR09428
                                                                                                                                                                                                                                                  AAR09428 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-023541/02.
N-PSDB; AAV63397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
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                                                                                                                                                                                                                                                                                                                                                                                                                        117 VSA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                         Chain V Region (mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                       (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0133804.
92US-0831967.
95US-0461386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0461386
                                                                                                                                                                                                                                                  Protein; 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.4%;
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The present sequence represents an anti-cetbs-2 sPv, cerbs-2 is an antisen that is overexpressed on the surface of tumour cells, an antibody designated 741F78 binds cerbs-2 variable heavy and light sequences of antibody 741F8 are connected, together with a linker, to produce the present single chain ry gene, but ceabs-2 sPv exemplifies the invention, biners of the single chain Pv gene, but contains the contrained for targeted delivery of drugs or imaging agents (e.g. cytozounes drugs or the SPM-technetism) to antigen expressing cells, particularly for treatment or diagnosis of tumours (especially of overy or breast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclaic acid encoding single-chain Fv fragment specific for antigens and having C-reminal tail for crosslinking to form dimer with improved pharmacokinetic properties, used to deliver drugs and imaging agents, especially to tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Columns 27-30; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORF.
(CREA-) CREATIVE BIOMOLECULES INC.
63 ABEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG----GFANWGQGTLVT
                                                                ADDEKGREAESLETSASTAYLQINNLKNEDTATYECA----LYGNSPKGEAYWGQGTLVT 116
                                                                                                                                EIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNTGEPTY
                                                                                                                                                                                            EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
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                                                                                                                                                                                                                                                                                                                  Score 552; DB 20;
Pred. No. 2.3e-38;
                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ring DB
                                                                                                                                                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                                                                                                                                                             Length 250;
                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                       Gaps
118
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RESULT 10
AAMO6217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                         tumour; antigen; colon carcinoma; stomach carcinoma; pancreas carcinoma; oesophagus carcinoma; cancer; diagnosis; therapy; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is used in the produ, of a chimeric antibody mol. comprising two light chains and two heavy chains, each having a comprising two light chains and two heavy chains, each having a specificity to an antigen bound by murine monoclonal antibody (MAD). The chimeric antibodise can be used for any purpose for which the original nursine Mads can be used, with the advantage that they are more competible with the human body. They are esp. used for Updated on 25-94MR-2001 to courset M field.)
                                                                                                                                                                                     25-MAR-2003
13-FEB-1997
                                                                                                                                                                                                                                                                           AAW06217 standard;
                       ds sp
                                                      Elerapy;
                                                                                                          Chimeric antibody; monoclonal antibody; ME4; antibody engineering;
                                                                                                                                                  MAb KM10 heavy chain variable region.
                                                                                                                                                                                                                                           AAW06217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Page 123 + Fig 36; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric mouse-human antibodies - prepd. using constant human region murine variable region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-1988;
19-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Better MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8861-4ES-90
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INGENE INT GENETIC.
                                                                                                                                                                                                                                                                                                                                                                                                 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYMGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVKLYESGPELKKPGETVKISCKASGYIFTNYGMWWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                 ADDEKGREAFSLETSVSTGHLQINNLKNBDTATYFCARWGGS-YGMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                            QIQLVQSGPELMKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Horwitz AH,
                                                                                                                                                                                     (updated)
(first entry)
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88US-0241744.
88US-0243739.
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89US-0382768.
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                                                                                                                                                                                                                                                                              Protein; 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 548.5; DB 11; Length 139; Pred. No. 2.5e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes coding for esp. to 3 tumour
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US5843685-A ds sp treatment;

human cancer.

chimeric immunoglobulin; human tumour antigen; chimeric antibody, Heavy chain variable region; murine antibody KM10; antibody ING-1; Mouse KM10 heavy chain variable region

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Matches 101;
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Best Local Similarity
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19-JUN-1989;
21-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The heavy chain variable region (AAW06217) of mouse monoclonal antibody RM10 is the product of a cDNA clone (ARJ442) isolated from a RM10 hybridona cDNA library. MAD RM10 (IgGI) binds to an antigen that is expressed on the surface of human colon, stocach, pencreas and oseophagus carcinomas, but not on most normal adult tissues. The heavy chain and light chain variable regions (see also AAW06218) of RM10 can be Linked to human constant regions and expressed in transformed host cells. Novel mouse-human chmeric amenicative (see also AAW06218) to RM10 can be produced that have agentificity to Maman tumour antigens for use in the treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers
20-MAR-2003
16-APR-1999
                                                                AAW85064;
                                                                                                        AAW85064 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 36; 102pp; English.
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N-PSDB; AAT43442.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (XOMA ) XOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5576184-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agnosis of human cancer.

Jodated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                             1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                  QIQLVQSGPSLMKPGSTVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGSPTY
                                                                                                                                                                                                                                                ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLYTVSA 119
                                                                                                                                                                                                                 ADDFKGRFAFSLETSVSTGHLQINNLKNEDTATYFCARWGGS-YGMDYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chang CP,
(updated)
(first entry)
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89US-0367641.
89US-0382768.
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88US-0241744.
88US-0243739.
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                                                                                                        Protein; 139 AA
                                                                                                                                                                                                                                                                                                                                                                                                           84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                           Score 548.5; DB 1
Pred. No. 2.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lei
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                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                139;
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RESULF 12
ABUS898
ID 58898
XX XBUS8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the heavy chain variable region of murine anthody 2010. The sequence was used to create chimeric nouse-luman immunoglobulins which recognise the human tumour antigen bound by anthody 1MG-1 (produced by bybridoma cell line ATCC HB 9912). The chimeric antibodies also have an antigen-binding site that complement-dependent cytolysis of target cells or antibody dependent cellular cytolysis of target cells or chimeric antibodies can be used for therapeutic purposes in the freateent of human capacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Better MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995;
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               US6461824-B1
                                                                                                         Mouse; human tumour antigen; anti-human tumour antigen-antibody; ING-1 antibody; cell line HB9812; immunoassay; imaging;
                                                                                                                                                          Mouse antibody heavy chain variable region #5
                                                                                                                                                                                           16-APR-2003
                                                                                                                                                                                                                                                       ABU58898 standard; Protein; 139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 36; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoassay, imaging or antitumour agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric antibody specific for human tumour antigen - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV71160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-DEC-1994;
06-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-
                                                                             heavy chain variable region
                                                                                            tumour diagnosis; tumour therapy; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-044574/04.
                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                       80 ADDFKGRFAFSLETSVSTGHLQINNLKNEDTATYFCARWGGS-YGMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                    20 QIQLVQSGPELMKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 79
                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                                                                                                   ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                         (first entry)
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89US-0367641.
89US-0382768.
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88US-0241744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 548.5; DB 2
Pred. No. 2.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20; Length 139;
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RESULT 13 AAR64232

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ADDEKGREAFSLETSVSTGHLQINNLKNEDTATYFCARWGGS-YGMDYWGQGTSVTVSS

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Query Match Best Local Matches 101;

Similarity

84.9%;

Score 548.5; DB 24; Pred. No. 2.5e-38; 7; Mismatches 10;

Indels Length 139; ۲,

Conservative

Sequence

139 AA;

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The invention describes an antibody comprising a human content region and a variable region having specificity for the human through a formal content region bound by the 1887 antibody, where the 1807 is produced by cell lines the state of the state of the human tumour antigen. The same affinity as the 1891 as deposited with ACC, and the antibody has the same affinity as the 1891 as deposited with ACC, and the antibody has the same affinity as the 1807 in the human tumour antigen. The antibody, detecting a label and relating the detected label to the presence of a label-detectable antigen that an animal by contenting the antibody with a part of the animal supported of containing the antigen that the same antigen in an animal by contenting the antigen; and for killing cells supported of containing the antigen; and for killing cells surjected of a label for the presence of the antigen; and for killing cells and the same of the antigen; and for killing cells and the same of the antigen; and for killing cells and the same of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody for detecting antigen in animal or killing cella carrying antigen comprises human constant region and variable region having apecificity for human tumor antigen bound by ING-1 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Better MD,
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06-SEP-1988;
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antigen-antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0241744.
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RESULT 14
AAR64257
ID AAR66
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AC AAR66
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Best Local &
Matches 101
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27-JAN-1994;
09-FEB-1994;
29-MAR-1994;
                                                                                                                                                                                                                                                                                                  L233 is a mouse MAb raised against human MHC class II. The nucleotide and amino acid sequences of L343 VL and VH regions given in AAQ80359/R64231 and AAQ80360/R64232, respectively.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanized antibody; antibody engineering; MHC class I; major histocompatibility region; HLA; monoclonal antibody; MAb; LMA3; immunological disease; transplantation; light chain; beavy chain; variable region; complementarity determining region;
         AAR64257;
                             AAR64257 standard;
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                          CDR-grafted humanized antibodies based on these sequences have
                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig. 2; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                   conditions
                                                                                                                                                                                                                                                                                                                                                                         New humanised anti-HLA DR antibodies - used for diagnosis and treatment of immunological diseases and transplantation related
                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ80360
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-036480/05
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17-JUL-1995
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                                                                                                                      ADDFKGRFAFSLETSASTAYLQINNLKNEDTAKYFCARDITAVVPTGFDYWGQGTTLTVS
                                                                                                                                          ADDEKGREAFSLETSASTAYLQINNLKNEDTATYFCA--LYGNSPKGFAYWGQGTLVTVS 118
                                                                                                                                                              QIQUVQSGPELKXPGETVKISCKASGFTFTNYGMNWVKQAPGKGLKWMGWINTYTRBPTY
                                                                                                                                                                             EVKLVESGPELKKFGETVKISCKASGXIFTNYGMWVKQAPGKGLKWMGWINTYTGEPTY
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ilarity 83.5%;
Conservative
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94GB-0001597.
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94GB-0006222.
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                             Protein; 140 AA
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Pred. No. 4.1e-38;
8; Mismatches 10
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RESULT 15
AAR37717
ID AAR37
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Best Local :
                                                                                                                                                                                                                                                                                     Matches
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27-JAN-1994;
09-FEB-1994;
29-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                          COMMA for mouse anti-human MHC-III MAD £243 (ATCC HB 55; heavy variable region was cloned by CTK. Clone pBITO2 was obtained contained a WH insert having the sequence given in AAQ00426; t deduced amino acid sequence is given in AAQ04276; hitcred antibodies have been prepared that retain immunosuppressive properties but show reduced binding to FcKI.

Updated on 23-MAR-2001 to correct PM field.)
           25-MAR-2003
30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1243; heavy chain; VH; monoclonal antibody: Mab; MHC-II; major histocompatibility complex class II; immunosuppressive; variable region; Fc receptor I; FcRI; antibody engineering;
                                              AAR37717,
                                                                        AAR37717 standard;
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig. 3; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     constant
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N-PSDB; AAQ80426.
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31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CLLT ) CBLLTECH LTD
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                                                                                                                                                                                    ADDFKGRFAFSLETSASTAYLQINNLKNEDTAKYFCARDITAVVPTGFDYWGQGTTLTVS
                                                                                                                                                                                                         ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA--LYGNSPKGFAYWGQGTLVTVS
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                                                                                                                                                                                                                                                                                                                                    140 AA;
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                                                                      Protein;
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Pred. No. 4.1e-38;
8; Mismatches 10
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Mouse 4C10 anti-idiotype Ab heavy chain V region.

PXPXPXQXXXXXX

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Search completed: November 7, 2003, 07:26:59 Job time : 52.3178 secs
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Best Local Similarity 84.08; Pred, No. 5.9e-38;
Matches 100; Conservative 8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of the 4C10 anti-idictipe Ab heavy chain V region which was used in the construction of a murine/human emocloral anti-idictive anti-body (MALA). The MALA elicits an anti-ganglicate response and produces anti-bodies which induce cyclocoxic destruction of cancer cells bearing the ganglicaides. It can be used for treation of cancer cells bearing the ganglicaides, It can be used as a immunomodulator to enhance anti-cancer immunity, suppress organ transplant rejection and enhance anti-cancer immunity, suppress organ transplant rejection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  suppress autoimmune disease. of cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimerio murine-human anti-idiotype monocional antibodies useful as immuno-modulators for treating and diagnosting cancers, and for suppressing organ transplant rejection and auto-immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                          80 TEEFKGREAFSLETSANTAYLLINNLKNEETATYECARGEGHAWGEAYWGQGTLVTVSA 138
                                                                                                                                                                                 61 ADDFKGRFAFSLETSASTAXLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                               20 QIQLVQSGPBLKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNTGEPTY 79
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1 Ogn2_6/podate/2/pubpas/USO7_PUBCOMB.pep.*

2 Ogn2_6/prodate/2/pubpas/USO7_WEW_PUB_pep.*

3 Ogn2_6/prodate/2/pubpas/USO6_PUBCOMB.pep.*

4 Ogn2_6/prodate/2/pubpas/USO6_PUBCOMB.pep.*

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195.799 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-05-1608-9

2 US-10-234-671-9

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US-09-975-221A-106

1 US-09-775-221A-106

1 US-09-775-221A-106

2 US-10-138 777A-1

US-09-965-099-11

4 US-10-965-099-11

4 US-10-965-099-11

4 US-10-965-099-10

4 US-10-965-099-10

4 US-10-967-7293A-1

1 US-09-977-233A-1

2 US-10-138 777A-2

2 US-10-138 777A-2

2 US-10-138 777A-3

2 US-09-977-233A-1

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Sequence 25, Appli
Sequence 9, Appli
Sequence 90, Appli
Sequence 106, App
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Sequence 107, Appli
Sequence 109, App
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Sequence 32, Appli
Sequence 32, Appli
Sequence 31, Appli

SEULT 1 125-25-2 Sequence 2. Application US/09887853 Sequence 2. Application US/09887853 Patent No. US20020168375A1 GENERAL INFUSANTION: GENERAL INFUSANTION: GENERAL INFUSANTION: Storyermann, Mermann Brigs David B. TITLE OF INVENTION: Storyerthetic Binding Proteins For NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:

Result No.

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Description

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US-10-887-853-2 US-10-422-048-19 US-10-282-0268-35 US-10-288-883-9 US-10-288-883-8 US-10-288-883-8 US-10-138-727A-26 US-10-288-883-3 US-10-288-883-3 US-10-288-883-3 US-10-288-883-13 US-10-288-883-13

Sequence 2, Appli Sequence 35, Appli Sequence 35, Appli Sequence 3, Appli Sequence 4, Appli Sequence 6, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli

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CIBERRY APPLICATION INVOICES: 105/10/422,049
CIBERRY ELIZA DATE, 2001-44-22
PRIOR FILIRO BATE, 199-00-14
PRIOR FILIRO TATE, 199-00-12
PRIOR PELIFORITON INVOICES: 09/456,418
PRIOR FILIRO DATE: 199-00-12
PRIOR PELIFORITON INVOICES: 09/373,882
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                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Publication No. US20030199679A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Adair, John Robert
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Emtege, John Spence:
APPLICANT: Emtege, John Spence:
APPLICANT: Bodner, Mark Hilliam
TIIIB OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
FILB REFERENCE: CARPOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Humanized OTHER INFORMATION: Antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Murine
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TYPE: PRT
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 105; Conser
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
118 S 118
                                                                   119 A 119
                                                                                                                            62 DDPKGREAFSLETSASTAYLQINNLKNEDTATYECLLYGNSPKGF---AYMGQGTLYTVS 118
62 DDPKGREAFSLETSASTAYLQINNLKNEDTATYECA.---RKEGFYAMDYMGGGTSYTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 VSA 123
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                                                                                                                                                                                                                                                                          2 IQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVTQAPGKGLKWMGWINTYTGEPTYA
                                                                                                                                                                                                                                                                                                            2 VKLVESGPELKKPGETVKISCKASGYIFTNYGMNWYKQAPGKGLKWMGWINTYTGEPTYA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVKLVESGEELKKEGETVKISCKASGYIETNYGMMVKQAEGKGLKMMGMINTYTGEETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDEKGREAESLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLVT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 250 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 543.5; DB
Pred. No. 8e-41;
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Pred. No. 2.9e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 118;
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                                                                                                                                                ; ORGANISM: Mouse
US-10-268-883-9
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LENGTH: 160
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                                                          Query Match
Best Local Similarity
Matches 100; Consert
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL IMPONANTION:
APPLICANT: For, J. Yun
APPLICANT: Green, Jennifor Macphate
TITLE OF INTENTION: Anti-HIA-DR Antibodies and the Methods of Using Thereof
FILE REFERENCE: 05882.0662.RPUSOI.
FILE REFERENCE: 05882.0662.RPUSOI.
                                                                                                                                                                                                           SEQ ID NO 9
LENGTH: 118
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Publication No. US20030138862A1
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Best Local Similarity
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APPLICANT, Hisching, Peter

APPLICANT, Lerner, Richard A.

APPLICANT, Geo, Champshou

TITLE OF INVENTION: ENTOOS FOR DISPLAY OF HETERODIMERIC

TITLE OF INVENTION: ENFOOSITIONS, VECTORS AND COMBINATORIAL LIBERRIES

FILE REFERENCE, TSRI 693.0 IL

FILE REFERENCE, TSRI 693.0 IL
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Publication No. US20030186322A1
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: USSN 60/329,178
PRIOR FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: USSN 60/331,965
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/222,026A
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 09/318,786
PRIOR FILING DATE: 1999-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                          TYPE: PRT
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1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDFRGRFAFSLATSASTAYLQIINLKNEDTATYFCETY-DSPLG-DYWGQGTTVTVSS 119
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                                                          Conservative
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                                                                           82.4%;
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                                                       Score 532.5; DB 1
Pred. No. 7.5e-40;
6; Mismatches 9
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Pred. No. 4.9e-40;
5; Mismatches 10;
                                                                                             DB 12; Length 118;
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Patent No. US20020168375A1
GENERAL INFORMATION:
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LENGTH: 137
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Publication No. US20030138862A1
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Best Local Similarity 82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: USSN 60/331,965
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                 Oppermann, Hermann
Flouston, L. L.
Ring, David B.
RITILS OF INVENTION: Blosynthetic Binding Proteins For
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Huston, James S
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 11
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61 ADDPKGREAPSLETSARTAYLQINNLKNEDMATYFCARGDYYG---PPDYMGQGTLTTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
                                                                                                                                                                         STREET: Exchange Place, 53 State Street
                                                                                                                   COUNTRY: USA
                                                                                                                                     CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                           ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
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                                                                                                                                                                                                                                                  Imaging
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TELECOMPUTCATION HEROPHATION:
TELECHARS: 617-248-7407
INFORMATICLERAY: 617-248-7406
INFORMATICLERAY: 617-248-7406
INFORMATICLERAY: 283 MAINO SAIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09971543
Patent No. US20020146846A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APELICANT: PLICKTHIM, ADDREAS
APELICANT: HORSESE, ANNEASE
APELICANT: HORSESE, ANNEASE
APELICANT: HORSESE, ANNEASE
APELICANT: HORSESE, ANNEASE
TITLE OF INVESTION: OF ELEMENOGLOBULING OR IMMINOGLOBULIN PRACHENTS, AND
TITLE OF INVESTION: FREITLICED MATI-EDF-2 SCTV FRAGMENT
FILE REFERENCE: FLUCK-3 COM.
THE REFERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: EP 99 10 7030.1
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILIMO DATE: 21-Jun-2001
PICASES PECATION: CHRISTON
PRIOR PAPLICATION HOMEN:
APPLICATION HOMEN:
APPLICATION HOMEN: US/09/13,804
FILIMO DATE: -Unknown:
ATTORNEY/ARMT IMPORMATION:
NAME: Kelley, Robin D.
RESISTRALION HOMEN: 34,637
                                                                                                                                                                                                                                                                                                                                                                        Match 82.0%;
Local Similarity 84.0%;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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61 ADDFKGRFAFSLETSASTAYLQINNLKHEDTAYYFOALYGUSEKGFAYMOGGTLYTVSA 119 61 ADDFKGRFAFSLETSASAAYLQINNLKHEDTAYYFOARF--AIKG-DYMGQGTTLTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSFKGFAYWGQGFLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ADDPKERFAFSLETSATTAHLQINNLRNEDSATYPCA----RRFGFAYWGQGTLVSVSA 115
                                                                                                                                                            1 BIQLVQSGPELKKFGETVKISCKASGYTFANYGMMMKQAPGKGLKWMGWINTYTGQSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98;
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                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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82.4%; Pred. No. 2.5e-39;
ative 10; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                      8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Score 529.5; DB 10; Length 116; Pred. No. 1.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 243;
                                                                                                                                                                                                                                                                                                                                      Indels 3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
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RESULT 9
US-10-127-890-124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ); ORGANISM: Mus sp
US-09-971-543-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-971-543-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 124, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.0%;
Best Local Similarity 84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09971543
Patent No. US20020146846A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PLICKTUM, ANDREAS
APPLICANT: MICKESSE, ANEWHALE
APPLICANT: MILLUDA, JORG
TITLE OF INVESTICAN: DEMONSCRIPE, AND FOR THE STABILIZATION OF CHIMERIC
TITLE OF INVESTICAN: IMMINICALIZED ANT: 569-2 a GET PERAGRETY
TITLE OF INVESTICAN: STABILIZED ANT: 569-2 a GET PERAGRETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PLUCK-3 CON
GURRENT APPLICANTION NUMBER: U8/09/971,543
CURRENT ALTIMO DATE: . 2001-10-04
PRICE APPLICATION NUMBER: PCT/EP00/03176
PRICE LILING DATE: . 2000-04-10
PRICE APPLICATION NUMBER: EP 99 10 7030.1
PRICE FILING DATE: . 1999-04-09
PRICE FILING DATE: . 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                    COMPTER READABLE PORM:
COMPTER READABLE Floppy disk
COMPTERS: IBM PC compatible
OPERATING SETEM: PC COMPATIBLE
OPERATING SETEM: PC COMPATIBLE
OPERATING SETEM: PC-DOS/MS-DOS
SOFTWARE: PATEMITIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/17,890
FILING APPLICATION BATH:
PRIOR APPLICATION BATH:
PRIOR APPLICATION BATH:
PRIOR APPLICATION BATH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carroll, Stephen F.
Studnika, Gary M.
STUTLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 QVQLQQSGPBLKKPGETVKISCKASGYTFTNYGMNWVKQAPGRGLKWMGWINTYTGESTY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVXQAPGKGLKWMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDFKGRFAFSLETSASAAYLQINNLKNEDTATYFCARF--AIKG-DYWGQGTTLTVSS 253
        APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996 APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
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Pred. No. 2.9e-39;
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61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSFKGFAYWGQGTLVTVSA 119
                                                                                                                                1 BVKLVESGPELKKPGETVKISCKASGYIFTNYGMMWVKQAPGKGLKWMGWINTYTGEPTY 60
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US-10-138-727A-2
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Query Match 81.5%; Score 526.5; DB 12; Length 116; Best Local Similarity 81.5%; Pred. No. 2.5e-39; Matches 97; Conservative 11; Mismatches 8; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: (01)lies, Stephen
APPLICANT: (01A), Susan
APPLICANT: (01A), Susan
APPLICANT: (01A), Susan
TITLE DG INVERTION: Recombinant Tumor Specific Antibody and Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION HOMBER: US/10/138,727A
CURRENT APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-03
MUMBER: OF SEQ 1D NOS: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0
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INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   OTHER INFORMATION: KS VH mouse
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                            FEATURE:
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PELLING DATE: 13-MAY-1993
PELLING DATE: 13-MAY-1993
PELLING DATE: 03-DEC-1992
ATTORNEY/AGRIT DATE: 03-DEC-1992
ATTORNEY/AGRIT DATE: 03-DEC-1992
PELLING DATE: 03-DEC-1992
PELL
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Local Similarity 83.2%;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 124:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ADDYKGRPAPSLETSASTAYLQINNLKNEDTATYFCTRRGYD-WYFDVWGAGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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        Gaps
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QIQLVQSGPELKKPGETVKISCKASGYTFINYGMNWVRQAPGKGLKWMGWINTYTGEPTY

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ADDFKGRFVFSLETSASTAFLQLNNLRSEDTATYFCVRF--ISKG-DYWGQGTSVTVSS 116

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61 ADDEKGREAESLETSASTAYLQINNLKNEDMATYECATTTLITYYEDYWGQGTTLTVSS 119

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US-10-268-883-3
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US-10-138-727A-26
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CURRENT FILING DATE: 2002-05-03
PRICE PLICATION WINDER: US 6/289,564
PRICE FILING DATE: 2001-05-03
VINNEER OF SEQ ID NOS: 42
VINNEER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 26
SEQ ID NO 26
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rubilcation No. U820030157054A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: LJ, Kin-Ming
APPLICANT: Qian, Susan
                                                                                                                                                                                      Matches
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Best Local :
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Publication No. US20030138862A1
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                                                                                                                                                                                                                                                                                                                                                                                                                  NPELICANT: Teo. J. Yun
APPLICANT: Teo. J. Yun
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-Ne Antibodies and the Methods of Using Thereof
FILE REFERENCE, 15882,1062. APUS01
CURRENT APPLICATION NUMBER: US/10/266,883
CURRENT FILING DATE: 2001-01-02-6
PRIOR APPLICATION NUMBER: USSN 60/323,178
PRIOR APPLICATION NUMBER: USSN 60/323,178
PRIOR APPLICATION NUMBER: USSN 60/331,965
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TITLE DF INVENTION: Recombinant Tumor Specific Antibody and Use Thereof
FILE REFERENCE: LEX-019
                                                                                                                                                                                                                                                                                                                      ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                           Match 81.4%;
Local Similarity 82.4%;
61 ADDFKGRFAFSLETSASTAYLQINNLKNBUTATYFCALYGNSFKGFAYMGQGTLVTVSA 119
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                                                                              1 QIQLVQSGPELKKPGETVKISCKASKYTFTNYGMNWVXQAPGKVLRWMGWINTYTGEPTY 60
                                                                                                                                1 EVKLVESGPELKKEGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
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Pred. No. 2.8e-39;
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                                                                                         Query Match
                                                                                                                                                                                                                                   SEQ ID NO
                                                                                                                                                                                                                                                                            CURRENT PAPILCATION NUMBER: US/10/268,883
CURRENT PILLING DATE: 2001-03-26
PRIOR REPLICATION NUMBER: USSN 60/329,178
PRIOR PILLING DATE: 2001-11-121
PRIOR REPLICATION NUMBER: USSN 60/331,965
PRIOR RELLING DATE: 2001-11-21
TUNBER: OF SED ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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CURRENT PILLIA DATE: 2001-10-10
PRIOR APPLICATION NUMBER: USAN 66/229.178
PRIOR PILLIAN DATE: 2001-11-01
PRIOR APPLICATION NUMBER: USAN 66/229.178
PRIOR PILLIAN DATE: 2001-11-121
PRIOR PILLIAN DATE: 2001-11-121
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Teo, J. Yun
APPLICANT: Green, Jennifer Wacphate
TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
FILE REFERENCE: 05892.0062.NPUS01
FILE REFERENCE: 05892.0062.NPUS01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tso, J.
APPLICANT: Tso, Jenniffer
                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                ORGANISM: Mouse
                                                                                                                                                                                      TYPE: PRT
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                                                                   Local Similarity
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1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
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                                            Conservative
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                                                               Score 526; DB 12; Length 138; Pred. No. 3.2e-39;
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Pred. No. 2.8e-39;
                                            Mismatches
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RESULT 15

US-09-977-283A-13

I Sequence 13, Application US/09977283A

Publication No. 202030031664A1

Publication No. 202030031664A1

Publication No. 202030031664A1

Publication No. 20203031664A1

Publication No. 202
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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22 /ggp2 6/ptcdate/l/iss/5A_COMB.psp:*

31 /ggp2 6/ptcdate/l/iss/6A_COMB.psp:*

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34 /ggp2 6/ptcdate/l/iss/backfiles/.psp:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                Gapext 0.5
                                                                  18-00-56-796-16
18-00-599-17-76
18-00-599-17-80-90
18-00-902-486-9
18-00-902-486-9
18-00-902-481-53
18-00-875-811-53
18-00-875-913-50
18-00-875-913-50
18-00-875-913-50
18-00-887-93-20
18-00-481-33-86-6
18-00-481-33-86-6
18-00-481-386-6
18-00-481-386-124
18-00-481-386-124
18-00-481-386-124
18-00-481-386-128
18-00-481-386-128
18-00-481-386-128
18-00-481-388-28
18-00-481-388-28
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US-08-461-838-2
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COMPUTER READMENTS FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READMENTS FORM:
COMPUTER IDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DACEDIA Release #1.0, Version #1.25
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACEDIA Release #1.0, Version #1.25
OPERATING DATE:
PLINED DATE:
PLINE
                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-133-804-2
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US-08-133-804-2
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Best Local :
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Patent No. 5534254
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APPLICANT: Gouston, L. L.
APPLICANT: Gouston, L. L.
APPLICANT: Houston, L. L.
APPLICANT: Houston, Blosynthetic Binding Proteins For INTELLO P. INVESTION: 1 Hospitch State On INVESTION: 1 Hospitch State On INVESTION: 1 Hospitch State On Investion: 1 Houston Brown Bro
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CITY: Boston
STATE: Massaci
COUNTRY: USA
                                                                                                                                                       Eocal Similarity 85.4%; B5.4%; B5.4%; B5.4%; B5.4%;
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STREET: Exchange Place, 53 State Street
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US-09-116-39-124
US-09-610-38-124
US-09-610-38-124
US-09-610-689-66
US-08-472-7818-68
US-08-472-7818-68
US-08-91-845-28
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US-09-91-845-28
US-09-91-85-33-15
US-09-91-85-33-15
US-09-33-35-15
US-09-33-35-15
US-09-33-35-15
US-09-33-35-11
US-09-344-0100-7
US-09-344-0100-7
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Result No.

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Score 552; DB 1; I Pred. No. 2.2e-43; 5; Mismatches 5;

DB 1, Length 250 Indels

8 Gaps

62 60 543.5 543.5 539.5 539.5

Database

Scoring table: Perfect score:

ALIGNMENTS

sequence 124, App
sequence 124, App
sequence 124, App
sequence 16, App
sequence 66, App
sequence 66, App
sequence 66, App
sequence 66, App
sequence 11, App
sequence 12, App
sequence 21, App
sequence 17, App
sequence 11, App

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OM protein -

RESULT 3 US-08-463-675-8	Db 119 V8A 121	Qy 117 VSA 119	Oy 61 ADDEGREASELETASSPALLQINALMSEDTATYFOLYGNSPKOFAUMOQOTLUT 116 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	OY 1 WKLYSGJELKKEGETYKISCKAGYITTNYGMENVKQAFGKGLKMANGHINTYTGEPTY 60 1		50;	US-08-461-184-8	MOLECULE	; LENGTH: 250 amino acids TYPE: amino acid	22	KEPREMUEL/DOCKET NUMBER: CRP093 TELECOMMUTCATION INFORMATION: TELEPHONE: 617/248-7000 TELEPHONE: 617/248-7100	INFORMATION: Y, ROBIN D NUMBER: 34,6	; APPLICATION NUMBER: US/08/143,498 ; FILING DATE:	; PRIOR APPLICATION: 435	APPLICATION NUMBER: US/08/461,184 FILING DATE:	CURRENT APPLICATION DATA. CURRENT APPLICATION DATA.	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC comparible	四に	ત્રા∾	ADDEESSEE: PATENT AUMINISTRATOR, CREATIVE BIOMOLECULES, INC STREET: 45 SOUTH STREET ; CIT: HOPKINTON	NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:	TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN TITLE OF INVENTION: PRODUCTION FROM NON-MATTUE DNA	RMAN.		RESULT 2 US-08-461-184-8	TT MON ETT CO	117 VSA	63 ABBEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYGGFANWGQGTLVT 118	QY 61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKSFAYMQQQTLVT 116
ADDRE STREE	, TITLE (; APPLICA	; Patent No ; GENERAL ; GENERAL	RESULT 4 US-08-464-5	Db 1	Qy 1	Db	Q	Db	Q	Query Mat Best Loca Matches	, MOLECU US-08-463-6	TYPE	; sequen	TELE	; REFE	; ATTORN ; NAME ; REGI	FILI	PRIOR	APPL	SOFT	; COMP	; COMPUI	; STAT	CITY	NUMBER	; APPLIC ; TITLE	; APPLI	; Sequence ; Patent No

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WEDIUM TYPE: Floppy disk
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COMPUTER: IMP COMPACTION
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INGTH: 250 amino acids
'PE: amino acid
'PE: amino acid
'PDOLOGY: linear
COULE TYPE: protein
'-675-8
CANT: DORAL, HAIMANT
CANT: OPERANN, HERMAN
OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH FROTEIN
OF INVENTION: PRODUCTION FROM NON-MATIVE DRA
RO SEQUENCES: 1
RESSEE: PRODUCTION FROM NON-MATIVE DRA
RO SEQUENCES: 1
RESSEE: ADTENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
RESSEE: HOPKINFON
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EFAX: 617/248-7100
TION FOR SEQ ID NO: 8:
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8, Application US/08464589
5. 5733782
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SEPONDENCE ADDRESS;
SERSISEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC.
EET: 45 SOUTH STREET
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ISTRATION NUMBER: 34,637
ERENCE/DOCKET NUMBER: CRP093
OWNUNICATION INFORMATION:
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CANT: OPPERMANN, HERMANN
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o. 5658763
INFORMATION:
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CRY: USA
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 8:
                      COMPUTER READMENTS FOOM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATER: IBM PC compatible
OPERATURG SYSTEM: PC-DOSS/MS-DOS
SOFTWARE: Pacent IR Release #1.0, Version #1.25
CURRENT APPLICATION DAY'S.
                                                                                                                                                                                                                                           CORRESPONDERGE ADDRESS:
ADDRESSEE: Testa, Narwitz & Thibeault/Patent Department STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                          APPLICANT: thatcon James S.
APPLICANT: Opermann Hermann
APPLICANT: Houston L. L.
APPLICANT: Houston L. L.
APPLICANT: Risg. David B.
APPLICANT: Risg. David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
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REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEPHONE: 617/248-7000
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COMPUTER: IR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTUMARE: Batentin Release #1.0, Version #1.25
CURRENT AFFLICATION DATA:
AFFLICATION INDEER: US/00/464,589
FILING DATE: 05-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/143,498
FILING DATE: 25-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: USCALA DOCUMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07148
COMPUTER READABLE FORM:
                                                                                                                                                                                                      CITY: Boston
STATE: Massachusetts
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TYPE: amino acid
TOPOLOGY: linear
APPLICATION NUMBER: US/08/461,838
                                                                                                                                                                ZIP: 02109
                                                                                                                                                                                   COUNTRY:
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milarity 85.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 552; DB 1; Length 250; Pred. No. 2.2e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-461-386-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INPORMATION:

NAME: Religy Reptin D. 3.

REGISTRATION NUMBER: 24.634

TELECOMMUNICATION INPORMATION:

TELEPHONE: 617-248-7477

INFORMATION POR SEC ID NO: 2:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGTH: 250 mains eaids

TYPE: amains eaid

TOPOTLOST: Alleat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08461386 Patent No. 5837846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                              INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109

COMPUTER REALIBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN FO COMPUTER: IN FO COMPUTER: IN FO COMPUTER: IN FO COMPUTER: IN FO COMPUTER: IN FO COMPUTER: IN FOR CO
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ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nuston, James S.
APPLICANT: Appermann, Arraman
APPLICANT: Houston, L. L.
APPLICANT: Houston, L. L.
APPLICANT: Houston, L. L.
TITLE OF INVENTION: Biosynthetic Binding Proteins For TITLE OF INVENTION: Imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                              TELEPHONE: 617-248-7100
                                                                                                                                                                                                                                                                                                      NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EIQLVQSGPELKKPGETVKISCKASGYTFINYGMNWVKQAPGKGLKWMGWINTNYGEPTY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
amino acid
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TOPOLOGY:

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US-08-356-786-16
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US-08-461-386-2
                                                                                                                Matches 105;
                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08356786 Patent No. 5877305
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                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 248-710
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                          LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTING BATA:
APPLICATION MATA:
APPLICATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosyn'
TITLE OF INVENTION: Marker
                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
CITY: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
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Local Similarity 85.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMMVXQAPGXGLKMMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG----GFANWGQGTLVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oppermann, Hermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houston, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      James S.
                                                                                                                                          85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biosynthetic Binding Protein for Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRP-053
                                                                                                          Score 552; DB 2; Length 622
Pred. No. 5.7e-43;
5; Mismatches 5; Indels
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Pred. No. 2.2e-43;
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                                                                                                          Gaps
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                                ; Sequence 6, Application US/08279772A ; Patent No. 6080560
                                                                                                US-08-279-772A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 101;
GENERAL INFORMATION:
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; MOLECULE TYPE: protein
US-08-569-147-76
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                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPRAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER FADABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER IBM PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
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FILING DATE: 25-March-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6180377ris, LLP STREET: One Liberty Place - 46th Floor CITY: Philadelphia
140 S 140
                                          119 A 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 VSA 121
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                                                                                                                        61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA--LYGNSPKGFAYWGQGTLVTVS 118
                                                                                                                                                                         20 QIQLVQSGPELKKPGETVKISCKASGFTFTNYGMNWVKQAPGKGLKWMGWINTYTREPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 AEEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG----GFANWGQGTLVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSFKGFAYWGQGTLVT 116
                                                                                                                                                                                                             1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGNNWVKQAPGKGLKWNGWINTYTGEPTY
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                                                                                 ADDEKGREAFSLETSASTAYLQINNLKNEDTAKYFCARDITAVVPTGFDYWGQGTTLTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PA
                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                    84.5%;
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388: CARP-0047
                                                                                                                                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                       Score 546; DB 3;
Pred. No. 4.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25 (EPO)
                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                             Length 140;
                                                                                                                                                                                                                                                                  Indels
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APPLICANT:

Russell, David R

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US-08-902-486-9
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NAME SORT, NICHOLAND.

RECISTRATION NUMBER: 27.36.

RECISTRATION INFORMATION:
TELEPHONE GOR 251.900.
TELEPHONE GOR 251.916.
INFORMATION FOR ESD ID NO: 6.
SEQUENCE CHARACTERISTICS.

ENGINE 252 amino acids
TTRE. amino acids
TTRE. INFORMATION INFORMATION:

LENGTH: 252 amino acids
TTRE. INFORMATION INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08902486
Patent No. 6140075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDITM TYPE: Plopy disk
COMPTEN CONTINUE OF THE PROPERTY OF TH
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT: Russel, David R.
APPLICANT: PAILST, James T.
TITLE OF INVENTION. METHOD FOR PRODUCTING ANTIBODIES AND TITLE OF INVENTION. PROTEIN TOXINS IN PLANT CELLS
MUMBER OF SEQUENCES: 15
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: Method for Producing Antibodies in Plant
TITLE OF INVENTION: Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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ADDRESSEE: Quarles and Brady
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                                                                                                                                                                                                   COUNTRY: US
ZIP: 53701-2113
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                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/279,772A
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Pred. No. 1.3e-42;
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FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:

US 60/011,800

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588

COMPITER: IRW FO COMPLETA:
OPERATING SYSTEM: PO COMPLETA:
SOFTMARE: PACCHICI RELEASE #1.0, Version #1.30
CURRENT APPLICATION DAYA.
APPLICATION UNMERS: US/08/875,611
FILING DAYE: 19-FEB-1998/875,611

ZIP: 94111-3834 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY: CITY: San Francisco

California USA

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                                                                                                                                                                                                                                                                                 RESULT 11
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                                                                                                                                                                                       Sequence 53, Applicati
Patent No. 6045793
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELBEAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                   APPLICANT: Pybak, Susanna M.
APPLICANT: Netron, Dianna L.
APPLICANT: Boque, Liuis
APPLICANT: Holeawer, Alexander
TITLE Of INVENTION: Recombinant Ribonuclease Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 67
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 84.1%;
Local Similarity 84.3%;
es 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             191 ADDFKGRFAFSLETSAYTAYLQINNLKNEDMATYFCARFSYGNS-KYADYWGQGTTLTVS 249
                                                                                                                                                                                                                                                                                                                                             250 S 250
                                                                                                                                                                                                                                                                                                                                                                                  119 A 119
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                                                                                                                                                                                                                  53, Application US/08875811
>: 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ADDPKGREAFSLETSASTAYLQINNLKNEDTATYFCA--LYGNSPKGFAYWGQGTLVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVKIVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            670513.90261
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/ MOLECULE TYPE: protein US-08-875-811-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 83.5%;
Best Local Similarity 86.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                       TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                        NAME: FATIS, SUSAN K. 1,739
REGISTRATION NUMBER: 01:
REFERENCE, DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (4.15) 576-0200
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 6:
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rybak, Susanna M.
APPLICANT: Neveton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Roque, Lluis
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
                                                           - TYPE: a
                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                           TOPCLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: WO PCT/US97/02588
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/OFFILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6045793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 539.5; DB 3
Pred. No. 4.5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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US-08-483-749A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: fusion ; OTHER INFORMATION: polypeptide US-09-318-786-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-09-318-786-35
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                                                                                                                                                                                                                                                                   PARENT NO. 6053561
CEMERAL INFORMATION:
CEMERAL INFORMATION:
APPLICANT, EING, DAVID B.
TITLE OF INVENTION: MATICEN-EINDING SITES OF ANTISODY
TITLE OF INVENTION: MALEGULES SPECIFIC FOR CANCER ANTICENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 35
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT, Janda, Kim D
APPLICANT, Harching, Reter
APPLICANT, Harber, Richard A
APPLICANT, Jarner, Richard A
APPLICANT, Jarner, Richard A
APPLICANT, Jerney, Richard A
APPLICANT, Jerney, METHODS FOR DISPLAY OF HETERODHERIC PROTEINS ON
TITLE OF INVENTION, PILLAMENTONS PHAGE USING PUIL AND PIX, COMPOSITIONS,
TITLE OF INVENTION, PILLAMENTONS PHAGE USING PUIL BEARIES
FILE REFERENCE, TSSE00105COS AND COMBINATIONIAL LIBRARIES
FILE REFERENCE, TSSE00105COS AND COMBINATIONIAL LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/08483749A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 103; Conservative
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CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
COMPUTER THE FORM:
COMPUTER TIBH PC Compatible
COMPUTER: IBH PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
                                                                                                ZIP: 94662-8097
                                                                                                                  COUNTRY:
                                                                                                                                                           STREET: INTELLECTUAL PROPERTY - R440, CITY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y march
33.0%; Score 536; DB 4; Length 160;
Local Similarity 85.7%; Pred. No. 3.9e-42;
nes 102; Conservative 5; Kismatchea 10. ...
                                                                                                                                                                                                           ADDRESSEE: CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNS£KGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 ADDFRGRFAFSLATSASTAYLOIINLKNEDTATYFCETY-DSPLG-DYWGQGTTVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 ADDFKGRFAFSLETSASAAYLQINNLKNEDTATYFCARF--AIKG-DYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSFKGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5, Application US/09318786
6472147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLQQSGPBLKKPGETVKISCKTSGYSFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTY
                                                                                                                                          g
                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.5%; Score 539.5; DB 3; 86.6%; Pred. No. 4.5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                   PO BOX 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 15
US-08-133-804-6
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Patent No. 5534254
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INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amin acids
TYPE: amin acid
TOPOLOCH: TYPE: procein
MOLECULE TYPE: Drocein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
TELERAX: 617-249-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                   FILINO DATE:

CLASSIFICATION: 424

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kallary, Robin D. 637

REGERBRICE/DOCKET NUMBER: 20.64

TRICOMMUNICATION INFORMATION:

TRILECOMMUNICATION INFORMATION:

TRILECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,934
REFERRENCY/DOCKET NUMBER: 050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READMALE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSECENTION DATA:
CUERENT APPLICATION DATA:
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ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department STREET: Exchange Place, 53 State Street
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APPLICANT: Opermann Hermann
APPLICANT: Houseon L. L.
APPLICANT: Bing David B
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APPLICATION UNMERS: US/08/483,749A FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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Search completed: November 7, 2003, 07:30:07 Job time: 18.4766 secs
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Best Local Similarity
Matches 98; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.0%; Score 530; DB 1; Length 243; ilarity 82.4%; Pred. No. 2.2e-41; Conservative 10; Mismatches 7; Indels
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GenCore vergion 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18; Search time 1,9866 Seconds without alignments of the distinct of the seconds 742.581 Million cell updates/sec

Title: US-09-661-992B-82_COPY_135_242
Perfect soor: 572
Sequence: 1 DIGWTQSPKFLLVSAGDRVT......QDDYGSPFTFGGGTKLEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 28330

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: piR_76:*
1: pir::*
2: pir::*
3: pir3:*
4: pir4:*

Freel. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4450 4450 4224 4224 4224 4224 4224 4224	510.5 487 479 473 466 456	Score
777 77 77 77 77 77 77 77 77 77 77 77 77	89.2 85.1 83.7 82.7 79.7	Query
107 107 108 108 108 108 107 1152 107 117 117 117 117 121 121 121 121 121 12	225 127 107 115 149 107	Length
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PQ0265 S32191 S32192 S32191 A25924 A25924 A25926 A26967 A27966 A31796 A3	S37484 S04577 S09964 B25924 KVMS11 D53285	IJ.
y kappa ig k	Ig kappa Ig kappa Ig kappa Ig kappa Ig kappa Ig kappa	pescription
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Query Match Best Local Similarity

85.1%; 87.7%;

Score 487; DB 2; Pred. No. 4.3e-37;

45	44	43	42	4	40	39	38	37	36	35	34	33	32	31	30
389	389.5	389.5	389.5	390	391	391	391	391.5	391.5	392	392	392	392	393	393
68.0	68.1	68.1	68.1	68.2	68.4	68.4	68.4	68.4	68.4	68.5	68.5	68.5	68.5	68.7	68.7
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ALIGNMENTS

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Public Constitutions 171 immunoglobulin V region; immunoglobulin homology competently: immunoglobulin V region; immunoglobulin homology competent commenced with the competent of the competent o
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CiSpecies Man musculus (Nouse mouse)
CiPate: 05-Unn-1988 #sequence_revision 05-Unn-1988 #text_change 21-Jan-20
CiAccession 182524
R.T.; Goldrick, M.M.; Gottlieb, P.D.
Proc. Matl. Acad. Sci. U. S.A. 83, 913-9138, 1986
A,Fülle: Structural differences in a single gene encoding the V-kappa-Sex
A,Fäcerence mumber: A94141; MUID:87067464; PMID:3097643
A,Baccession: B25924
A,Föblecule type: NNA
A,Fäcenses: GBNA-360; NID:g197464; PIDN:AAA39034.1; FID:g197465
A,Föbreimental source: strain BALB/C
Cjenetics: ...
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A;Feasidues; 1:07 - REIL
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C;Superfamily; mumuoglobulin V-region; immunoglobulin homology
C;Superfamily; mumuoglobulin Two polytopy
C;Feyevords: heterotetramer; immunoglobulin
F;Fe-90/Demail: immunoglobulin bomology ciPey
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A.Accession: 809964
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C;Bpacclas: Num suschlus (house mouse)
C;Date: 12-Feb-1993 #Sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: 509564
R;Bealninger, L-; Shibata, T-; Ozaki, S-; Shitai, T-; Jaton, J.C.; Izui, S.
Eug. J. Immunol. 20, 712-777, 1990
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IVMTQTPKELLVSAGERVTITCKASQSVSNDVAWYQQKPGQSPKLLIYYASNRYTGVPDR
                                                      IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR 61
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                                                                                                                                                                             Score 473; DB 2;
Pred. No. 7.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 479; DB 2;
Pred. No. 1.9e-36;
                                                                                                                                            Mismatches
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D53285
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82
                   62
                 FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSP
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Ig kappa chain precursor V region (MPC11) - mouse C;Species: Mus musculus (house mouse) C;Datte: 19-Feb-1984 #sequence revision 19-Feb-1984 C;Accession: A90823; A90753; Ā90298; A01916 #text_change 21-Jan-2000

Cell 29, 681-689, 1982
A;Title: Functional significance and evolutionary development A;Reference number: A90823; MUID:83001944; PMID:6288267 R; Kelley, D.E.; Coleclough, C.; Perry, R.P. of the 5'-terminal

gene

A;Accession: A90823 A;Molecule type: DNA A;Residues: 1-71 <KEL>

A.Note: the sequence was determined from the differentiated R; Rabbitts, T.H.; Hamlyr, P.H.; Matthyssens, G.; Roe, B.A. Can, J. Blochem. 58, 176-187, 1980.
A.; Title: The variability, arrangement, and rearrangement of

immunoglobulin

genes

A.Reference number: A90753; MUID:80176554; PMID:6245773 A.Accession: A90753 A.Molecule type: MRNA

A; Residues: 41-149 < RAB>

R,Smith, G.P. Biochem. J. 171, 337-347, 1978

A; Title: Sequence of the full-length immunoglobulin kappa-chain A; Reference number: A90298; MUID: 78186617; PMID: 418775 o H mouse

myerome

A) (Contents: myslosa protein MPC11
A) A(Contents: myslosa protein MPC11
A) A(Contents: myslosa protein
A) (Molecule type: protei

F;64-129/Disulfide bonds: #status predicted

Local Similarity 82.4%; 42 ۲ DIQMTQSFKFLLVSAGDRVTITCKASQSVSNDVAMYQQKFGQSFKLLMYYASNRYTGVPD DIVMTQSHKFMSTSVGDRVSITCKASQDVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPD Conservative 6, Score 466; DB 1 Pred. No. 4e-35; Mismatches 13, Indels 0, Gaps 101 60

DB 1;

Length 149

0

102 61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108 RFTGSGSGTDFTFTISSVQAEDLAVYYCQQHYSTPPTFGGGTKLEIKR

Ig kappa chain V and J regions, monoclonal antibody SCET.M8.1 - CySpectes: Mus musculus (house mouse)
C.Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change
C.Pacesion: D53285 20-Jun-2000 mouse (fragment)

RiSawada, J.; Mizusawa, S.; Terao, T.; Mol. Immunol. 28, 1063-1072, 1991 Naito, M.; Kurosawa,

A; Title: Molecular characterization of monoclonal anti-steroid antibodies:

primar

and their pH-reactivity profiles.
A;Reference number: A53285; MUID:92017897; PMID:1922102
A;Accession: D53285

A;Status: preliminary A;Molecule type: DNA;

A;Residuas:

1-107 <SAW>

60 60

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A.Readdues: 1-107 c2721b.
A.(Tease-references: BMEL:X70097; NID:g288262; PIDN:GAM49701.1; PID:g288263
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Seywords: heterocetramer; immunoglobulin
F.16-90/Domain: immunoglobulin bomology c1M9>
                                                                                                                                                                                        A; Reference number: S32185
A; Accession: S32192
                                                                                                                                                                                                                                                                                                  Ig kappa chain V region - mouse (fragment)
C:Spectse: Mus muscallus (house mouse)
C:Date: 06-reb-1995 #sequence_revision 06-reb-1995 #text_change
C:Accession: 832192
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C;Bate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: 190245
R;Johnent, K.L.; Carrillo, M.A.; Kennedy, R.C.
Gene 1959, 2813-284, 1993
A;Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal by sections of the mouse; P00255; MIDI:29039046; PMID:1937027
                                                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                   A,Status: preliminary
                                                                                                                                                                                                                                               submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                               832192
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;36-46/Region: complementarity-determining 1 F;62-68/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Comment: This protein recognizes a restricted idiotype associated with antibodies specisuperfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: heterocetramer; immunoglobulin homology C:Reywords: heterocetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:M59985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-119 < LOH>
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jauperfamily: immunoglobulin V.region; immunoglobulin homology
Keywords: heterotektramer; immunoglobulin
;16-90/Domain: immunoglobulin homology <1M/h>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMIQSEKFLLVSAGDRVIITCKASQSVSNDVAWYQQKFGQSFKLLMYYASNRYIGVED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFTGSGSGTDLTFTISSVQABDLAVYYCQQHYSTPPTFGGGTKLBIK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIVMTQSHKFMSTSVGDRVSITCKASQDVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPD 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTGSGYGTDFTLTTRSVEAEDLAVYPCQQNFKSPYTFGGGTKLETK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVMTQTPKFLHVSVGDRVTTTCKASQSVRNAVVWYQQKTGLSPRLLIYYASNRYTGVPDR
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Pred. No. 3.1e-34;
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Pred. No. 2.3e-34;
7; Mismatches 12
                                                                                                                                                                                                                                               February 1993
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IQMTQSPXFLLVSAGDRVTITCXASQSVSNDVAMYQQXPQQSPKLLMYYASNRYTGVPDR 61

Matches

82;

Conservative

Similarity

Length 115

Indels

0

Gaps

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A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                 F;21-115/Product: Ig kappa chain V region Ser-e
F;36-110/Domain: immunoglobulin homology < IMM>
                                                                                              F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Product: Ig kappa chain V region Ser-a #status predicted <WAT>
                                                                                                                                                                                                                           C;Genetics:
                                                                                                                                                                                                                                         A; Experimental source: strain C.CS8
                                                                                                                                                                                                                                                       A;Cross-references: GB:M14361; NID:g197466; PIDN:AAA39035.1; PID:g197467
                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-115 < BOY>
                                                                                                                                                                                                                                                                                                                              A; Accession: A2592
                                                                                                                                                                                                                                                                                                                                        R.Poyd, R.T.; Goldrick, M.M.; Gottlieb, P.D.
Proc. Natl. Acad. Sci. U.S.A. 33, 9134-9134, 1986
A.Title: Structural differences in a single gene encoding the V-kappa-Ser group A.Reference number: A94141; MUID:87067464; PMID:3097643
                                                                                                                                                                                                                                                                                                                                                                                                                                             ig kappa chain preutreor V region (Ser-a) - mouse
C:Spectes: Mus mascallu (house mouse)
C:Date: 05-Vun-1998 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
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A;Moleuile type: makh
A;Rosidues: 1-107 - ZIDJ
A;Cross-references: MMEL:X70095; NID:9288260; PIDN:ChA49700.1; PID:9288261
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Koywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain W region - mouse (fragment)
C:Spectes: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
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A;Accession: S32191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S32191
                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: A25924
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87; Conserv
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                       75.9%;
87.2%;
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6,
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Pred. No. 2.2e-33;
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Pred. No. 7.8e-34;
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60

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RESULT
PL0204
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A.Wolerule type: mENN
A.Residues: 1.122 cGBA.
A.Geose-references: EMBL.XOS877; NID:g52195; PIDN:CAA29301.1; PID:g52196
C.Supwards: heterotetzamer: immunoglobulin v region; immunoglobulin homology
F:45-1197Domain: immunoglobulin homology cIMMs
F:45-1197Domain: C region (C-kappa) (fragment) #status predicted <CBS>
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A. Disperimental source: strain BALB/c
A. Disperimental source: strain BALB/c
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Meywords: heterotetramer; immunoglobulin
F. 16-91/Domain: humunoglobulin homology < 1001>
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Nuclaic Acids Res. 13, 5496, 1997
A.Fitie: Improved RNA sequencing method to determine immunoglobulin
A.Feterence number: $30751, MUDI-07500030) FWI-1801633
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J. Dep. Med. 163, S19-S33, 1989.
A; Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A; Reference number: PAOSO, MUID:89094248; PMID:2492056
A; Accession: PAOSO.
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C:Spectes: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain precursor V region - mouse
CiSpecies: Mus musculius (house mouse)
CiDate: 11-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
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78; Conservative
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                                                                                 RFTGSGSGTDYTLTISSVQAEDLALYYCQQHYSTPLTFGAGTKLELKR 137
                                                                                                                                                                          DIVMTQSHREMSTSVGDRVSITCKASQDVTTAVSWYQQKPGQSPKLLIFWASTRHTGVPD
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                                                                                                                                                                                                                                                                                    74.0%; Score 423; DB 2
72.2%; Pred. No. 3e-31;
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Ig kappa chain V region (anti-haloperidol antibody A) - mouse C;9pecies; Num smeculus (house mouse) C;pates; 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jan-2000 C;Accession: A28159 F. A. (1982) F. (1982) F. A. (1982) F. 
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A28195
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A!Feeddues 1-117 - CHI:

A:Crose-references: BRBL:K79108; NID.9460824; FIDN:CAA54998.1; FID.9460825

C:SuperEmaily: immunoglobulin V region; immunoglobulin homology

C:Keynozds: heerocetramer; immunoglobulin

F;26-100/Domain: immunoglobulin homology <NMH>
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Cispace (6-Jan-1995 Hecquence_revision 06-Jan-1995 #text_change 21-Jan-2000
Cipaces (06-Jan-1995 Hecquence_revision 06-Jan-1995 #text_change 21-Jan-2000
Cipacesion: 54466
R:Shiyanov, P.A.; Bespalov, T.A.; Terlersbarg, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A.Reference number; 542466
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C;Superfamily; immunoglobulin V region; immunoglobulin bomology
F;16-90/Domain: immunoglobulin homology; cIMM-
F;16-91/Domain: complementarity-determining 1
F;50-55/Regjon: complementarity-determining 2
F;50-55/Regjon: complementarity-determining 3
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MOI. Immunol. 27, 463-470, 1990
M.Title: Variable region primary structures of monoclonal A; Reference number: PL0196; WUID:30309768; PWID:2114528
A; Accession: PL0204...
A; Accession: PL0204...
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A;Molecule type: mRNA
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A; Residues: 1-108 <SMI>
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Similarity 75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPQQSPKLLIYWASTRHTGVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 117
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76.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 419; DB 2;
Pred. No. 5.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 419; DB 2;
Pred. No. 4.9e-31;
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A, Accession: A2019S
A, Molecule type; mRXN
A, Residues: 1.107 < SB: M19766, NID:g197039, PIDN:AAA38891.1; PID:g197040
C. Superfamily: immunoglobulin v region: immunoglobulin homology
C. Superfamily: immunoglobulin
C. Superfamily: immunoglo
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OM protein -
protein search, using sw model
                                                                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: November 7, 2003, 07:21:18; Search time 7.78638 Seconds (without alignments) 652.278 Million cell updates/sec

Title: Perfect score: US-09-661-992B-82_COPY_135_242 572

Scoring table: Sequence: BLOSUM62 1 DIQMIQSPKFLLVSAGDRVT.....QQDYGSPPTFGGGTKLEIKR 108

Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB Post-processing: Minimum Match 0% seq length: 0 length: 2000000000

Maximum Match 100% Listing first 45 summaries SwissProt_41:* 100%

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length I	80	ID	Description
3 to	166	81.5	149	بر د	KVSA MOUSE	P01633 mus musculu
w h	391.5	68.4	133	٠,	KV4B HUMAN	
4.	391	68.4	114	-	KV4A HUMAN	homo
(ri	387	67.7	134	1-2	KV4C HUMAN	homo
o,	386	67.5	108	44	KV1M_HUMAN	bomo
7	378	66.1	108	4سر	KV1Y_HUMAN	homo
00	376	65.7	108	μ	KV1H_HUMAN	homo
9	376	65.7	108	μ	KVIN HUMAN	homo
10	372	65.0	114	μ	KV1A_MOUSE	P01632 mus musculu
11	370.5	64.8	109	۲	KV3D_HUMAN	homo
12	370	64.7	129	۳	KV1W HUMAN	homo
13	368	64.3	108	-	KV1A HUMAN	homo
14	367.5	64.2	129	М	KV3H_HUMAN	nomo
15	367	64.2	108	μ	KV1P HUMAN	homo
16	366	64.0	108	,	KVIS HUMAN	
17	365	63.8	108	н	KVIK HUMAN	nomo
18	365	63.8	108	μ.	KV5M_MOUSE	mus n
19	363.5	63.5	109	,.	KV3B_HUMAN	Domo
20	363	63.5	108	۳	KVIG HUMAN	Omo
21	362.5	63.4	129	,	KV3L HUMAN	DOMO
22	361	63.1	108	,	KV1B HUMAN	nomo
23	361	63.1	108	,	KV10 HUMAN	nomo
24	360	62.9	108	بر	KV1C HUMAN	P01595 homo sapien
25	359	62.8	108	μ	NAMOH ATAX	homo
26	358.5	62.7	109	μ.	KV3F HUMAN	home
27	358	62.6	108	μ	KV5P MOUSE	
28	357.5	62.5	129	۳	KV3M_HUMAN	P18136 homo sapien
29	356.5	62.3	113	۳	KV2G_MOUSE	P01631 mus musculu
30	356	62.2	108	<u>ب</u>	KV5K_MOUSE	P01644 mus musculu
31	354	61.9	108	۱.,	KV1F_HUMAN	P01598 homo sapien
32	354	61.9	108	μ	KV1R_HUMAN	P01610 homo sapien
33	354	61.9	108	۳	KV50 MOUSE	P01648 mus musculu

45	44	43	42	41	40	39	38	37	36	35	ω.	
344	345	345	345	346.5	348	348.5	350	350	350	351	353	
60.1	60.3	60.3	60.3	60.6	60.8	60.9	61.2	61.2	61.2	61.4	61.7	
121	128	109	108	107	108	109	129	108	108	108	108	
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KV40_HUMAN	KV3K HUMAN	KV4D_HUMAN	KV5J_MOUSE	KV1D_HUMAN	KV1L_HUMAN	KV3E_HUMAN	KV1X_HUMAN	KV5S_MOUSE	KV1E_HUMAN	KV5N_MOUSE	KV5L_MOUSE	
P06312	P06311	P83593	P01643	P01596	P01604	P01623	P04432	P01652	P01597	P01647	P01645	
homo sa	homo sa	homo sa	mus mus	homo saj	homo saj	homo sa	homo saj	mus mus	nomo saj	mus mus	mus musculu	
pien	pren	pien	culu	nero	oren	pien	pien	nTn	pien	nTu	ulu	

RESULT 1 KV5A MOUSE STANDARD; PRT; 149 AA. AC P0153;
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ALIGNMENTS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 15-JUL-1999 (Rel. 38, Last annotation upda Ig kappa chain V-V region MPC11 precursor. Mus musculus (Mouse). Jast annotation update)

SEQUENCE OF 1-71 FROM N.A. NCBI_TaxID=10090;

mbilinesion1944; Pubwede528267; Kalley D.B., Coleclough C., Perry R.P.; Functional significance and evolutionary development of the 5 -terminal regions of immunoglobulin variable-region genes."; Cell 29:681-689(1982).

SEQUENCE OF 41-149 FROM N.A.

REDOUBLED OF 41-147 row. Research of the
Can. J. Biochem. 58:176-187(1980)

MEDLINE=78186617; PubMed=418775; SEQUENCE OF 30-149.

Smith G.P.; myeloma MPC 11 "Sequence of the full-length immunoglobulin kappa-chain of mouse

Biochem. J. 171;337-347(1379).

-1- MISCELLAMEGUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS AND SKN, DUE TO A TANDEM UPELICATION 07 54 NUCLEMOTIDES ATERN THE COOM FOR RESIDUE 36. RESIDUE 42. CRORRESPONDS TO THE MATHO-TENHALMENT OF THE MATHOR THE AND THE MATHOR THE RESIDUE OF TYPICAL KAPPA CHAINS.

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EMBL, J00561, AAA38776.1; -.
PIR; A90823; KVMS11.
HSSP; P80362; IWTL.
HSSP; P80362; IWTL.
INTERFEC; IER003706; Ig_MIC.
INTERFEC; IER003506; Ig_WC.
INTERFEC; IER003596; Ig_V.

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RESULT 2
KV5B_MOUS
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Best Local
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   CHAIN
                     FEam; FP00047; ig; 1.
SWART: SW0046; IGv; 1.
PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
SIGNAL
                                                                                                                       RMBL, V00610, CARA492.1; ALT_TERM.
PIR; A93736; KVMS21.
PBB; 11GC; 03-JUN-95.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                          This SWISG-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMULOURIESTON.

the ENUrpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is him own modified and this statement is not removed. Usage by and for commercial strictics requires a locance are present is content in the commercial profits and the commercial or send an easility and to commercial or send an easility and to incense spreamon (See http://www.isb-stb.ch/amounce/or send an easilito license spreamon (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hamlyn P.H., Gait M.J., Milstein C.;
"Complete sequence of an immunoglobulin mRNA using specific priming
and the dideoxymucleotide method of RNA sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KV58 MOUSE STANDARD;
P01634;
21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=73053310; PubMed=4638343;
Svasti J., Milstein C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=82059477; PubMed=6170937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 9:4485-4494(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-7UL-1986 (Rel. 01, Last sequence update)
15-3EP-2003 (Rel. 42, Last annotation update)
ig kappa chain V-V region MOPC 21 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete amino acid sequence of a mouse kappa light chain. \pi_t them. J. 128:427-444(1972).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF 30-136.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 AA,
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Pred. No. 1.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG KAPPA CHAIN V-V REGION MPC11.
PRAMEWORK-1.
IG KAPPA CHAIN V-V REGION MOPC 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                           Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                           EMBL; 200022; CAA77317.1; ...
PIR; A01904; K4HUJI.
                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 13:6515-6529(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
13 kappa chain V-IV region JI precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1988
01-JAN-1988
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                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                            InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zachau H.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=86041853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            "Subgroup IV
                                                                                                                                                                                                        GO:0006955; P:immune response; NAS
                                                                                                                                                                                                                 GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity; NAS
                                                                                                                                                                                                                                                P80362; 1WTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            of human immunoglobulin K light chains is encoded by a
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Pred. No. 1.4e-35
                                     FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1
FRAMEWORK-2.
           COMPLEMENTARITY-DETERMINING-2
FRAMEWORK-3.
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                                                                                IG KAPPA CHAIN V-IV REGION JI
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FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3

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Best Local Similarity
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21-JUL-1986
01-OCT-1996
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DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schneider M., Hilechmann N.;
"The primary etructure of a monoclonic immunoglobulin-L-chain of subgroup IV of the kappa type (Sence-Jones protein Len).";
Honna-Sevler's Z. Physiol. Chem. 356:507-557(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
KV4A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1996) to the SWISS-PROT data bank.
-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS
-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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Schneider M., Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V-IV region Homo sapiens (Human).
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                                                              DISULFID
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(Rel. 34, Last sequence update)
(Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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         N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 391.5; DB :
Pred. No. 8.4e-35
                                                              FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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    0647F1D17F236485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Indels
         CRC64;
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Query Match Best Local Similarity

68.4%;

Score 391; DB 1; Pred. No. 8e-35;

Length 114,

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1 DIQMTQSPKFLLVSAGDRVT1TCKASQSV-----SNDVAWYQQKPGQSPKLLMYYASNR

Conservative

13;

Mismatches

Indels

6,

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Query Match
Best Local Similarity
Matches 76; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SHISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEW outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lab-sib.ch/announce/or send an email to licenseasexib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
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MEDLINE=86041854; PubMed=2997713;
Marsh P., Mills F., Gould H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-IV region B17 precursor.
                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BMBL; X02990; CAA26733.1; -. HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marsh P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISION TO 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Detection of a unique human V kappa IV germline gene
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GO:0003823; F:antigen hinding activity; NAS
GO:0006955; P:immune response; NAS.
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                                                                                                      134 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGv; 1
                                                                                                                                                                                                                                                                                                                                                                                                                region;
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                                                                                                                                                                                                                                43
60
75
82
                                                                                                      14966 MW;
                        67.7%; Score 387; DB 1; 66.7%; Pred. No. 2.6e-34;
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                                                                                                                                                       FRAMEWORK-4
BY SIMILARI'
                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                COMPLEMENTARITY-DETERMINING-2
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                       IG KAPPA CHAIN V-IV REGION B17 FRAMEWORK-1.
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                                                                                                      6413A22FD0738832 CRC64;
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                                            Length 134
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RESULTA 6

KVIN HUWAN

AC POLSOS;

POLSOS;

CALLETTO NO CONTROLLA 
RESULT 7
KV1Y_HUMAN
ID KV1Y_H
AC P80362
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Best Local
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last_annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, A01871; K1HULY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=77038198; PubMed=824717;
Capra J.D., Klapper D.G.;
"Complete amino acid sequence of the variable domains of
TopM anti-gamma globulins (Lay/Pom) with shared idiotypio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986
   KV1Y HUMAN
P80362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO: GO:0005576; C:extracellular; NNS.
GO; GO:0003823; P:amtign binding activity; NNS.
GO; GO:0008925; P:ammune response; NNS.
IntestPro; IPPO03006; Ig_MC.
IntestPro; IPPO03006; Ig_MC.
IntestPro; IPPO03006; Ig_MC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specificities."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nd. J. Immunol. 5:677-684 (1976).
MISCELLAROUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL HITH THOUSE OF THE HUMAN FOM V-III KAPPA CHAIN, RITH HUILUI IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
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                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YTGVPDRFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
                                                                                                                                         RFSGSGSGTDFTFTISSLQPEDIATYYCQQYNWWPPTFGQGTKVEVKR
                                                                                                                                                                    RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR
                                                                                                                                                                                                                                   DIQMTQSPSSLSVSVGDRVTITCQASQNVNAXLNWYQQKPGLAPKLLIYGASTREAGVPS
                                                                                                                                                                                                                                                                                   DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                          108 AA;
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FRANGEWORY-2.
COMPLEMENTARITY - DETERMINING-2.
FRANGEWORY-3.
COMPLEMENTARITY - DETERMINING-3.
FRANGEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                            Score 386; DB 1;
Pred. No. 2.6e-34;
3; Mismatches 21
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                          PRT;
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InterPro; IBR003006; Ig_WC.
InterPro; IBR003965; Ig_V.
Pfam; P00047; Ig; I.
SMART; SMO4065; Ioc; I.
BMOATC; BMO4065; Ioc; IICE; I.
Immunoglobalia V zegjon; Bence
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01-MOV-1995 (Rel. 32, Last sequence update)
01-MOV-1995 (Rel. 41, Last annotation update)
19 keppa chain v. region WAT.
19 keppa chain v. region WAT.
Hamos sepiens (Human).
Bukbaryota, Metasoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukbaryota, Metasoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukbaryota, Metasoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Bulitz M., Soldmenn M., Sewens P.J., Schliffer M., Freens P.J., Schliffer M., Freens P.J., Schliffer M., Schliffer M., Standardson or Comparison of Crystal Schroduses of two homologous procedus. Structural origin of altered domain increactions in immunoglobulin Structural origin of altered domain increactions in immunoglobulin Light-Cobain dimension.
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"Characterization and preliminary crystallographic data on the Vi-
"characterization and preliminary orystallographic data on the Vi-
related fragment of the human KI Bence Jones protein Wat.";

"Edited fragment of the human KI Bence Jones protein Wat.";

J. Mol. Biol. 147:185-193 [1881], where more more and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemistry 33:14848-14857(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95086080; PubMed=7993911;
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GO:0003823; F:antigen binding activity; NAS
GO:0006955; P:immune response; NAS.
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          Similarity
                                            108 AA;
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107
31
                                                                 11737 MW;
66.1%; Score 378; DB 1; [
66.7%; Pred. No. 1.8e-33;
Live 15; Mismatches 21;
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BY SIMILARITY.
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COMMENSURATIV-DETERMINING-1...

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Matches 69
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KV1H_HUMAN
    KV1N HUMAN

P01606;

21-JUL-1986

21-JUL-1986

15-JUL-1999
                                                   HUMAN
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GO; GO:0003825; F:antigen binding activity; NAS.
GO; GO:000385; F:immne response; NAS.
InterPro; [PRO:01010; Ig-Ike.
InterPro; [PRO:03006; Ig_MKC.
InterPro; [PRO:03006; Ig_MKC.
InterPro; [PRO:03006] Ig_MKC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           subgroups ";
Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970)
-i- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS TH
-i- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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Watenabe S., Hilschmann N.;
Watenabe S., Hilschmann N.;
When primary extructure of a monoclonal kappa-type immunoglo
chain of subgroup I (Bence-Jones Protein Hau): subdivision
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                   NTAMOO
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                                                                                            RFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITFTSFGQGTRVBIKR
                                                                                                          RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPFTFGGGTKLEIKR
                                                                                                                                    DIQWTQSPSSLSASVGDRVTTTCRASQSISSYLSWYQQKPGKAPQVLIYAASSLPSGVPS
                                                                                                                                                       DIQMIQSPKFLLVSAGDRVIITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYIGVPD 60
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    Last
                        Created)
   annotation update)
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              sequence update)
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BY SIMILARIT
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COMPLEMENTARITY-DETERMINING-3
                                             PRT;
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This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
                                                           SEQUENCE FROM N.A.
MEDLINE=81241357; PubMed=6788890;
Kwan S.-P., Rudikoff S., Seidman
                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                         12-UIL-1986 (Rel. 01, Created)
21-UIL-1986 (Rel. 01, Last asquence update)
15-UIL-1999 (Rel. 38, Last association update)
Ig kappa chain V-I region S107A.
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Mammalia; Eutheria; Primates;
                              J. Exp. Med. 153:1366-1370(1981)
                                         chains.
                                                "Nucleic acid and protein sequences
                                                                                                    NCBI_TaxID=10090;
                                                                                                                                  Mus musculus (Mouse)
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HSSP; P01607; 1REI.
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phosphocholine-binding light

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Scharff M.D.;

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InterFro; IR007110; Ig-11ke.
InterFro; IR003596; Ig-MEC.
InterFro; IR003596; Ig-MEC.
InterFro; IR003596; Ig-V.
Fram; PR00047; ig; 1.
SMART; SMORT; STORT; IG-11KE; 1.
Immung-Jobaltin V resjon.
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-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
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Kohler H., Shimizu A., Paul C., Putnam F.M.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain V-I region Homo sapiens (Human).
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GO:0003823; F:antigen binding activity; NAS
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                                                                                                            RESGSGSGTBETETISSLZPZBEATYYCZZSYSSPTTEGZGTRLZIKK
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COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-2.

FRAMEWORK-3.
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BY SIMILARIT
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PRT,
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                                                                                                                                                                                                                                  NEDILINE-72186439; PubMed-8027703;
Surer I., Banthol H. U., Watanabe S., Hilschmann N.;
Twake of antibody structure. The primary structure of a monoclonal immunoglobulin. To-data for Exppe-type, subgroup 3 [Bence-Jones protted mechanism of antibody production sequence and its significance for the mechanism of antibody production.

HODE-Selfert S. Physiol. Chem. 333:18-208(1972).

HODE-Selfert S. Physiol. Then. 333:18-208(1972).
               GG: GG:005576 G: Gentracellular; NBS:
GG: GG:0003827 F: amtigen binding activity;
GG: GG:0006855; F: amtigen binding activity;
GD: BG:0006855; F: Amtigen binding activity;
InterPro: IRMO31010; I3_MC.
InterPro: IRMO3506; I3_W.
Ffam: FF00047; I3_V.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1996 (Rel. 38, Last smoctation updat
Ig kappa chain V-III region Ti.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A01915; KVMS7A.
HSSP; P01607; 1REI.
                                                                                                                                                                                        PIR; A01895; K3HUTI.
HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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COMPLEMENTARITY-DETERMINING-1.
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Mismatches
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ALC COCCURRATE TO THE PROPERTY OF THE PROPERTY
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KV1W_HUMAN
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SMESS-PROT entry is copyright. It is produced through a collaboration between the Smiss Institute of Bioinformatics and the EMBLO utstation - the Buropan Bioinformatics Institute, There are no restrictions on its use by non-posit institutions as long as its content is in no wy modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or end an email to licensesib-sib.ch/).
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Immunoglobulin V region; Benc DISULFID 23 89
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DISULFID
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SEQUENCE
                                                                                                              DOMAIN
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last amoutation updat
Ig kappa chain V-I region Walker precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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SMART; SM00406; IGV;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v
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PIR; A01883; K1HUWK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 12:6995-7006(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klobeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the kappa light c
lymphoid cell lines are closely related.";
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Mammalia; Eutheria;
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PROSITE; PS50835; IG LIKE;
Immunoglobulin V region; S
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GO:0003823; F:antigen binding activity; NAS
GO:0006955; P:immune_response; NAS.
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AA,
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                                                                                                                                                          FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1
FRAMEWORK-2.
                                                                                        FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                        COMPLEMENTARITY-DETERMINING-2
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RESULT 14
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P01593;
21-JUL-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region; Benc
                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.

    J. BIO.L. Chem. 244:3550-3560(1969).
    INISCELLANDOUS: THE CREGIOU OF THIS CHAIN HAS THE INV (3) MARKER
    MISCELLANDOUS: THIS IS A BENCE-JONES PROTEIN.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The amino acid sequence of a kappa type Bence-Jones protein. complete sequence and the location of the disulfide bridges.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P01607; 1RBI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=69234734; PubMed=4893682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Ig kappa chain V-I region AG.
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                                                                                                                        RFSGSGFGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGQGTKLEIKR
                                                                                                                                                                RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
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          STANDARD;
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01, Last sequence update)
38, Last annotation update
                                                                                                                                                                                                                                                                                                                                64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                  11992 MW;
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Pred. No. 1.6e-32;
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                                                                                                                                                                                                                                                                                                                                                      Score 368;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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          PRT;
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Best Local :
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GD; GO:0003633; F:antigan binding activity; NA
GD; GO:0003635; P:immune response; NAS:
InterPro; Ipen07100; Jg_MRC.
InterPro; Ipen07100; Julius; J.
InterPro; Ipen07100; Signal.
InterPro; Ipen07100; Ipen0710
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20-MAR-1987
01-NOV-1990
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light-chain gene.",
Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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MEDLINE=86177570;
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15.-UL-1999 (Rel. 18, Last ambetation update)
15.-UL-1999 (Rel. 18) Last ambetation update)
15. Manaphan (Humani).
150 kappa chain V-III region CLL precursor (Rheumatoid factor).
160m aspidans (Humani).
150 kappa chain V-III region Chardiata; Vertebrata; Buteleostomi;
150 kappa chain V-III region (Chardiata).
150 kappa
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                                                                                                                                                                                 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches
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Pred. No. 2.5
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FRAMEWORK-1.
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BY SIMILARI
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PO1650; PO1650

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Homo sapiens (Human).

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Page 8
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Search completed: November Job time: 7.78638 secs
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Best Local Similarity
Matches 70; Conserv
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HSSP, P8018.2; NWTL.
GO; GO:0005576; C:cettacellular; NhS.11tty; NAS.
GO; GO:000383; F:amtigen binding activity; NAS.
GO; GO:000383; F:ammune response; NAS.
InterPro; IPRO07101, 1g-Like.
InterPro; IPRO07106; 1g-WC.
InterPro; IPRO03566; 1g-W.
Ffam; PF00447; 31g, 1.
SMART; SMO465; JOy 1.
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SEQUENCE
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DOMAIN
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(In) Franck F., Shugar D. (eds.)
Gamma globulins: structure and function, pp.57-74, Academic Press,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RQB_BaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York (1969)
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                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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Immunoglobulin V region; Bence-Jones protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS TO 39 AND 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=68362076; PubMed=5595110;
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                                                                                                           61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
                                                                           DIQMTQSPSSLSASVGDRVTTTCQASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60
                                                                                                                                                                                                       DIOMIOSEKELLVSAGDRYTITCKASQSVSNDVAWYQQKPGQSEKLLMYYASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                   108 AA;
                                                                                                                                                                                                                                                 Conservative
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ลนธ	Q9JL76	11	97	48.3	276
Bum	Q92589	11	127	50.7	290
Q921a6 mus musculu	Q921A6	11	241	50.8	290.5
BUM	Q8R028	11	234	52.1	298
mus	Q8K0F8	11	239	52.4	299.5
	Q9JL78	2	101	52.4	300
	Q8K1F0	Ľ	112	52.7	301.5
	Q9U410	s	106	52.7	301.5
mus	QBVDD0	11	134	53.1	303.5
	087060	4	114	53,1	304
Bum	Q9JL80	11	103	53.3	305
ฒนธ	Q91W12	11	235		309.5
ยม	Q8VCP0	11	234	54.5	312
Q8tcd0 homo sapien		4	239	55.0	314.5
		11	112	55.7	318.5
Q9Qyf0 mus musculu		11	298	55.9	320
Q9jl84 mus musculu		11	107	56.5	323
Q9jl82 mus musculu		11	104	56.6	323.5
Q8k1f3 mus musculu		11	112	56.9	325.5
ğ		11	109		327
Q96pf6 homo sapien	Ø	4	116	57.5	329
Butt	Q8K1F1	11	114		330.5
mus	Q9R1A5	11	214	57.9	331
homo	QBNEKO	4	239		
Omo	98TD60	4	109		332.5
Q8r062 mus musculu	Q8R062	;;	234	58,2	333
Q920e9 mus musculu	Q920E9	1	111	58.6	335
Q91ws9 mus musculu	6SMT6D	H	233	59.1	338

ALIGNMENTS

Q96SA9 Q9UL79 Q9UL70 Q9UL77

Q9UL78 Q9UL81

Q9UL85 Q8VC16 Q9ERZ9 Q9UL83 Q8NEK1 Q91WF8 Q99M37 Q8VC55

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RESULT 3

O965A9

O965A9

ID O965S

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Q8VIJO,
Q8VIJO,
Q1-MAR-2002
Q1-MAR-2002
Q1-MAR-2003
                                                                                                                                                                                                                                                   O968A9 PRELIMINARY, PRT, 107 AA.

Q968A9.

Q1-DEC-2001 (TENBLIZE1. 19 Created)

Q1-DEC-2001 (TENBLIZE1. 19 Lost sequence update)

Q1-MAC-2003 (TENBLIZE1. 23 Lost sequence update)

Auti-streptococcal/anti-myosin immunoglobulin kappa

variable region (Fragment).
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                           SEQUENCE FROM N.A.

NEDLINE-983716839; PubMed-9712075;

NEDLINE-983716839; PubMed-9712075;

Nedecline analysis of polyreactive monoclonal antibodies from 
Ynblencine analysis of polyreactive monoclonal antibodies from 
Ynblencine; o carditis: human anti-N-acetylglucosamine/anti-myosin 
Ynblencine; o carditis: human anti-N-acetylglucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mioch M.K., Alexander A.L., Pippen A.M., Pisetaby D.S., Gilkeeen G.; 
"Differences in Vappa gene utilization and W GORI sequence among anti-DNA from CSH-Ipr mide and lupus mide with nephritis."; 
Bur. J. Immunol. 26:2255-2231395).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U59155; AAB02917.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C3H/HeJ-lpr/lpr;
MEDLINE=96409289; PubMed=8814271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-DNA light
   antibody V region genes.";
                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPYTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIVMTQSQTFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKALIYSASYPYSGVPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG_LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11859 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Fragment).
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20, Last sequence update)
23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 399; DB 11;
Pred. No. 3.8e-36;
8; Mismatches 22
                                                                                                                                                                                                       Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68506D75613DBFBE CRC64;
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                                                                                                                                                                                                       Euteleostomi, Homo.
                                                                                                                                                                                                                                                                                                           light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108;
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RESULTATION OF THE CASE OF THE
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Best Local :
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Best Local
                                                                                                                                                                     Matches
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EMBL, U06396; ABB66788.1;

InterPro; IPR007101; Ig-like.

InterPro; IPR003096; Ig_MHC.

ITHERPRO; IPR003996; Ig_V.

Pfam; PP0047; Ig;

SMART; SMO465; IGy 1.

SMART; SMO465; IGy 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; PO1607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UL79;
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                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                          Ptam; PF00047; 1g; 1.
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                         Local Similarity
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61
                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunol. Immunopathol. 87:184-192(1998)
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                                                                                                                                                                  70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIOMIOSPKELLVSAGDRVTITCKASOSVSNDVAWYQQKEGQSPKLLMYYASNRYIGVPD
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                                     RETGSGYGTDETETISTVQAEDLAVYECQQDYGSPETEGGGTKLEIKR
                                                                                                                      DIQMIQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESGSGSGTDFTLTISSLQPEDFATYYCQQSY-STLTEGGGTKVEIKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQXPGKAPKLLIYAASSLQSGVPS
RESGSGSGTDETLTISCLQSEDEATYYCQQYYSEPPTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                            IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                            IPR007110;
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                                                                                                                                                                                                                                                      108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD56271.1; -.
                                                                                 PSTLSASTGDRVTISCRMSQGISSYLAWYQQXPGKAPETLIYAASTLQSGVPS
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.9%;
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                                                                                                                                                                                                                                                   11787 MW;
                                                                                                                                                                                      64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                            Ig-like
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                                                                                                                                                                                         Pred.
                                                                                                                                                                                                          Score 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                      DB5845F19724FB4E CRC64;
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                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                          DB 4;
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Best Local
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InterPro; IPRO03106; Ig_MHC.
InterPro; IPRO03596; Ig_V.
InterPro; IPRO03596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SW00406; IGY; 1.
PROSITE; PS50835; IG_IKE; 1.
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09UL77.
09UL77.200 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence up
01-MAY-2000 (TYEMBLrel. 23, Last annotation
Myosin-resorther immunoglobulin light chain v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1)
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
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01-MAY-2000 (TERMBLrel. 13, Last sequence update)
01-MAR-2000 (TERMBLrel. 23, Last annotation update)
01-MAR-2003 (TERMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                EMBL; AF035037; AAI
HSSP; P01607; 1REI.
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Young D.C.;
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HSSP; P01607; 1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates;
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     PROSITE; PS50835; IG_LIKE; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                        Immunol. Immunopathol. 87:184-192(1998)
AF035037; AAD56273.1; -.
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Pred. No. 1.3e-33;
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Catarrhini; Hominidae;
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01-MAY-2000
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01-MAY-2000 (TrBMBLrel. 13, Last sequence update)
01-MAR-2000 (TrBMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01607; 1REI
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Mammalia; Eutheria; Primates;
         (Fragment)
                 Myosin-reactive immunoglobulin
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SMART; SM00406; IGv; 1.
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lin light chain variable
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Pred. No. 1.3e
15; Mismatches
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Pred. No. 5e-33;
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Best Local &
Matches 7:
    Quary Match
Best Local Similarity
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                                                                                                                                                                                                  RWBI, PRO3029, AADS265.1;
HSSP, PRO362, NTL.
INCEPTO, IPRO07010, IG-11ke.
INCEPTO, IPRO0306; IG-WC.
INCEPTO, IPRO03069; IG-WC.
PEAM; PRO0407; IG-T.
PEAM; PRO0406; IG-T.
PROM3TEN; PROM3TEN; PROM3TEN; PROM3TEN; PROM3TEN; PROM3TEN; PROM3TEN;
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MEDLINE=98277139; Pu
Wu X., Liu B., Van d
Young D.C.;
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HSSP, P80362; 1MTL.
InterPro, IPR007110; Ig-like.
InterPro, IPR003006; Ig_MHC.
InterPro, IPR003596; Ig_v.
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Clin. In
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OSULAS, CREated

OL-MAY-2000 (TENNIL:el. 13, Created)

OL-MAY-2000 (TENNIL:el. 12, Last sequence update)

OL-MAY-2003 (TENNIL:el. 23, Last sequence didate)

OL-MAY-2003 (TENNIL:el. 23, Last amocation update)

Myosin-resective immunos/obulin kappa chain variable
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SMDRT; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Mammalia; Eutheria;
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SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
MEDLINE-98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa;
Mammalia, Butheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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AF035029; AAD56265.1; -.
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                                                                                                                      109
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n der Merwe P.L.,
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64.1%; Sci
64.2%; Pri
ative 19;
                                                                                                                      11761 MW;
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; Pred. No. 5.16
19; Mismatches
    Score 366.5;
Pred. No. 1.4e
19; Mismatches
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i; Hominidae; Homo.
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                                                             DB 4;
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EMBL, ECO13760, NAH07961.1.
InterPo. IPE003006; Ig_MMC.
InterPo. IPE003306; Ig_w.
IPE0047; ig_v.
IP
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01-MAR-2002 (TrEMBLrel. 20, La
01-MAR-2003 (TrEMBLrel. 23, La
01-MAR-2003 (TrEMBLrel. 23, La
Hypothetical 26.2 kDa protein.
Mus musculus (Mouse)
SEQUENCE FROM N.A. Year Z.L., Han H., Yeo L.B., Chen F., Deng J.B., Wang Z.L., Han H., Yeo L.B., "Construction and sequencing of the single-chain human TMF-alpha specific monoclonal antibody." 114 Chun i Ta Haueh Haueh Pao 19:373-376(1998).
                                                                                                                                                                                                                                          SEQUENCE FROM N.A. C.S.; Chen P., Deng J.B., Wang Z.L., Han H., Su C.S.; Clen P., Deng J.B., Wang Z.L., Han H., Su C.S.; Clen P., Deng J.B., Chen J. St., Cell. Marking and sequencing of the light chain fragment genes of an anti-hTMP-a monoclonal antibody.", J., Cell. Mol. Immunol. 12:21-26(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01.MAR-2001 (TREMBLICEL 16, Created)
01.MAR-2001 (TREMBLICEL 16, Last seq
01.MAR-2003 (TREMBLICEL 23, Last and
Anti human TNF-alpha light chain var
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01-MAR-2001
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQSPKETLVSAGDRVTITCXASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGVPDRFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIQMIQSPKELLVSAGDRVIIICKASQSV--SND---VAWYQQKPGQSPKLLMYYASNRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPP-TFGGGTKLBIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPTFGGGTXLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQXPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Created)
, Last sequence up
, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 366.5; DB 1
Pred. No. 3.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
annotation update)
variable region (F
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                                                                                                          Su C.Z.;
antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment)
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                                                                                                                                                                                                        Query Match
Best Local S
Matches 68
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Best Local S
Matches 70
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O9UL63: ANY-2000 (TYEMBLrel. 13, Created)

O1-MAY-2000 (TYEMBLrel. 13, Last sequence update)

O1-MAY-2000 (TYEMBLrel. 23, Last annotation update)

MO1-MAY-2003 (TYEMBLrel. 23, Last annotation update)

MO2-10-10-2003 (TYEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                 NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Dfam: PP00047: ic. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEDLINCE FROM N.A. FubWed-9614934;
KEDLINE-98277139; FubWed-9614934;
KEDLINE-98277139; Van der Merwe P.L., Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESQUENCE FROM N. A.
Chen Ps. Deng J. B. Wang Z.L., Han H., Yeo L.B., Su C.Z.;
Chen Ps. Deng J.B., Wang Z.L., Han H., Yeo L.B., Su C.Z.;
Submitted (MX-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, PERG/178-BAG23804.1;
HSDP., B03631.1MTL. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF035031; AAD
HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
61
                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunol. Immunopathol. 87:184-192(1998)
AF035031; AAD56267.1; -.
                                                                                                                                                                                                             68;
                                                                                                                                                                                                                                      Similarity
                                                  RETGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR
                                                                                                                                                  DIOMIOSPKELLVSAGDRVIITCKASOSVSNDVAMYQQKPGQSPKLLMYYASNRYIGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPDRPMGSGSGTDFTLTISSVQTEDLADYFCQQHYRTFFTFGSGTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPDRFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WTQSPSSLAMSVGQKVTMSCKSSQSVLNSNTQKNVLAWYQKXPGQSPELLVYFASTRESG 60
RESGSGSGTEFTLTISSLQFEDFAVYYCQHYNNWPFTFGPGTKVDIKR
                                                                                                EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQXPGQAPRLLIXCASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTQSPKFLLVSAGDRVTITCKASQSVSND-----VAWYQQKPGQSPKLLMYYASNRYTG 57
                                                                                                                                                                                                                                                                                                                 108
108 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 AA; 11784 MW;
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                 11834 MW; 9F9C5A92EBA96EBA CRC64;
                                                                                                                                                                                                                                 62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.9%; Score 360; DB 11; 65.4%; Pred. No. 7.1e-32;
                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                                                                                                                      Score 359; DB 4; Length 108; 
Pred. No. 9.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2B15EEA6604A26C3 CRC64;
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 107,
                                                                                                                                                                                                        21;
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108
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                                                                                                    60
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RESULT 14
QOLUME
TO CODINI
AC CODINI
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Q8NEK1
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Best Local S
Matches 68
                                                                                                           Straubecy R.;

Submitted (OCT-2001) to the BMBL/GenBank/DDBJ da

LMBL, BG015921, AM112921.1;

InterPro; IRB003006; 1g_W.

InterPro; IRB00396; 1g_W.

InterPro; IRB00396; 1g_W.

IRB0718; PR00145; RIDS00MA1_52.

HAM; PR00147; 4g; 2.

RMSTT; SW00463, TGV HKC, 1.

RMSTT; BW00463, TGV HKC, 1.

RMSTT; BW00463, REDS00MA1_82_11 1.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       031WF9;
01-BEC-2001 (TERMELTel. 19, Created)
01-BEC-2001 (TERMELTel. 19, Last sequence update)
01-BMR-2001 (TERMELTel. 23, Last amonation update)
Hypothetical 25,9 kNa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 2.

SMART; SM00407; IGC1; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS0835; IG LIKE; 2.

PROSITE; PS0290; IG MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. MBEL, ECO30613; AMR0613.1; -:
InterPro; IPR007110; Ig-1ke. Therefro; IPR003597; Ig-gl.:
InterPro; IPR003597; Ig-gl.:
InterPro; IPR003597; Ig-gl.:
InterPro; IPR003596; Ig-yr.:
IPR010476; IPR003596; Ig-yr.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. Homo sapiens (Human).
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01-MAR-2003
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                                                                   Hypothetical protein.
SEQUENCE 234 AA; 25929 MW;
                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91WF8
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SEQUENCE 234 AA; 2
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68; Conservation
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61.0%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 358; DB 4;
Pred. No. 3.1e-31;
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Score 349; DB 1
Pred. No. 3e-30;
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                       DB 11,
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099M37, TERBUICE1. 17, Created)
01.-UN-2001 (TERBUICE1. 17, Last sequence update)
01.-UN-2001 (TERBUICE1. 23, Last amnotation update)
Mypothetical AG, 3 kOa protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                          80 SGVPDRFSGSGSTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGTKLEIKR 132
                                                                                                                                                                                                                                                                                                                                                  56 TGVPDRFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Total number of hits satisfying chosen parameters: 1107863

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Maximum DB seq length: 200000000

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SIIDSI JOGOdata (penesed/gen /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Anti VLA-4 antibod	AAY01034	20		91.4	523	9
Antibody HP1/2 lig	AAY23985	20		91.4	523	8
Anti-VLA4 Ab HP1/2	AAR58750	15		91.4	523	7
HP1/2 Vk. Synthet	AAR59937	15	106	91.4	523	on
Sequence of the va	AAR39567	14		91.4	523	U
HP1/2 Vk. Homo sa	AAR39818	14		91.4	523	4
Chimeric 31.1 anti	AAE29157	23		92.3	528	ω
MAD 4197X light ch	AAR70828	16		92.5	529	٥.
Anti-FIX/FIXa anti	AAB20433	22		100.0	572	
Description	₽	80	Query Match Length DB	Query	Score	Regult No.
150	SOPPOND S			de		

VK1 (DQL) VL. Chi Transplanted V-kap	AAR70254	16	128	80.6	461
mised HP1/2	AARS5209	: 5	128	80.6	461
×	AAR55211	15	128	80.9	463
4	AAR70256	16	129	81.5	466
4	AAY01036	20	128	٠	466
	AAW31691	19	128	81.5	466
	AAW72435	19	128	81.5	466
XGMVS	AAR58752	15	128	81.5	466
Fasi	AAW19018	18	105	82.9	474
Variable light cha	AAW00832	17	105	82.9	474
oclonal antibo	AAR40385	14	225	83.7	478.5
	AAR59935	15	128	83.7	479
	AAR59943	15	124	83.7	479
Modified sequence	AAW35377	18	107	84.1	481
eered super	ABP58454	24	672	85.7	490
expressed	ABU07262	24	488	86.9	497
Human expressed pr	ABU07253	24	488	86.9	497
acid sequer	AAB83836	22	488	86.9	497
ì	AAW86004	<u>۵</u>	488	86.9	497
nce of regi	AAW35376	18	107	87.1	498
Ε.	AAW86003	20	595	87.8	502
	AAB83838	22	592	87.8	502
scid seque	AAB83835	22	243	87.8	502
ine ar	AAW86002	20	243	87.8	502
CPV	AAY27407	20	243	87.8	502
5T4 sec	AAY42294	20	243	87.8	502
chain	AAY17494	20	126	88.3	505
	AAR25411	13	107	88.6	507
	AAY39452	20	206	89.3	511
Light chain variab	AAR25413	13	107	89.5	512
Anti-cataract immu	AAR70827	16	554		518
binding inhi	AAR58612	5	246	90.7	519
	ABU08539	24	106	91.4	523
e anti-	AAB73463	22	106	91.4	523
Light chain variab	AAW96742	20	106	91.4	523

ALIGNMENTS

AAB20433 standard; Protein; 242 AA.

AAB20433;

21-JUN-2001 (first entry)

Anti-FIX/FIXa antibody 193/AD3 scFv

Factor IX; FIX; Pactor IXa; FIXa; scPv; antibody; procagulant, Factor VII coffactor; blood coagulation disorder, haemophilia h, haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

Chimeric - 1 Chimeric - 1 Mus musculus. Synthetic.

WO200119992-A2. Region Region Key Protein Peptide Protein /label= VH 98..108 135..242 /label= VL Location/Qualifiers 120..134 /label= Linker 'label= CDR3 'label= CDR3 231

22-MAR-2001.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                              Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diathesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-290358/30.
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                     Region
                                                                                                                                                                           Tamunotoxin, heavy chain, light chain, variable region, antibody, ricin-A, cytestatic, cataract; lens opacification; epithelial cell; pHE19; 4197X; monoclomal antibody; MAD.
                                                                                                                                                                                                                                                         MAb 4197X light chain variable region.
                                                                                                                                                                                                                                                                                               25-MAR-2003
31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                          AAR70828;
                                                                                                                                                                                                                                                                                                                                                                                               AAR70828 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BAXT ) BAXTER
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                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 RFTGSGYGTDFTFTISTVQAEDLAVVFCQQDYGSPFTFGGTKLEIKR 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQSBKFILLVSAGDRVTITCKASQSVSNDVAWYQQKBGQSBKLLMYYASNRYTGVFD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
ilarity 100.0%;
Conservative 0
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(first entry)
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                                                                          Location/Qualifiers 53..64
   80..86
/label= CDR2
                                        /note= "complementarity
                                                           /label= CDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 572; DB 22;
Pred. No. 3.1e-39;
); Mismatches 0;
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                                        determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٦
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RESULT 3
AAE29157
ID AAE2
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An immunotoxin (given in AAR70827) comprises the heavy (WH) and light chain (VI) variable regions of anti-lens gybthealium 1923 Web 4197X Linked to rich-A. chas encoding the VI and W regions of 4197X (AAQ85387-88) respectively) were obtained from hybridoms mRDM, amplified by FCN; and engilescred for inclusion in the immunotoxin construct (AAQ85361, 2003 to correct PM field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after extra:capsular cataract extraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-082036/11.
N-PSDB; AAQ85387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gould RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-1995
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                                                                                                                                                                                                           31.1 antibody; pancreatic cancer; pancreatic
                                                                                                                                                                                                                                                                                     27-JAN-2003
                                                                                                                                                                                                                                                                                                                             AAE29157;
                                                                                                                                                                                                                                                                                                                                                                     AAE29157 standard; Protein; 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOUS-) HOUSTON BIOTECHNOLOGY INC.
WO200274251-A2
                                                    Protein
                                                                                         Peptide
                                                                                                                                                   Unidentified
                                                                                                                                                                                        light chain variable region.
                                                                                                                                                                                                                                                Chimeric 31.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTGSGYGTDFTFTTSTVQAEDLAVYFCQQDYSSPYSFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVMTQTPKFLLVSAGDRVTITCKASQSVNNDVAWXQQKPGQSPKLLIYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQMIQSPKFLLVSAGDRVIITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYIGVPDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                antibody light chain variable region
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/note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "complementarity determining region 2" 119..127
                                                                      /label= Signal-peptide
                                                                                                           Location/Qualifiers
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                                 "31.1 antibody light chain variable region"
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Mismatches
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                                                                                                                                                                                                           carcinoma; antibody therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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26-SEP-2002

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Best Local
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Use of anti-VLA-4 antibodies e.g. HP1/2, HP2/1, HP2/4, L25 or P4C2 antibodies - for inhibiting late phase response to allergens
                                                                                N-PSDB;
                                                                                                              WPI; 1993-242914/30.
                                                                                                                                                                                                                   (BIOJ ) BIOGEN
                                                                                                                                                                                                                                                                                                                             12-JAN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             very
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody; allergen; light chain; asthma; VLA-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HP1/2 Vk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR39818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR39818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relakes to movel muchaic acid esquences encoding light and heavy chain variable regions of the antibody 31.1. Sequences of the thromtion are useful in expressing chimerised 31.1 antibodies, which can be used for treating pancreatic cancer or for diagnosing puncreatic careful antibody. Therapy. The presequence is chimeric 31.1 antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 2; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding light and heavy chain variable regions of antibody 31.1, useful for expressing chimerized 31:1 antibodies for treating pancreatic cancer or for diagnosing pancreatic carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arlen M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             late antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSSPLTFGAGTKLELKR 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVMTQTPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLIYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsang KY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.3%;
(larity 93.5%;
Conservative
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Pred. No. 6.5e
3; Mismatches
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RESULT 5
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Best Local S
Matches 99
expressed in combination with constant regions of human timunoglobulin heavy and light chains. Such a chimeric HP1/2 antibody is simular in specificity and potency to the murzine H antibody, and may be useful in methods for treating ulcerative
                                                   Amti-VuA-4 antibody = anti-very late antigen-4 antibody. One anti-
VuA-4 monoclonal antibody is designated HP/2 (obtained from Biog
Inc. Cambridge, Ms). The warrable regions of the heavy and light
chains of the anti-VuA-4 antibody HPI/2 were closed, sequenced as
                                                                                                                                                     Treatment of inflammatory bowel disease - using anti-very late antigen-4 antibody, polymeptide or other molecule recognising anti-very late antigen-4, reducing acute inflammation in ulcerative colitis, Crohn's disease, etc.
                                                                                                                             Disclosure; Page 26; 35pp; English.
                                                                                                                                                                                                                               N-PSDB; AAQ46080
                                                                                                                                                                                                                                          WPI; 1993-272566/34
                                                                                                                                                                                                                                                                         ddor
                                                                                                                                                                                                                                                                                                                                                         02-FEB-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of the variable region of the light monoclonal antibody HP1/2 (HP1/2 V kappa).
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08-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody, esp. monoclonal antibody HP1/2. The antibody is able to bind to the alpha 4 submit of VMA-4 os as to (a) inhibit late phase response to an allergem to which the subject is hypersensitive or (b) decrease alreay hypersensitivity after allergen challenge. Updated on 23-MAR-2000 to correct PM field.)
                                                                                                                                                                                                                                                                                                  (BIOJ ) BIOGEN
                                                                                                                                                                                                                                                                                                                               12-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variable light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody; anti-very late antigen-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR39567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asthma is treated by admin. of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 29; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating chronic allergen-induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVMTQTFKFLLVSAGDRVTITCKASQSVTNDVAWYQQKPGQSFKLLIYYASNRYTGVPDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSSPYTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 AA;
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(first entry)
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Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLA-4; HP1/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the anti-VLA-4
                                                                                from Biogen
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               HP1/2
                                                       and
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Best Local S
Matches 99
                                This sequence represents the HP1/2 antibody kappa chain variable region (VR). This process sequence was used in the production of a humanised recombinant anti-VLA4 antibody (rab). The humanised rab comprises non-human complementarity determining regions at VH positions 3-35 (CDR1), 59-55 (CDR2) and 59-102 (CDR3). It may further comprise non-human residues at Framework positions 2-30, 75, 77-79 or 65-67, or 69-71 and 65-71, or 64-65, or 39 and 40 or 24. The VIO of the rab has non-human CDRs at positions 24-24 (CDR1), 59-55 (CDR2) and 59-79 (CDR3). It may also have non-human residues at framework positions 60 and 67. It may also have non-human residues at framework positions 60 and 67. It may also have non-human residues at framework positions 60 and 67. It may also have non-human residues at framework positions 60 and 67. It may also have non-human completed framework with no unusual residues. The rab completed framework with no unusual residues. The rab completed framework with no unusual residues. The rab completed framework with no unusual residues.
                                                                                                                                                                                                                                             Recombinant and humanised anti-VLA4 antibodies - contg
non-human CDRs in their light and heavy chains, used to
                                                                                                                                                                                                                                                                                WPI; 1994-249240/30.
P-PSDB; AAR59937.
                                                                                                                                                                                                                                                                                                                                                                                            07-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised; human; mouse; recombinant; antibody, anti-TuAn; heavy;
light; variable; framework; rab; monoclonal; CDR; HR1/2; asthma; CDR;
complementarity determining region; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HP1/2 Vk
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07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR59937;
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Sequence
                                                                                                                                                                                                         Example 1; Page 78; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9416094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bowel disease.
                         (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                  (non-)specific inflammation, e.g. asthma
                                                                                                                                                                                                                                                                                                                                              (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                     12-JAN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crohn's disease or an acute flare-up of inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTGGGYGTDFTFTISTVQAEDLAVXFCQQDXSSPYTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                     Lobb RR,
   106 AA;
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                                                                                                                                                                                                                                                                                                                       PR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 523; DB 14;
Pred. No. 1.4e-35;
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RESULT 7
AAR58750
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Best Local &
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Best Local
                                                                                                                                                                                                                                                                                    Chimeric HPI/2 antibody comprises the variable regions of and light chains of mouse anti-VLAA bb HPI/2 and constant human heavy and light chains CNNA encoding the HPI/2 VH kappa sequences are given in AAQ67343-44, and the encoded AAR56749-50.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment and prevention of insulin dependent diabetes - by nadministering monoclonal antibodies specified for the integrin VLA4 blocking interactions with VCAM-1 and fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric antibody; HP1/2; integrin; VLA4; very late antigen-4; heavy chain; light chain; constant region; variable region; antibody engineering; VCAN-1; fibromectin; monoclonal antibody; insulin-dependent diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR58750;
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                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ67344.
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                                                                                                                  N
                                                                                                                                                         99;
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FIGSGYGIDFIFIISTVQAEDLAVYFCQQDYGSPTTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSFFTFGGGTKLEI 106
                                                               IVMTQTPKFLLVSAGDRVTTTCKASQSVTNDVAWYQQKPGQSPKLLIYYASNRYTGVPDR
                                                                                                               IQMIQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKFGQSPKLLMYYASNRYIGVPDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
                                                                                                                                                                                                                                 106 AA;
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                                                                                                                                                      3.
                                                                                                                                                                     Score 523; DB 15;
Pred. No. 1.4e-35;
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Pred. No. 1.4e-35;
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12-FEB-1992;
02-FEB-1993;
11-AUG-1994;
18-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the light chain variable region of the markine anti-human very late antisen, 4 (VLA-4) monoclonal antibody RF1/2. The protein can be used in the method of the invention. The specification describes methods for treating inflammatory bowel disease with a composition comprising an antibody, or its fragments, able to bind to the BI or E2 Spitope of the alpha 4 submit to "VLA-4. The method is usseful for treating ulcerative colitis and Crohn's disease.
    04-JUN-1999
                                                     AAY01034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain variable region; very late antigen-4; VLA-4; antibody Hpl/2; inflammatory bowel disease; B1 epitope; B2 epitope; alpha 4 subunit; ulcerative colitis; Crohn's disease.
                                                                                                   AAY01034 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating inflammatory bowel disease with VLA-4 blockers
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22-SEP-1999
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                                                                                                                                                                                                                                                                    FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                                           IQMTQSPKFLLVSAGDRVTXTCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR 61
                                                                                                                                                                                                                                                                                                                                      IVMTQTFKFLLVSAGDRVTITCKASQSVTNDVAWYQQKPGQSPKLLIYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 AA;
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(first entry)
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92US-0835139.
93WO-US00924.
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94.3%;
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Pred. No. 1.4e-35;
3; Mismatches 3;
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ID AAW96
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XX 20-M9
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DT 16-AE
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09-FEB-1993;
09-FEB-1994;
                                                                 Light chain variable region; antibody HP1/2; Alpha 4 beta 1 integrin very late antigen-4; VLA-4; chronic allergen-induced asthma; VAM-leukocyte enigration; leukocyte infiltration; signal transduction inhibition.
                                                                                                                                                                                                         Light chain
                                                                                                                                                                                                                                                          20-MAR-2003
16-APR-1999
                                                                                                                                                                                                                                                                                                                                        AAW96742;
                                                                                                                                                                                                                                                                                                                                                                                         AAW96742 standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for the treatment of insulin-dependent type I diabetes, comprising administering to a predibett memmal for membering partial beta-cell destruction) one or more empesitions of an antibody that bluds to the alpha 4 submunit of work every expensive antigen-b) its antigen-binding fragments, or a soluble VDM-I (vascular cell addesson molecular) bolypertide that binds to the alpha 4 submit cell addesson molecular) bolypertide that binds to the alpha 4 submit cell was the contraction between the contraction of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Column 27-28; 28pp; English.
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N-PSDB; AAX27914.
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insulin-dependent type I diabetes; very late antigen-4; soluble VCAM-1;
vascular cell adhesion molecule-1; insulin-dependent diabetes; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating insulin-dependent diabetes by blocking VLA-4 antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQMTQSPKFILIVSAGDRVTITCKASQSVSNDVAMYQQXPGQSPKILMYYASNRYTGVFDR
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                                                                                                                                                                                                     variable region of antibody HP1/2.
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(first entry)
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Pred. No. 1.4e-35;
3; Mismatches 3
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Matches 95
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13-JAN-1992;
12-JAN-1993;
12-JUL-1994;
                                                                                                                                                                                                                                            Integrin antegonist; VLA-4 antegonist; alpha-4-bets-1 integrin; very late antigen; moncolonal antioly HP1/2; mouse; murine; kidney disease; chronic renal failure; end etage renal disease; chronic dishetic nephropethy disbetic glomerulopathy; disbetic renal hypertrophy, hypertrophy hypertropathy enphroselerosis; hypertensive glomerulopathy appartensive glomerulopathy; appartensive glomerulopathy appartensive glomerulopathy; hypertensive negotiation and hypertensive glomerulopathy; hypertensive glomerulopathy; hypertensive negotiathy hypertensive production and hypertensive glomerulopathy; hypertensive negotiathy hype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine anti-VLA-4 monoclonal antibody HP1/2 VL
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to inhibit late phase response and decrease airway hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX15094.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5871734-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-166573/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVMTQTPKFLLVSAGDRVTITCKASQSVTNDVAWYQQKPGQSPKLLIYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9508-0374331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0456193
92US-0821768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 523; DB 20;
Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٥,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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22-MAR-2901

Mus musculus

Nouse; antibody, VLA-4; alphadbetal integrin; VCM-1; IED; vascular call adhesion molecula-1; inflammatory bowal disease; vascular call adhesion molecula-1; inflammatory disorder; vascular call of the state of the control of inflammatory disorder; antilocer; antilnflammatory, VCMA 2D IGG; kappa chain variable region.

Mouse anti-VLA-4 antibody HP1/2 kappa chain variable region

02-JUN-2003

(first entry)

밁 B 밁

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RESULT 12
ABU08539
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             administration of at least one integrin antegonist The integrin antegonists that may be used in the method include antegonists of alpha-1-submit containing integrine or antegonists of alpha-1-submit containing integrine or antegonists of alpha-1-submit containing integrine. In particular, the antegonists are antibodies specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or VLA-4 (alpha-1-beta-1 integrin) which inhibit the interaction of the integrin and its cognate ligand (collagen I, collagen IV, and lamin in the case of VLA-1, and tiborenetin and VCMM-1 in the case of VLA-1). The method of the invention may be used to treat chronic renal failure, end-stage renal disease, chronic diabetic nephropathy, diabetic renal glomenilopathy, diabetic renal positions, breeditary hypertensive glomenilopathy disease, chronic glomenilosphitis, chreditary hypertensive glomenilopathy and contained the present sequence represents the light magnitus or renal (vepplasia, The present sequence represents the light thain variable region (VI) of the mutue anti-VLA-4 monotonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for treating a mammal with or at risk of developing, chronic renal failure, involving the contract of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page -; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF86602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-SEP-2000; 2000WO-US25140
ABU08539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Temmen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOJ ) BIOGEN INC.
(UNLO ) IMPERIAL COLLEGE SCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is given
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is not given in the specification, ven in US5932214, columns 25-26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOMTQTPKELLVSAGDRVTITCKASQSVBIDVANYQQKFGQSPKLLTYYASNRYTGVPDR 61
standard; Protein;
                                                                                                                                                                                                                                                                                       FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSSPYTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                      FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pusey C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0153826
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106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 523; DB 22;
Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TECHNOLOGY & MED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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RESULT 13
AAR58612
ID AAR5
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                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to treating inflamancory bound disease (TBD). To comprising a vascular cell adhesion molecule (VCM)-1)/simmosphaking comprising a vascular cell adhesion molecule (VCM)-1)/simmosphaking comprising a vascular cell adhesion molecule (VCM)-1)/simmosphaking composition of the composition is useful to for treating inflamancory bowel disease in a mammal, preferably a human composition is disease for the chronic circles of the composition is desease to the analysis of the composition is administered during an acute transit of the inflamantory bowel disease. The disease force is termed VCMM 2D 196 and comprises 2 N-terminal domains of VCM-1, fused to the human logo heavy chair constant regions, hinge CH2 and CH3.

The present sequence represents the kappa chair variable regions of a consess conjocitional, antibody, 2017.
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                      Matches
           BP617126-A2
                                                                     Human interleukin-6 binding inhibitor;
                                                                                                                     25-MAR-2003
28-APR-1995
                                                                                                                                                         AAR58612;
                                                                                                                                                                               AAR58612 standard; Protein; 246 AA
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            use as a treatment for IBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Column 23-24; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating inflammatory bowel disease, comprises administering composition comprising a vascular cell adhesion molecule-1/immunoglobulin G fusion protesn
                                   Homo sapiens
                                                        septic shock;
                                                                                            Il-6 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lobb RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-1994,
18-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-1997;
02-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-340372/32
                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                       62 FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                      99;
                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                    IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPDR 61
                                                                                                                                                                                                                                                                                       IVMTQTPKFLLVSAGDRVTITCKASQSVTNDVAWYQQKPGQSPKLLIYYASNRYTGVPDR 61
                                                                                                                                                                                                                                        FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSSPYTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burkly LC:
                                                                                                                                                                                                                                                                                                                                                                                      106 AA;
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                              inhibitor
                                                        multiple myeloma; ss
                                                                                                                   (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0456124.
97US-0950660.
93US-0835139.
93WO-US00924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0284603
95US-0373857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0157452
                                                                                                                                                                                                                                                                                                                                                91.4%;
                                                                                                                                                                                                                                                                                                                                      ω
                                                                                                                                                                                                                                                                                                                                     Score 523; DB 24;
Pred. No. 1.4e-35;
3; Mismatches 3;
                                                                    IL-6; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                           Length 106;
                                                                                                                                                                                                                                                                                                                                      Indels
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RESULT 14
AAR70827
ID AAR70
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Best Local S
Matches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A070612 codes for human interleukin-6 binding inhibitor, the polypeptide described in A826812. This polypeptide libbits to binding of human II-6 to its receptor, and can therefore be useful in the treatment of a variety of autoimmune diseases; specifically in the treatment of thousatoid arthritis, seption shock due to bacterial lifection and multiple mysloma. Updated on 25-MAX-2001 to correct PM field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide inhibiting its receptor - useful or aggravated by IL-6
                               Domain
                                                                                                          Domain
                                                                                                                                                     Peptide
                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                рНВ19; 4197X;
                                                                                                                                                                                                                                                 ricin-A;
                                                                                                                                                                                                                                                                                             Anti-cataract immunotoxin.
                                                                                                                                                                                                                                                                                                                          25-MAR-2003
31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                        AAR70827;
                                                                                                                                                                                                                                                                                                                                                                                                   AAR70827 standard; Protein; 554 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 18; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ70612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hamuro J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1994
                                                            Peptide
                                                                                                                                                                                                                                                              Immunotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1994-295777/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYRSPFTFGSGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                            din heavy chain; light chain; variable region; antibody;
cytostatic; catarate; lens opacification; epithelial cell;
197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DILLTQSPKFLLVSAGDRVTITCKASQSVSTDVSWYQQKPGQSPKLLIYYASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakazawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                        (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-0028173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94EP-0102346
                                                                                                                                                                  Location/Qualifiers
/label= LIGHT
/note= "MAD 419X
                                                            148..166
                                                                                                                      /label= Sig_peptide
/note= "phoA signal sequence"
                                             'label= LINKER
                                                                          'note= "MAb 4197X heavy chain
                                                                                           /label= HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.7%;
                                 . 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding of human interleukin-6 (IL-6) to for treating auto:immune disease induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimamura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 519; DB 15;
Pred. No. 6.6e-35;
3; Mismatches 5
light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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/label= RICIN-?

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Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The immunotoxin given in AAR/0827 comprises the heavy and light chain variable regions of anti-lens epithelium 1963 who 4527X linked to ricin-A and a hoxa-histidine tag The DNA construct encoding the immunotoxin was expressed from pHB19 in B. coli. (Dpdated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after extra copsular cataract extraction.
             21-DEC-1990;
03-MAY-1991;
                                                                                                                                        monoclonal antibody; humanised; chimeric; CDR; neoplastic therapy;
shock; antilymphocyte therapy; endotoxin shock; septic shock;
sepsis; cardiovascular shock; tumour necrosis factor alpha;
multi-organ failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig.4; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gould RM,
                                             20-DEC-1991;
                                                                      09-JUL-1992
                                                                                            WO9211383-A1
                                                                                                                   Chimeric.
                                                                                                                                                                                                    Light chain variable domain of MAb hTNF3 to TNFalpha epitope.
                                                                                                                                                                                                                           25-MAR-2003
11-JAN-1993
                                                                                                                                                                                                                                                               AAR25413;
                                                                                                                                                                                                                                                                                      AAR25413 standard; Protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-082036/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HOUS-) HOUSTON BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9503828-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 98; Conserv
                                                                                                                                                                                                                                                                                                                                                229
                                                                                                                                                                                                                                                                                                                                                                                              169 IVMTQTPKFLLVSAGDRVTITCKASQSVNNDVAWYQQKPGQSPKLSIYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                     62 FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                           2 IQMTQSPKFLLVSAGDRVTITCXASQSVSNDVAWYQQKPGQSFKLLMYYASNRYTGVPDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ85386
                                                                                                                                                                                                                                                                                                                                              FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSSPYSFGGGTKLEIK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kelleher PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            554 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                           (updated)
(first en
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           90WO-GB02017.
91GB-0009645.
                                             91WO-GB02300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US07919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549..554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "hexa-histidine tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= TAG
                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wallace TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 518; DB 16;
Pred. No. 1.7e-34;
4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                             4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                       Search completed: November Job time: 47,5741 secs
                                                                                                                                                                                         Matches
                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                antibody to an epitope of human tumour necrosis factor. The sequence shows 2 differences compared with CBS (EMZS411.3) - in the light chain at positions 50, 96, and in the framework at 1, 19, 40, 45, 46, 76, 103, and 106, and in the heavy chain in the CDB at 52, 60 and 95, and in the framework at 1, 10, 38, 40, 67, 73, 87,
                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                               This sequence is that of the light chain variable domain of a chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 4; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant antibody specific for human TNF-alpha - for treatment of shock and immuno:regulatory and inflammatory disorders, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-250102/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adair JR,
                                                                                                                                                                                                                                                                                     (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                      and 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CLLT ) CELLTECH LTD
                                                             61
                                                                                    61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPFTFGGGTKLEIK 107
                                                                                                                                               1 DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPD
                                                                                                                                                                                         94;
                                                                                                                           1 NIVMTQTPKFLLVSAGDRITITCKASQSVSNDVAWYQQKPGQSPRLLIYYVSNRYTGVPD
                                                                                                                                                                                                        Similarity
                                                             RFTGSGYGTDFTFTINTVQAEDLAYYFCQQDYSSPYTFGGGTRLEVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Athwal DS,
                                                                                                                                                                                                                                                       107 AA;
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                      89.5%;
                 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bodmer MW,
              2003, 07:27:00
                                                                                                                                                                                         8
                                                                                                                                                                                       Score 512; DB 13;
Pred. No. 1.1e-34;
8; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emtage JS
                                                                                                                                                                                                                    Length 107;
                                                                                                                                                                                         Indels
                                                                                                                                                                                         0
                                                                                                                                                                                         Gaps
                                                                                                                           60
                                                                                                                                                           60
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: OM protein - protein search, using sw model November 7, 2003, 07:30:19; Search time 94.7343 Seconds (without alignments) 195.799 Million cell updates/sec

Title: Perfect score: US-09-661-992B-82_COPY_135_242 572

DIQMTQSPKFLLVSAGDRVT.....QQDYGSPPTFGGGTKLEIKR 108

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Post-processing: Minimum Match 0% Maximum Match 100% Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database

Listing first 45 summaries

published Applications An:

1 (Sqn2 6) prodates // jhubpas/USO7 pUBCOMB .psp:

2 (Sqn2 6) prodates // jhubpas/USO7 MBW FUB .psp:

3 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

4 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

5 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

6 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

6 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

8 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

9 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

10 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

11 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

12 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

13 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

14 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

15 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

16 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

17 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

18 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

19 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

10 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

10 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

11 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

12 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

13 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

14 (Sqn2 6) prodates // jhubpas/USO6 .puBCOMB .psp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

															Result
15	14	13	12	11	10	9	8	7	6	ຫ	,ih	w	N	,	No.
442	442	445	448	461	466	479	479	490	498	507	512	523	523	523	Score
77.3	77.3	77.8	78.3	80.6	81.5	83.7	83.7	85.7	87.1	88.6	89.5	91.4	91.4	91.4	Query
128	108	128	108	128	128	128	124	672	107	107	107	106	106	106	Length
8	12	12	12	12	12	12	12	11	15	12	12	15	15	12	DB
US-08-779-784-36	US-10-422-049-14	US-10-010-729-72	US-10-422-049-18	US-10-428-662-31	US-10-428-662-63	US-10-428-662-67	US-10-428-662-71	US-09-900-766-1	US-10-283-838-6	US-10-422-049-13	US-10-422-049-17	US-10-252-978-4	US-10-095-496-2	US-10-428-662-10	ID
Sequence 36, Appl	Sequence 14, Appl	Sequence 72, Appl	18,	Sequence 31, Appl	Sequence 63, Appl	Sequence 67, Appl	71,	۲	Sequence 6, Appli	Sequence 13, Appl	Sequence 17, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 10, Appl	Description

Ś 밁 8

62 FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEI 106

Query Match 91.4%; Score 523; DB 12; Length 106; Best Local Similarity 94.3%; Pred: No. 9.4e-44; Matches 99; Conservative 3; Mismatches 3; Indels

0 Gaps

61

2 IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR 61 2 IVMTQTPKFLLVSAGDRVTITCKASQSVTNDVAWYQQKPGQSPKLLIYYASNRYTGVPDR

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421	421	421	421	421	421	421	422.5	422.5	422.5	422.5	422.5	422.5	423	423	423	424	424	425	427	427	430	431	435	437	439	439	439	439	442
73.6	73.6	73.6	73.6	73.6	٠		73.9	73.9	73.9	73.9	73.9	73.9	74.0	74.0	74.0	74.1	74.1	74.3	74.7	74.7	75.2	75.3	76.0	76.4	76.7	76.7	76.7	76.7	77.3
126	126	126	126	126	126	126	234	234	234	213	213	213	127	107	106	133	133	107	127	107	109	107	250	331	131	131	131	107	333
16	5	12	11	ä	9	9	12	12	12	12	12	12	10	10	ø	11	H	15	10	10	9	11	0	15	16	11	H	H	15
US-10-218-253-106	US-10-315-125-6	US-10-428-085-6	US-09-509-098-12	US-09-269-921-106	US-09-355-925-6	US-09-760-723-6	US-10-286-132A-24	US-10-275-180A-24		US-10-286-132A-76	-10-275-180A-	US-10-281-479A-76	US-09-956-206A-65	US-09-956-206A-81	US-09-824-286-4	US-09-874-141-51	US-09-874-141-45	US-10-268-501-1	US-09-956-206A-49	US-09-956-206A-79	US-09-811-123-4	US-09-509-098-134	US-09-887-853-2	US-10-059-261-169	•	US-09-509-098-2	US-09-269-921-104	US-09-509-098-130	US-10-059-261-61
	Sequence 6, Appli			Sequence 106, App		6, AI	24,	Sequence 24, Appl	24,	76,	76,	76,	Sequence 65, Appl	8	Sequence 4, Appli	51	45	Sequence 1, Appli	49	e 79	Sequence 4, Appli	۳,		169	10	Sequence 2, Appli	104		Sequence 61, Appl

ALIGNMENTS

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62

FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSSPYTFGGGTKLEI 10t

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APPLICANT: Alien Andrew
APPLICANT: Busey Charles
APPLICANT: Busey Charles
APPLICANT: Busey Charles
APPLICANT: Bogen, Inc.
APPLICANT: Imperial College of Science, Technology and Medicine
TITLE OF INVENTION: Therapies for Chronic Renal Failure
TITLE OF INVENTION: URLEG One or More Integrin Antagonists
CIREME PRINCENTON MUNISER: US/10/095,496
CREATER FILLIAN DATE: 2002-09-14
PRIOR PELLIAND DATE: 2002-09-14
PRIOR PELLIAND DATE: 1002-09-14
PRIOR PELLIAND DATE: 1009-09-14
PRIOR PELLIAND DATE: 1099-09-14
PRIOR PELLIAND DATE: 1099-09-14
PRIOR PELLIAND DATE: 2009-09-14
PRIOR P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-095-496-2
                                                                                                                                                                                                                                 PRIOR PIPELCONTION INMMERS: US/09/257,452
PRIOR FILING DATE: 1998-09-21
PRIOR PIPELCANTION INMMERS: US 08/950,660
PRIOR PRICE ADVITE: 1997-10-15
PRIOR PIPELCANTION INMMERS: US 08/979,557
PRIOR PIPELCANTION INMMERS: US 08/284,603
PRIOR PIPELCANTION INMMERS: US 08/284,603
PRIOR PIPELCANTION INMMERS: US 08/284,603
PRIOR PIPELCANTION INMMERS: PCT/US33/00524
PRIOR PIPELCANTION INMMERS: PCT/US33/00524
PRIOR PIPELCANTION INMMERS: PCT/US33/00524
PRIOR PIPELCANTION INMMERS: PCT/US33/00524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10252978 Publication No. US20030095969A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10095496
Publication No. US20030007969A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                 SEQ ID'NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT, BARYLY, LAINGA C.
TITLE OF INVESTION: TEXAPARENT FOR INFLAMMATORY BOWEL DISEASE
FILE REFERENCE: 10274-004003
CURRENT APPLICATION NOWBER: US/10/252,978
CURRENT FILING DATE: 2007-09-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lobb, Roy
APPLICANT: Allen, Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lobb,
APPLICANT: Burk!
                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                PRIOR FILING DATE: 1992-02-12
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 07/835,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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ENGTH: 106
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Pred. No. 9.4e-44;
3; Mismatches 3
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US-10-422-049-13
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US-10-252-978-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: CARPOGÉS

CURRENT PELLING LATE: 2001-04-22

PRICE APPLICATION NUMBER: US/10/267, 281

RICE PILLIG LATE: 1999-01-125

PRICE PILLIG LATE: 1999-01-125

PRICE PILLIG LATE: 1999-01-125

PRICE PILLIG LATE: 1999-01-125

PRICE PILLIG LATE: 1999-01-15

PRICE PILLIG LATE: 
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PRIOR PLING DATE: 1992-09-28
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PACENTIN VET: 2.1
SEQ ID NO 17
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/10422049 Publication No. US20030199679A1 GENERAL INFORMATION:
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Best Local Similarity
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Publication No. US20030199679A1
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NPPLICANT: Addit, John Robert
APPLICANT: Abral, Diljest Singh
APPLICANT: Bmteage, John Spencer
APPLICANT: Bomteage, John Spencer
APPLICANT: Bomte, Mark Hilliam
TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
FILE REFERENCE: CARPOOS
CURRENT APPLICATION NUMBER: US/10/422,049
CURRENT FILMS DATE: 2090-304-22
FILOR APPLICATION NUMBER: US/07/867,281
FILOR APPLICATION NUMBER: US/07/867,281
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APPLICANT; Metage, John Spentoer
APPLICANT; Bodmer, Mark William
APPLICANT; Bodmer, Mark William
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ORGANISM: Murine
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Pred. No. 9.4e-44;
3; Mismatches 3;
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Pred. No. 1.1e-42;
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; ORGANISM: Murine
US-10-422-049-13
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PRIOR APPLICATION NUMBER: 08/373,882
PRIOR FILING DATE: 1995-01-17
PRIOR APPLICATION NUMBER: 07/920,378
PRIOR FILING DATE: 1995-09-28
PRIOR FILING DATE: 1996-09-28
ONTWARE: PRIORITIN '87.2.1
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                                                                                                                TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/283,838
FILING DARE: 30-0cc-2002
CLASSIFICATION: -CIDHOWN-
PRIOR APPLICATION DATE:
APPLICATION WINHER: US/08/635,692
FILING DATE: Mugnets 12, 1996
APPLICATION WINHER: 9601245-5
APPLICATION WINHER: 9601245-5
APPLICATION WINHER: 86276 22, 1996
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIF "77027-9098
COMPUTER READAILE PORM:
NEDITW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Petentin Release 41.0, Version #1.25
CURRENT REPLICATION DARN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                NAME: Krieger, Paul B.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41986/1
TELECOMMUNICATION:
TELECHONE 7,713-850-0909
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
Johan Hansson, Terje Kalland, Lars
Abrahnsen and Goran Forsberg
TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Houston
STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTGSGYGTDFTFTTTTVQAEDLAVYFCQQDYSSPWTFGGGTKLBIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 507; DB 12;
Pred. No. 3.4e-42;
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; NAME/KEY: PEPTIDE
; LOCATION: (1): (672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1
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                           CIRERENT PAPELICATION (TUMBER: US/10/428,662)
CIRERENT PELLONIUM DATE: 0000-15-02
PRIOR PELLONIUM NUMBER: US/08/454,899G
PRIOR PELLONIUM NUMBER: US 08/004,798
PRIOR PELLONIUM NUMBER: US 08/004,798
PRIOR PELLONIUM NUMBER: PCT/US94/00266
PRIOR PELLONIUM DATE: 1994-01-07
AUMERICATION MOMBER: PCT/US94/00266
PRIOR PELLONIUM DATE: 1994-01-07
AUMERICATION LI DASS: 109
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 71. Application US/10428662
Publication No. US20030188819A1
BRENEARL IMFORMATION:
APPLICANT: LOBD, Roy R.
APPLICANT: Carr, Frank J.
APPLICANT: Carr, Frank J.
APPLICANT: Propert, Pallip R.
APPLICANT: PROPERT, PALID R.
APPLICANT: PROPERT, PALID R.
APPLICANT: TOTAL PROPERT PALID R.
APPLICANT: TOTAL PALID R.
APPLICANT: TOTA
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LENGTH: 672
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Publication No. US20030039655A1
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SOFTWARE: PatentIn version 3.0
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APPLICANT: AUGUSSOM, EVA
APPLICANT: AUGUSSOM, DER
APPLICANT: AUGUSSOM, DER
APPLICANT: AUGUSSOM, DER
AUGUSTOM
TITHE CE INVENTION: A MOVEL ENGINEERE SUPERANTIGEN FOR HUMAN THERAPY
FILM REPERENCE: P02186US0,10104199
GURERNY APPLICATION MORBER: US,09/90,766
GURERNY APPLICATION DATE: 2001-07-66
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APPLICANT: ERLANDSS
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
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87.9%;
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Pred. No. 2.6e-41;
4; Mismatches 9;
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Pred. No. 1.1e-39;
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SEQ ID NO 71

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US-10-428-662-63; Sequence 63; Application US/10428662; Publication No. US20030185819A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-428-662-67
                 GERERAL IMPORMATION:
APPLICANT: LODD, Roy R.
APPLICANT: Carr, Frank J.
APPLICANT: Carr, Frank J.
APPLICANT: Garr, Frank J.
APPLICANT: TOTAL STATE OF INVESTIGATION: RECOMBIANT ANTI-VLA4 ANTIBODY MOLECULES
FILE REFERENCE: 10274-007001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
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PRIOR FLING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/004,798
PRIOR FLILING DATE: 1993-01-12
PRIOR APPLICATION UNMBER: EC7/US99/00266
PRIOR FLILING DATE: 1994-01-07
PRIOR FILING DATE: 1994-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CARY, FYANK J.
APPLICANT: CARY, FYANK J.
APPLICANT: TEMPOST, PHILIP ANTI-VLAM ANTIBODY MOLECULES
TILE REFERENCE: 10274-0075.
CURRENT SPLICATION NUMBER: UD/10/10/128,662
CURRENT SPLICATION NUMBER: UD/10/10/128,662
CURRENT SPLICATION NUMBER: UD/10/128,662
CURRENT SPLICATION NUMBER: UD/10/128,662
CURRENT APPLICATION NUMBER: US/10/428,662
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 128
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124
                                                                                                                                                                                                                                                                             RFSGSGYGTDFTFTISSLQPEDIATYYCQQDYSSPYTFGQGTKVEIKR 121
                                                                                                                                                                                                                                                                                                                                                                                                        DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSGSGYGTDFTFTISSVQAEDVAVYYCQQDYSSPYTFGGGTKLEI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVMTQSPDSLAVSLGERVTINCKASQSVTNDVAWYQQKPGQSPKLLIYYASNRYTGVPDR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/10428662
No. US20030185819A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.7%; Score 479; DB 12;
81.5%; Pred. No. 2.2e-39;
ative 10; Mismatches 10
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Pred. No. 2.1e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 128;
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US-10-428-662-31
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US-10-428-662-63
                                                                                                                                                                                                                                                    ; OTHER INFORMATION: light chain variable region US-10-428-662-31
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/10428662
Publication No. US20030185819A1
                                                                                                                                                                 Matches
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URRENT APPLICATION NUMBER: US/10/428,662
URRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: US/08/454,899G
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 00/004,798
PRIOR RPLIANG DATE: 1993-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CADb. SOY R.
APPLICANT: CAT. Frank J.
APPLICANT: CAT. Frank J.
TITLE OF INVENTION: RECOMBINANT ANTI-VLAA ANTIBODY MOLECULES
FILE REPERRICE: 1027+-007001.
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                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US94/00266
PRIOR FILING DATE: 1994-01-07
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                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 128
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                                                                                                                                                                                     Local Similarity
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                                       61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
                                                                                                                                                                 85;
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                                                                                                                      1 DIQWIQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR
RFSGSGSGTDFTFTISSLQPEDIATYYCQQDYSSPYTFGQGTKVBIKR 127
                                                                               DIQLTQSPSSLSASVGDRVTITCKASQSVTNDVAWYQQKPGKAPKLLIYYASNRYTGVPS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSGSGYGTDFTFTISSLQPEDIATTYCQQDYSSPYTFGQGTKVEIKR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVMTQSPSSLSASVGDRVTITCKASQSVTNDVAWYQQKPGKAPKLLIYYASNRYTGVPDR
                                                                                                                                                                 Conservative
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                                                                                                                                                                                     80.6%;
                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                  Score 461; DB 12;
Pred. No. 1.3e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 466; DB 12;
Pred. No. 4.1e-38;
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                                                                                                                                                                                                         Length 128;
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                                                                                                                                                                 Indels
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RESULT 12 US-10-422-049-18

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CHRENT APPLICATION NUMBER: 15/10/010,729
CURRENT ILLING DATE: 20011-13-1
PRIOR PELICATION NUMBER: 09/730,473
PRIOR PELICHION NUMBER: 09/730,473
PRIOR PELICATION NUMBER: 09/580,787
PRIOR PELICATION NUMBER: 09/580,787
PRIOR PELICATION NUMBER: 09/580,787
PRIOR PELICATION NUMBER: 09/322,862
PRIOR PELICATION NUMBER: 09/79,784
PRIOR PELICATION NUMBER: 09/692,084
PRIOR PELICATION NUMBER: 08/692,084
PRIOR PELICATION NUMBER: 08/692,084
PRIOR PELICATION NUMBER: 08/236,520
PRIOR PELICATION NUMBER: 08/236
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US-10-010-729-72
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; OTHER INFORMATION: Antibody
US-10-422-049-18
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Publication No. US20030185827A1
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Best Local S
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APPLICANT: ADDITION: Miller, David J.
APPLICANT: Miller, David J.
APPLICANT: Passes, Larry R.
APPLICANT: Pesses, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Publication No. US20030199679A1
GENERAL INFORMATION:
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APPLICANT: Athwal, Diljeet S
APPLICANT: Emtage, John Spen
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ORGANISM: Artificial Sequence
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76.9%;
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Pred. No. 1.9e-36;
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                                               RESULT 15
US-08-779-784-36
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; ORGANISM: Mus musculus
US-10-010-729-72
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Sequence 36, Application US/08779784
Publication No. US20020164325A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. SEQ ID NO 14
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Publication No. US20030199679A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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NUMBER OF SEQ ID NOS: 20
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PRIOR FILING DATE: 199-03-12
PRIOR APPLICATION NUMBER: 08/456,418
PRIOR FILING DATE: 1995-06-01
PRIOR PILING DATE: 1995-06-01
PRIOR PILING DATE: 1995-01-17,882
PRIOR PILING DATE: 1995-01-17
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CURRENT FILING DATE: 2003-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Adair, John Robert
APPLICANT: Athenal, piljoes Singh
APPLICANT: Emenge, John Spencor
APPLICANT: Emenge, John Spencor
APPLICANT: Bedeer, Mark Hilliam
TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
FILE REFERENCE: CARPOGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 07/920,378
                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Humanized OTHER INFORMATION: Antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 108
                                                                                                                                       61 RESGSGSGYDYTETISSLOPEDIATYYCOODYSSEWTEGOGYKLOITK
                                                                                                                                                                                61 RFTGSGYGTDFTFTISTVQABDLAVYFCQQDYGSPFTFGGGTKLBIKR 108
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                                                                                                                                                                                                                                                                           1 DIQWIQSPKFLLVSAGDRVIITCKASQSVSNDVAWYQQXPGQSPKLLWYYASNRYIGVPD 60
                                                                                                                                                                                                                               DIOMIOSPSSLSASVGDRVTITCKASOSVSNDVAWYQQTPGKAPKLLIYHVSNRYTGVPS
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                                                                                                                                                                                                                                                                                                                                                     77.3%; Score 442; DB 12; 75.9%; Pred. No. 7.5e-36;
                                                                                                                                                                                                                                                                                                                           11; Mismatches
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Pred. No. 4.6e-36;
7; Mismatches 15;
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APPLICANT: Rodijum,
APPLICANT: Miler, David J.
APPLICANT: Maler, David J.
APPLICANT: ARABURA, KUNIHIKO
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REVOELINATION USING MONOCLONAL AUTOANTIBODIES
TITLE OF INVENTION: 37

GENERAL INFORMATION:

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INCOMPATION FOR SEC ID NO. 36:
SEQUENCE CHARACTER STICS:
SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUE
Search completed: November 7, 2003, 08:16:51 Job time: 95.7343 secs
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COMPATINE NEW TO THE MARKET PORM:

CHENTINE NEW TO THE MARKET PORM:

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COMPANIES: Described NATA:

APPLICATION NUMBER: US 08/08/79/984

FILING APPLICATION NATA:

PRICOR APPLICATION NUMBER: US 08/09/79/984

PRILING APPLICATION NUMBER: US 08/692,084

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REGISTRATICA NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION HEFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
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ADDRESSE: DAVId A. Jockson, Esq.
ADDRESSE: HOAVE
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Joersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 27.3%; Score 442; DB 8; Length 128; Local Similarity 78.7%; Pred. No. 8.9e.36; hes 85; Conservative 8; Mismatches 15; Indels
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61 RETGSGSGTDETETISSVOAEDLAVYYCQQHYTTPLTEGAGTRLEIKR 128
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Maximum Match 100%
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Maximum DB
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Perfect score:
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      seq length:
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Gapop 10.0 , Gapext 0.5
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      328717 seqs, 42310858 residues
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1. /ogp2_6/picodate//liaa/5a_COMB_pep:*

2. /ogp2_6/picodate//liaa/5a_COMB_pep:*

3. /ogp2_6/picodate//liaa/6a_COMB_pep:*

4. /ogp2_6/picodate//liaa/6a_COMB_pep:*

5. /ogp2_6/picodate//liaa/6a_COMB_pep:*

5. /ogp2_6/picodate//liaa/6a_COMB_pep:*

5. /ogp2_6/picodate//liaa/bcTilg_cOMB_pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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      B
                 US-08-840-713-2

US-08-940-713-35

US-08-840-713-37

US-08-235-938-14

US-08-425-473B-7

US-08-425-473B-7

US-08-425-473B-7

US-08-435-804-2
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US-08-463-298-10
US-08-36-3399-10
US-08-63-128-6
US-08-63-128-6
US-08-63-298-6
US-08-436-3399-6
US-08-437309-6
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US-08-950-660-4

US-09-157-452B-4

PCT-US93-00030-4

PCT-US93-00924-4
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Sequence 6, Appli
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Result No.

APELICATION INTA. APELICATION INTRA. APELICATION INTREEN; 07/821768 FILING DATE: 13-VAN 1992 TYTONBREY/AGENT INFORMATION: REGISTRATION WINDERS: 35/95 REFERENCE/DOCKET TUMBER: 869-021USCN RELECOMONICÁTION INFORMATION: TELEPOMONICÁTION INFORMATION: TELEPOMONICÁTION INFORMATION: TELEPOMONICÁTION INFORMATION: TELEPOMONICÁTION INFORMATION: TELEPOMONICÁTION INFORMATION: TELEPOMONICÁTION INFORMATION: LENGTETE: 105 AMBINITATION: LENGTETE: 105 AMBINITATION: LENGTETE: 105 AMBINITATION ACIDA TYPE: amino acida TYPE: amino acida	LORGING ARPLICATION DATAS. APPLICATION MADER: US/08/822,8308 APPLICATION DATAS. 03-048-1997 PRICE APPLICATION DATAS. 09-048-1997 ENGINE APPLICATION DATAS. 09-048-1,93 ENGINE APPLICATION DATAS. 1995 PRICE APPLICATION NUMBERS. US 08/374,331 PILING DATES. 10-304-1995 PRICE APPLICATION NUMBERS. US 08/256,631 PILING DATES. 113-UN-1994 PRICE APPLICATION BATCH. 113-UN-1995 PRICE APPLICATION BATCH. 113-UN-1995 PRICE APPLICATION MEMBERS. PCT/US99/00030 PILING DATES. 113-UN-1994	C12-30B-4 street - 15-90214 st	435 76.0 250 1 US-08-463-675-8 435 76.0 250 1 US-08-464-559-8 435 76.0 250 1 US-08-461-386-2 435 76.0 250 1 US-08-461-386-2 435 76.0 250 1 US-08-461-386-2 437 74.7 127 2 US-08-25-398-2 427 74.0 127 2 US-08-25-398-2 427 74.0 127 2 US-08-25-398-2 427 74.0 127 2 US-08-25-398-2 428 74.0 127 2 US-08-25-398-2 429 74.0 127 2 US-08-25-398-2 420 74.0 127 2 US-08-25-398-2 420 73.0 127 2 US-08-25-398-2 420 73.0 127 2 US-08-25-398-2 420 73.0 127 2 US-08-461-191-4 420 73.0 107 3 US-08-461-191-4 420 73.0 107 3 US-08-25-399-1
		Blocking	Sequence 8, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 48, Appli Sequence 41, Appli Sequence 61, Appli

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-822-830B-4
                                                                    ; MOLECULE TYPE: protein US-08-950-660-4
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Best Local Similarity
Query Match
Best Local Similarity
Matches 99; Conserv
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APPLICANT: Lobb,
                                                                                                                                                           TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/U893/0092.
FILING DATE: 02-PEB-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,139
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/373,857
FILING DATE: 18-JAN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lobb, Roy R.; Burkly, Linda C.
TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease
                                                                                                                                                                                                                                NAME: MYERE, LOUIS (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                          FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: I
                                                                                                                           TYPE: amino acid
                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IVMTQTPKFLLVSAGDRVTITCKASQSVTNDVAWYQQKPGQSPKLLIYYASNRYTGVPDR 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSSPYTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                             linear
                                                                                                                                                                                                                    (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.4%;
                 91.4%; Score 523; DB 2; Length 106; 94.3%; Pred. No. 1.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                      PCT/US93/00924
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/284,603
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  Mismatches
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Pred. No. 1.3e-46;
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  Indels
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APPLICANT: Lobb. ROY R.

APPLICANT: BURLLY, LANDAC.

APPLICANT: BURLLY, LANDAC.

TITLE OF INVESTIGN: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
FILE REFERENCE: 10.27-4.004.003

CURRENT ELIZATION KUMBER: US 09/950,660

PRIOR PELIZATION KUMBER: US 08/950,660

PRIOR PELIZATION KUMBER: US 08/950,660

PRIOR PELIZATION KUMBER: US 08/950,660

PRIOR PELIZATION KUMBER: US 08/373,857

PRIOR PELIZATION KUMBER: US 08/374,603

PRIOR PELIZATION KUMBER: US 08/284,603

PRIOR PELIZATION KUMBER: US 07/835,139

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GENERAL INFORMATION:
APPLICANT: Lobb Roy R.
TITLE OF INVENTION: Treatment for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 106
                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTFMARE: PALENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: PCT/US93/00030
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                  ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                         STREET: 10 Sou
CITY: Chicago
FILING DATE:
                                                                                                                                                                                            COUNTRY: U
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Pred. No. 1.3e-46;
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                                                       Matches
                                                                           Best Local
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GENERAL INFORMATION:
APPLICANT: Lobb, Roy R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
                                                                                                                                                                                                     TELEPAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                 TYPE: AMINO ACID
TOPOLOGY: lines-
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READMANDE FORM:
MEDIUM TYPE, Ploppy disk
COMPUTER: IRM FO Compatible
OPERATING SYZEM: G-7005/MS-DOS
SOFTMARE: PATENTIC BALBASE #1.0, Version #1.25
CURRENT APPLICATION BATES.
                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 92,308-A; D003 CIP PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Treatment for Inflammatory Bowel Disease NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Jamet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 92,307-A; D002 CIP PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 199302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 66
2 IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKFGQSPKLLMYYASNRYTGVFDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPDR 61
                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Allegretti & Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lobb, Roy R
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                                                                        91.4%;
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                                                                        Score 523; DB 5; Length 106;
Pred. No. 1.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 523; DB 5;
Pred. No. 1.3e-46;
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 106;
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                                                       Indels
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                                                                                                 US-08-695-692B-6
                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-197-834-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-08-197-834-7
                                                                                                                   RESULT 7
                                                           Sequence 6, Application US/08695692B
Patent No. 6514498
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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   GENERAL INFORMATION:
APPLICANT: Per An
APPLICANT: Johan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMPUTER READMALE FORM:
MEDIUM THER: Flopy disk
COMPUTER: IEM FC COMPACIAL'S
OMERATING SETEM: FC-DOS/MS-DOS
SUPTIMARE: PALENTING MATHA:
APPLICATION DATA:
APPLICATION MATHER: US/08/197,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSFFICATION: 514

PRIOR APPLICACTION INSTER: UP 028173/19
FILING DATE: 17-FEB-1093
ATTORNEY/AGENT INFORMATION:
NAMES: Oblon, No. 563945man F.
REGISTRATION HUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HENERAL INFORMATION:
APPLICANT: SHIMAMU
APPLICANT: NAKAZAW
APPLICANT: HAMURO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10-661-0 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                        61 RFTGSGYGTDFTFTISTVQABDLAVYFCQQDYGSPPTFGGGTKLBIK 107
                                                                                                                                                                            62 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYRSPFTFGSGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                         99;
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                                                                                                                                                                                                                                                          2 DILLIQSPKFLLVSAGDRVTITCKASQSVSTDVSWYQQKPGQSPKLLIYYASNRYTGVPD 61
                                                                                                                                                                                                                                                                                             1 DIQMIQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4: 246 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08197834
Per Antonsson, Per Bjork, Mikael Dohlsten,
Johan Hansson, Terje Kalland, Lars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAKAZAWA, HARUMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHIMAMURA,
                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                           90.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP 028173/1993
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                                                                                                                                                                                                                                                                                                                                      ű,
                                                                                                                                                                                                                                                                                                                                                           Score 519; DB 1
Pred. No. 9e-46;
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
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                                                                                                                                                                                                                                                          ; Patent No. 6068841

GENERAL INFORMATION:

; APPLICANT: SEINO, I

APPLICANT: KAYAGAKI

APPLICANT: YAGITA;
                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/09065059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local !
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIN Release #1.0, Very
CURRENT APPLICATION NUMBER: US/08/655.692B

FLING DAFE: ANGUSE 12, 1996

PLOS ASPLICATION NOTA: COLORE

PRIOS APPLICATION NOTA: COLORE

PRIOS APPLICATION NOTA: COLORE
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INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                      APPLICANT: OKUMURA, KO
APPLICANT: NAKATA, MOCOMI
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                 NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
                                                       ZIP: 22314
                                                                      CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 87.1%;
Local Similarity 87.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                              ADDRESSEE: McDermott, Will & Emery STREET: 99 Canal Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 77027-9095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEB: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD 60
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                                                                                                                                                                                                                                                             KAYAGAKI, No. 6068841uhiko YAGITA, Hideo
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Pred. No. 5e-44;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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Patent No. 5695755
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                              COMPITER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFYWARE: PatentII Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-518-5100
TELEFAX: 703-684-1124
NAME: Hally Jr., James F.
REGISTRAFION NUMBER: 27,794
REFERENCE DOCKET NUMBER: BI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 05-JUN-19;
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TITLE OF INVENTION: CELLS
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Papayannopoulou, Thalia (USA only)
APPLICANT: Board of Regents, U.
APPLICANT: Machington (except USA)
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/09/065,059
                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                            APPLICATION NUMBER: PCT/
FILING DATE: 11-11-1993
APPLICATION NUMBER: US 0
FILING DATE: 13-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 5035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RPTGSGSGTDFTFTISSVQVEDLAVYPCQQHYSSPYTFGSGTKLE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLE 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c/o FISH & NEAVE
                                                                                                                                                                                                                                             05-JUN-1995
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84.8%;
                                                                                                                                                                                                                                                                   US/08/463,128
                                                                                                                                 US 07/977,702
                                                                                                                                                                            PCT/US93/11060
                  B173CIP
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Pred. No. 1.4e-41;
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US-08-463-298-10
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GENERAL INFORMATION:
                                                                                                                                                                                                                 APPLICATION NUMBER: PCM/US93/11060
FILING DARE: 11-NOV-1993
APPLICATION NUMBER: US 07/977,702
FILING DARE: 13-NOV-1993
ATTORNEY/AGENT IMPORMATION:
NAME: 13-18-19 UT-, 7-794
FEGISTRATION NUMBER: 27.7-794
FEGISTRATION NUMBER: 13-3CIP
TELECHONEU: (212) 598.5-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Papayannopoulou, Thalla
APPLICANT: Board of Regents, U.
APPLICANT: Washington (except USA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PERIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
  y March 91.5%; Score 466; DB 2; Length 128; Local Similarity 90.4%; Pred. No. 1.2e-40; hes 86; Conservative 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 80.4
les 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 IVMTQSPSSLSASVGDRVTITCKASQSVTNDVAWYQQKPGKAPKLLIYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T: 1251 Avenue of the Americas
                                                                                                                              i: 128 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
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Pred. No. 1.2e-40;
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Gaps
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APPLICATION NUMBER: US 08/463,128
APPLICATION NUMBER: DCT/US93/11060
APPLICATION NUMBER: DCT/US93/11060
APPLICATION NUMBER: US 07/977,702
APPLICATION NUMBER: 27,794
ARRESTRANCE/DOCKST NUMBER: BT3CLP
ARRESTRANCE/TOCKST NUMBER: BT3CLP
ARRESTRANCE/TOC
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MEDITM TYPES FLORDY disk
COMPTIEN: IBM FC COMPALIAL
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION INTMER: US/08/436,339A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
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APPLICANT: Papayannopoulou, Thalia (USA only)
APPLICANT: Washington (except USA)
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOISTIC STEM
TITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                              Local
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STATE: New York
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                                                62 FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPTTFGGGTKLEIKR 108
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                                                                                                                                                                                                                                                                                          81.5%; Score 466; DB 2;
80.4%; Pred. No. 1.2e-40;
ative 10, Mismatches 11
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US-08-463-128-6

RESULT 12

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US-08-463-298-6
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US-08-463-128-6
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Best Local Similarity
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                                              NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH
                                                                                                                         APPLICANT: Papayannopoulou, Thalia (USA only)
APPLICANT: Board of Regents, U.
APPLICANT: Washington (Except USA)
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOISTIC STEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
TOPOLOGY: lin-
                                                                                                         TITLE OF INVENTION: PERIPE
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ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B173CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: PCT,
FILING DATE: 11-11-1993
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ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
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APPLICANT: Board of Regents, U.
APPLICANT: Washington (except USA)
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COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                  INFORMATION:
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                          1251 Avenue of the Americas
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Patent No.
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Best Local S
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INFORMATION FOR SEQ ID NO: 6:
                                                        MEDIUM TYPE: Ploppy disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN G-BASE #1.0, Version #1.25
CUERENT APPLICATION DATA:
APPLICATION MOMBER: UC)08/436,339A
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                         REPLICANT: Papayamnopoulou, Thalia (USA only)
APPLICANT: Meahing of Regence (USA)
REPLICANT: Weahing of Regence (USA)
TITLE OF INVESTIGATION OF HEMA
TITLE OF INVESTIGATION OF HEMA
THREE OF ENQUENCES: .

CORRESPONDENCE ADDRESS: .
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LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
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FILING DATE: 11-NOV-1993
APPLICATION NUMBER: US 07/977,702
FILING DATE: 11-NOV-1992
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIC Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Haley Jr., James F9
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B1
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
                   CLASSIFICATION:
                                                                                                                                                                                                            ZIP:
                                                                                                                                                                                                                         STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                    CITY: New York
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                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 DIQLTQSPSSLSASVGDRVTITCKASQSVTNDVAWYQQKPGKAPKLLIYYASNRYTGVPS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85; Conservative
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5843438
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                                                                                                                                                                                                                                                                                    1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                           C/O FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.6%; Score 461; DB 2; 78.7%; Pred. No. 3.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                              PERIPHERALIZATION OF HEMATOPOIETIC STEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT/US93/11060
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US-07-934-373C-5
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COMPUTER READABLE FORM:

WEDLING MYEE: 3.5 inch. 1.44 Mb floppy disk

COMPUTER: ISABORIC FORM:

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APPLICATION MYMBER: US/07/934,373C

FILING DATE: 21-Aug-1992

CLASSIFICATION MYMBER: DC7/US92/05126

FILING DATE: 15-UNR-1992

PRIOR APPLICATION MYMBER: 07/715272

APPLICATION MYMBER: 07/715272

PRIOR APPLICATION MYMBER: 07/715272

PRIOR APPLICATION MYMBER: 07/715272

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PRIOR MYMBER: 05/79

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Patent No. 5821337
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PILING DATE: 05-1WN-1955
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INFORMATION FOR SEQ ID NO: 6:
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acid
                                                           TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Paul J. APPLICANT: Leonard
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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650/952-9881
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Search completed: November 7, 2003, 07:30:08

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Search completed: November 7, 2003, 07:30:08 Job time : 16.8611 secs

# GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

| Run on:           | OM protein -     |
|-------------------|------------------|
| November 7,       | protein search   |
| 7, 2003, 07:21:18 | , using sw model |
| ; Search          |                  |
| time 15.6702      |                  |
| Seconds           |                  |

| Title: US-1<br>Perfect score: 643<br>Sequence: 1 E      |                                                       |
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| US-09-661-992B-84_COFY_1_121 643 1 EVQLVESGGGLVKPGGSLKL | (without alignments) 742.581 Million cell updates/sec |

Searched: Scoring table: 283308 seqs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| 48 490<br>48 890<br>48 890<br>48 890<br>48 890<br>48 990<br>48 900<br>48 900<br>40 900<br>40 900                                                                                                                                                                                                                                                                                                                                                                               |
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| 117<br>119<br>119<br>119<br>118<br>118<br>122<br>108<br>1112<br>112<br>112<br>112<br>113<br>114<br>115<br>117<br>117<br>117<br>117<br>119<br>119<br>119<br>119<br>119                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
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| PL0249<br>C36005<br>A43413<br>PH1010<br>S20641<br>PH1537<br>PH0248<br>PH1007<br>PL0252<br>C34903<br>S26327<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S31107<br>S3 |
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| ######################################                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| heavy chai<br>heavy chai<br>heavy chai<br>heavy chain<br>heavy chain<br>Heavy chai<br>heavy chai<br>heavy chai<br>heavy chai<br>heavy chai<br>heavy chai<br>heavy chai<br>heavy chai<br>heavy chai<br>heavy chai                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| heavy heavy heavy heavy heavy H chai heavy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |

# ALIGNMENTS

| A.P.Kolecut. type: DNA. A.P.Kolecut. type: DNA. A.P.Kolecut. the service of the s | "Accession: A.7. Brownlee, G.G.; Staudt, L.M.; Gerhard, W. R;Catcon, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W. BMEO J. 5, 1577-1587, 1986 BMEO J. 5, 1577-1587, 1986 BA;Title: Structural and functional implications of a restricted antibody respons A;Teference number: A91043; MUID:66301658; PMID:2427335 A;Reference number: A91043; MUID:66301658; PMID:2427335 | RESULT 1<br>127.889 tal. V region (H35-C6) - mouse<br>C:Species Mas muscullus (house mouse)<br>C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996 |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| binds influenza                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ıntibody respons                                                                                                                                                                                                                                                                                                                                                             | l6-Aug-1996                                                                                                                                                                |

ESTOT emline gene loma protein that binds influenza lobulin homology

RESULT 2

27888

Jo heavy chain V region (H158-89H4) - mouse
C.Secrise: MMs musculus thouse mouse)
C.Date: 15-Dec.1988 #sequence\_revision 15-Dec.1988 #text\_change 16-Aug-1996
C.Accession: 27788
R.Caton, A.J., Brownlee, G.G., Staudt, L.M., Gerhard, M.
EMBO J. 5, 1577-1587, 1986
A.Title: Structural and functional implications of a restricted antibody respons
A.Reference number: 27888
A.Reference number: 27888
A.Rocession: 27788
A.Rocession: 27788
A.Rocession: 12788
A.Rocession: 12788
A.Rocession: 119 CCNT>
A.Roperimental source: strain Balb/c
A.Rote: this sequence was determined from the germline gene

influenza

virus

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PH0097 phony chain V region (anti-cyclosporin B) - mouse (fragment)
[3] heavy chain V region (anti-cyclosporin B) - mouse (fragment)
[4] Species! is-an-1991 seguenoe_revision 15-Jan-1993 #text_change 16-Aug-1996
[5] Accession: PH0097
[5] Schmitter, D., Poch, O., Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux,
 BEAC471

Ig heavy chain precursor V region (MAX33) - mouse
C;Species Mus musculus (House mouse)
C;Species Mus musculus (House mouse)
C;Date; 05-Cun-1088 #sequence_revision 05-Jun-1388 #text_charge 23-Jul-1399
C;Accession; B26471, S70410
R;Bulckel, P; hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gense 51, 13-19, 1997
A;Fitle: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from
A;Reference number; A31572; MUID:87248058; PMID:3110009
 Ş
 A;Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin predicted dSTo-
F:10-19/Domain: signal sequence #fathus predicted dSTo-
F:10-19/Domain: signal sequence #fathus predicted dSTo-
F:10-19/Domain: signal sequence #fathus predicted
 A.Tetje: Boundaries of sonatio mutation in rearranged immunoglobulin genes: 5'
A.Reference number: 570410 MVID:91079775; PMID:2259702
A.Recession: 870410
A.Recession: 170410
A.Recession: Label A.Recession: 170410
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 A;Cross-references: GB:M16163; NID:g195405; R;Lebecque, S.G.; Gearhart, P.J. J. Exp. Med. 172, 1717-1727, 1990
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 C;Comment: This chain was isolated from a hybridoma procein that binds C;Superfamily: immunojabulin V region; immunojabulin bomology C;Keywords: heterotetramer; immunojabulin process (C;Keywords: heterotetramer; immunojabulin pr. 15-94)Domakin: immunojabulin bomology c1895
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 A;Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476
C;Genetics:
 F;34-117/Domain: immunoglobulin homology <IMM>
 A; Residues: 1-152 < BUC>
 A; Molecule type: mRNA
 A; Accession: B26471
 Best Loc
Matches
 Query Match
 Matches 105;
 Query Match
 Local Sin
 Local Similarity
 119 VSS 121
 80
 61
 61
 61 PDSVRGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGH--GYGSSFDYWGQGTTLT 118
 20
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 Similarity
 VSS 142
 PDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCARDKAYYGNYGDAMDYWGQGTSVT
 EVQGVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTPEKRLEWVATISDGGSYTYY
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCPR-GETYYDYAMDYWGQGTSVTVS
 PDSVRGRFT1SRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
 DVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSYTYY
 Conservative
 Conservative
 84.68;
 85.0%;
 5
 7;
 Score 542; DB 2;
Pred. No. 3.7e-40;
5; Mismatches 12
 Score 546.5;
Pred. No. 1.
 Mismatches
 PIDN: AAA38292.1;
 1.2e-40
 DB 2;
 12;
 7;
 Length 152
 Indels
 Indels
 Length 119;
 PID:g195406
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RESULT 6
HAZ7889 chain V region (H37-40) - mouse
CJSpecies: Mus muscullus (house mouse)
CJSpecies: Mus muscullus (house mouse)
CJSpecies: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
CJAccession: H27888
R. Caton. A.J.; Excented, 16, 6.G.; Stuut, L.M.; Gerhard, M.
SMBO J. 5, 1577-1897, 1986
A;Feieracne number: A91043 MUID:86300558; PMID:2427335
 RESUIT'S (STAIN V region pa20 - mouse (fragment)
(13 heavy chain V region pa20 - mouse (fragment)
(15 heavy chain V region pa20 - mouse (fragment)
(15 heavy chain V region pa20 - mouse (fragment)
(15 heavy chain V region pa20 - mouse (fragment)
(15 heavy chain V region pa20 - mouse (fragment)
(15 heavy chain V region pa20 - mouse (fragment)
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(15 heavy chain V region pa20 - mouse (fragment)
(15 heavy chain V region pa20 - mouse
 C:Keywords: heterotetramer; ımmunuyıvvu F:14-97/Domain: immunoglobulin homology
 A.Polacule type: mRNA
A.Polacule type: mRNA
A.Posedudes: 1-120 <0052-
A.Cross-xeferences: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
 U. Mol. Biol. 247, 932-946, 1995
A; Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibod
utations in the variable region genes.
 C. Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <INM\s.i.35/Region: complementarity-determining 1 F;31-36/Region: complementarity-determining 2.
 C; Keywords: heterotetramer; immunoglobu
 A; Molecule type: mRNA
A; Residues: 1-118 <SCH>
 Nol. Immunol. 27, 1029-1038, 1990
AyTitle: Analysis of the structural diversity of monoclonal antibodies to cyclos
AyReference number: PH0087, MUID:91042649; PMID:2122240
AyAccession: PH0087
 C; Superfamily: immunoglobulin V region; immunoglobulin homology
 A;Status: preliminary
 A; Accession: S55536
 A, Reference number: S55528; MUID:95239763; PMID:7536850
 F;99-105/Region: complementarity-determining
 Matches
 Query Match
 Matches
 Query Match
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 Local
 116 8 116
 121 $ 121
 61
 104;
 104;
 62 DSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVSS
 61 SDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYSTAS----GDSFDYWGQGTTLTVS
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSPDYWGQGTTLTVS
 N
 heterotetramer; immunoglobulin
 1 DVKLVESGGGLVKPGGSLKLSCAASGFTFSSYIMSWVRQTPEKRLEWVATISSGGRYTYY
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 Similarity
 Similarity
 DSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARLYYDYDPYVMDYWGQGTTVTVSS
 VQLVBSGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYYP
 VQLQESGGGLVKPGGSLKLSCAASGFTFSTYAMSWVRQTPEKRLEWVATISSGGSYTYYP
 Conservative
 Conservative
 86.0%;
 82.6%;
 ω.
 Score 535.5; DB
Pred. No. 1e-39;
 Score 531; DB 2;
Pred. No. 2.6e-39;
 Mismatches
 Mismatches
 <MM>
 immunoglobulin homology
 DB
 13;
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 Length 120;
 Indels
 Indels
 Length 118;
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 Gaps
 121
 61
 60
 115
 120
 60
 60
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antibody respons 16-Aug-1996

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Ig heavy chain V region (H37-45) - mouse
C:Species Mus musculus (House mouse)
C:pace: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
C:Accession: 127887
R:Caton. A.J. Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
BHO J. 5, 1577-1587; 1886
 A:Molecule type: mRNA
A:Residues: 1-118 «SCH»
A:Residues: 1-118 «SCH»
C:Superfeatly: immunoglobulin V region; immunoclobulin C:Reynords heteroretraner; immunoglobulin C:Reynords incorrectraner; immunoglobulin honology cINMY.
Fil5-98/Donain: immunoglobulin honology cINMY.
Fil5-98/Donain: complementarity-decemnining 1
Fil5-66/Region: complementarity-decemnining 2
A; Title: Structural and functional implications of a restricted antibody response
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 R.Schmitter, D.; Poch, O.; Zeder, G.; Hoinrich, G.P.; Kocher, H.P.; Quesniaux, V.F.J.; Wol. Immunol. 27, 1029-1018, 1990
A.Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine. A; Reference number: P80897, WIDD:91042649; PRID:1122240
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 A;Accession: PH0096
 C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996
C;Accession: PH0096
 Ig heavy chain V region (anti-cyclosporin A) - mouse (fragment) C;Species: Mus musculus (house mouse)
 B
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 C;Reywords: heterotetramer; immunoglobulin F;15-98/Domain; immunoglobulin homology <IMM>
 A,Note: this sequence was determined from the germine gene concern that binds influenza virus C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin bomology C;Superfamily: immunoglobulin bomology
 A; Experimental source: strain Balb/c
 A;Accession: H27888
A;Molecule type: DNA
A;Residues: 1-121 <CAT>
 Matches
 Query Match
Best Local
 99-105/Region:
 Matches
 Query Match
 00
 Local Similarity
 Local
 121 $ 121
 116 8 116
 120
 119 VS 120
 13
 61 PDSVRGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 101,
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 61
 102;
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 ,,
 1 EVOLVESGGGLVKEGGSLKLSCAASGFTFSTYTMSWVRQTPEKKLEWVATISSGGSYTYY 60
 Similarity
 PDNMKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTVSTG----TMDYWGQGTSVTVS
 DVKLVESGGGLVKPGGSLKLSCAASRFTFSSYSMSWVRQTPEKRLEWVATISSGGSYTYY
 SUQLVESGGGLVKFGGSLKLSCAASGETFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 PDTVTGRFTISRDNAKNTLYLEMSSLRSEDTAMYYCARBEGY-YGSSDAMDYWGQGTLVT 119
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSS--FDYMGQGTTLT 118
 ÝS 121
 EVOLVESGGGLVQPGGSLNLSCAASGFTFSSYAMSWVRQSPEKRLEWVABISSGGSYTYY 60
 Conservative
 complementarity-determining
 Conservative
 82.3%;
 82.5%;
 10;
 9,
 Score 529.5;
Pred. No. 3.
 Score 530.5; DB 2
Pred. No. 2.9e-39;
 Mismatches
 Mismatches
 immunoglobulin homology
 3.4e-39;
 DB
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 2;
 Indels
 Length 118;
 Indels
 Length
 121;
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Ig heavy chain V region pa24 - mouse (tragment)
ClSpecies: Nus muschlus (bouse mouse)
ClDate: 27-Oct-1955 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
ClAccession: 85639
RiPocttger, V.; Roettger, A.; Lane, E.B.; Spruce, B.A.
J. Nol. Biol. 247, 932-946, 1995
M. Mol. Biol. 247, 932-946, 1995
M.Ficle: Comprehensive spitope analysis of monoclonal anti-proenkephalin antibod:
Utations in the variable region genes.
A; Reference number: 855528; MUID:95239763; PMID:7536850
 Ig heavy chain V region pe21 - mouse (fragment)
Cispecies: Mus numerilus (house mouse)
Cipacie: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-dul-1999
CiAccession: SS537
K; Boetteger, V.; Boetteger, A.; Lane, E.B.; Spruce, B.A.
J. Nol. Biol. 247, 932-946, 1995
A; Mille: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibod utations in the variable region genes.
A; Reference number: SS538, NOID:95339763; PMID:7536850
A; Accession: SS55397
 A;Cross-references: RMBL:X8250; NID:g854306; PIDN:CAA57926.1; PID:g854307
C!$Uperfamily. immunoglobulin V region; immunoglobulin homology
C!$EPMOXd8: heterotetramer; immunoglobulin
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
 SSSS37
 A:Expecimental source: strain Balb/o
A)More: this sequence was determined from the germline gene
C;Comment: This Chain was isolated from a hybridoma protein that binds influenza
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IWM>
 F;14-97/Domain: immunoglobulin homology
 A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: 127887
A;McJecule type: DNA
A;Residues: 1-121 <CAT>
 Best Loc
Matches
 Query Match
 Matches 102;
 Query Match
Best Local Similarity
 Local
 119
 118
 61
 62
 103;
 61
 61
 μ
 Similarity
 DSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTRLYYDYDPYVMDYWGQGTTVTVSS
 VQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYYP
 TVS 121
 PDSVRGRFTISRDNAKNTLYLQMSSLKSBDTAMYYCTRDGG---HGYGSSPDYWGQGTTL 117
 EVQLVESGGGLVKFGGSLKLSCAASGFTFSTYTMSWVRQTFEKTLEWVATISSGGSYTYY
 DSVRGRETISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVSS
 VQLQESGGGLVXPGGSLKLSCAASRFTFSSYAMSWVRQTPEKRLEWVAT18SGGSYTYYP
 TVS 120
 PDSVKGRFTISRDNAKNTLYLOMSRLRSEDTAWYYCAREEGLRLEDY--AMDYWGQGTSV
 EVMLVESGGGLVKPGGSLKLSCAASGFTFSIYAMSWVRQTPEKRLEWVATISSGGTYTYY
 Conservative
 Conservative
 81.5%;
 82.2%;
 7;
 Pred.
 Score 524;
 Score 528.5; DB 2
Pred. No. 4.3e-39;
 Mismatches
 Mismatches
 No. 1e-38;
 <MMI>
 DB 2;
 13;
 2
 9.
 Length 120
 Indels
 Indels
 Length
 121;
 0
 5,
 Gaps
 Gaps
 60
 60
 60
 0,
 2
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A.Note: this sequence was determined from the germaline gene CiComment: This chain was isolated from a hybridenia that binds influenza virus (Superfamily: immunoglobulin v region; immunoglobulin homology Cikeywords: heterocetramer; immunoglobulin homology F.15-98/Domain: immunoglobulin homology F.15-98/Domain: immunoglobulin homology clMM>
 Ig heavy chain V region (H146-2483) , mouse
C.Species: Nu muschilus (house mouse)
C.Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 15-Aug-1996
C.Accession: B27889
 A, Křetetus; preliminary
A, Molecule type; mRNA
A, Reseiduse; 1-120 «DBO»
A, Cross-references; EMBL: X82593; NITD:9854312; PIDN:CAA57929.1; PID:9854313
A, Cross-references; EMBL: X82593; NITD:9854312; PIDN:CAA57929.1; PID:9854313
C. Steperfamily: immunoglobulin V region; immunoglobulin homology
C. Keynords: herotetramer; immunoglobulin homology C. L. Web
 AyTitle: Structural and functional implications of a restricted antibody response A;Reference number: A91043; MVID:06300658; PMID:212335
A;Accession: G27888
A;Molecular type: DNA
A;Residuss: 1-123 <CNP's
A;Residuss: 1-123 <CNP's
A;Residuss: 1-123 <CNP's
A;Residuss: 1-123 <CNP's
 R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, EMBO J. 5, 1577-1587, 1986
 Ig heavy chain V region (H28-A2) - mouse
C.Specte: Num nursollus (house mouse)
C.Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C.Dacession: G27888
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 A; Residues: 1-119 < CAT>
 A; Molecule type: DNA
 A/Title: Structural and functional implications of a restricted antibody response A;Reference number: A91043; MUID:86300658; PMID:2427335 A;Accession: B72889
 R,Caton, A.J
EMBO J. 5, 1
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 A, Experimental source: strain Balb/c
 RESULT 11
 A;Note: this sequence was
 Query Match
Best Local :
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 119
 118
 .J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, 1577-1587, 1986
 102;
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 61
 61
 23
 62
 N
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPBKRLEWVATISSGGSYTYY
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 VS 120
 PDSVKGRFTISRDNAKNNLYLOMSSLKSEDTAMYYCARDRVRRDGY---FDVWGRGTTVT
 DSVKGRETMSRDNAKNTLYLQMSSLRSEDTAMYYCVRLYYDYDEYVMDYMGQGTTVTVSS 120
 DSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVSS 121
 VQLQESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKKLEWVATIGSSGSYTYXP
 VQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYYP 61
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRD--GGHGYGSSFDYWGQGTTLT 118
 EVQLVESGGGLVKPGGSLKLSCAASGITFSDYIYYWVRQTPEKRLEWVATISDGGSYTYY
 Conservative
 Conservative
 80.2%;
 80.6%;
 determined
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 5
 Score 515.5; DB 2;
Pred. No. 5.7e-38;
 Score 518; DB 2; Length 120
Pred. No. 3.5e-38;
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CyComment: This chain was isolated from a hybridoma protein that CySuperfamily: immunoglobulin V region; immunoglobulin bancing cyReywords: heterotetramer; immunoglobulin CyReywords: heterotetramer; immunoglobulin protein immunoglobulin protein immunoglobulin protein immunoglobulin bancing protein immunoglobulin bancing protein immunoglobulin bancing protein protein immunoglobulin bancing protein protei
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118 TVS 120
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 PDTVTGRFTISRDNAKNTLYLEMSSLGSEDTAMYYCARGERDPQYGKAYVMDYWGRGTSV
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCT---RDGGHGYGSSFDYWGQGTTL
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 EVOLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 Conservative
 79.7%; Score 512.5;
79.7%; Pred. No. 1.1
 10,
 Pred. No. 1.1e-37
 Mismatches
 DB 2;
 Indels
 Length 123;
 ω.
 Gaps
 117
 120
 60
 60
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121

TVS 123

Ig heavy chain V region (17/9) - mouse CiSpecies: Mus musculiu (house mouse) CiDate: 31-Mar-1990 #equence\_revision 31-Mar-1990 #text\_change 23-May-1997 CiAccession: B31700 RiSchilze-Galman, U., Rini, J.M., Aravalo, J.; Stura, E.A.; Kenten, J.H.; Wilson

A;Accession: B31790 A;Molecule type: mRNA A;Residues: 1-254 <SCI Biol. Chem. 263, 17100-17105, 1988
 Affitle: Preliminary crystallographic data, primary sequence, and binding data A;Reference number: A92686; MUID:89034213; PMID:3182835

C;Superfamily: immunoglobulin C region; immunoglobulin C;Keywords: heteroretramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM> 1-254 <SCH>

homology

Matches Query Match POCGT 186 Similarity Conservative 79.2%; Score 509.5; DB 2 81.0%; Pred. No. 4.2e-37; Mismatches 2, Indels Length 254; ۲,

μ

EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY

Gaps

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121 S 121 6 13 ٠, PDSVRGRFTISRDNAKWTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS EVQLVESGGDLVKPGGSLKLSCAASGESESSYGMSWVRQTPDKRLEWVATISNGGGYTYY PDSVKGRFTISRDNAKNTLYLQMSSLKSEDSAMYYCARRERYD-ENGFAYWGQGTLVTVS 120 60 119

RESULT 14

120 A 120

anti-peptide Fabr B1312 heavy chain - mouse C.Spectes: Mus musculus (house mouse) C.Date: 22-Unn-1990 #sequence\_revision 22-Unn-1990 #text\_change 23-Unl-1999 C.Dacession: 83433

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Ighosys Chain V region (anti-cyclosporin G) - mouse (fragment)

[Ighasyy Chain V region (anti-cyclosporin G) - mouse (fragment)

[Species Mas musculus (house mouse)

[C.Datcs i.L.-dan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996

[C.Accession: PH0096

[C.Accession: PH0097

[R.Schmitter, D., Poch, O.; Zeder, G., Heinrich, G.F.; Kocher, H.P.; Queeniaux, V.P.J.; V. Mol. Immunol. 27, 1039-1038, 1990

[R.Schmitter, D., Poch, O.; Zeder, G., Heinrich, G.F.; Kocher, H.P.; Queeniaux, V.P.J.; V. Mol. Immunol. 27, 1039-1038, 1990

[R.Jocession: PH0097

[R.Jocession: PH0097

[R.Jocession: H0097

[R.Jocession: H0098]

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 116 TVSS 119
 118 TVSS 121
 61 POSVIGRETISERUNKNYTLYLÖNSSIKSEDTANYYCTEDGOHGYGGSETYWGGTTLTVB 120
61 PDSVKGRFTISEDNAKYTLYLÖNSSLOSEDTNYYTCTIPSNWG----VDYWGGTTLTVB 116
 61 PDSVRGRFTISRONAGYTLI,GNSSI,KSBDYAMYCYRDGGHGVSS---EDYRGGTTI 117
61 PDTVKGRFIISRONAGNTLI,GNSSI,KSBDYAMYCYRDGGHGVSS---EDYRGGTTI 115
61 PDTVKGRFIISRONAGNTLI,GLGMSSI,RSBDYAITYCYR-----YSSDPFYEDYRGGGTTI 115
 101;
 1 DVKHMESGGGLVKPGGSLKLSCAASGFTFSYYTMSWVRQTPEKRLEWVATISTGDGSTYY 60
 1 EVQLVESGGGLVKEGGSLKLSCAASGFTFSTYIMSWVRQTPEKRLEWVATISSGGSYTYY 60
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 EVQLVESGGDLVKPGGSLKLSCAASGFTFSRCAMSWVRQTPEKRLEWVAGISSGGSYTFY 60
 79.0%; Score 508; DB 2; Length 119; ilarity 81.5%; Pred. No. 2.5e-37; Conservative 6; Mismatches 9; Indels
 4;
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 Gaps
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 7, 2003, 07:21:18; Search time 8.72563 Seconds tithout alignments) 652.278 Million cell updates/sec

Run on:

Title: Perfect score: Sequence: US-09-661-992B-84\_COPY\_1\_121
1 EVQLVESGGGLVKÞGGSLKL......HGYGSSFDYWGQGTTLTVSS 121

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 127863 segs, 47026705 residues 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 33                 | υω         | 30                 | 29         | 28          | 27                 | 26         | 25         | 24                 | 23         | 22                 | 21         | 20                 | 19         | 18         | 17         | 16                 | 15         | 14         | 13         | 12         | 11         | 10         | 9          | 00         | 7          | σ,         | υ          | 4.         | ω          | 2          | ,                  | No.         | Result |
|--------------------|------------|--------------------|------------|-------------|--------------------|------------|------------|--------------------|------------|--------------------|------------|--------------------|------------|------------|------------|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--------------------|-------------|--------|
| 391                | 392        | 391.5              | 392        | 393         | 393.5              | 395        | 397        | 398                | 398        | 400                | 400.5      | 401.5              | 402        | 402.5      | 405.5      | 407                | 407.5      | 410.5      | 414        | 415.5      | 424        | 430        | 430.5      | 437        | 441.5      | 457.5      | 461        | 461        | 462.5      | 466        | 476                | Score       |        |
| 60.8               | 60.8       |                    | 61.0       | 61.1        | 61.2               | 61.4       | 61.7       | 61.9               | 61.9       | 62.2               | 62.3       | 62.4               | 62.5       | 62.6       | 63.1       | 63.3               | 63.4       | 63.8       | 64.4       | 64.6       | 65.9       | 66.9       | 67.0       | 68.0       | 68.7       | 71.2       | 71.7       | 71.7       | 71.9       | 72.5       | 74.0               |             | Query  |
| 123                | 113        | 119                | 115        | 119         | 116                | 117        | 123        | 117                | 115        | 144                | 114        | 119                | 115        | 122        | 122        | 117                | 111        | 116        | 118        | 119        | 121        | 117        | 122        | 117        | 126        | 97         | 117        | 117        | 136        | 117        | 98                 | Length 1    |        |
| ** *               | . د        | ,                  | <b>,</b>   | ,,,         | ۳                  | ۳,         | H          | مبو                | μ          | ,,                 | -          | ۳                  | <b>,</b> , | ۳          | ۳          | ۳,                 | <b></b>    | ۳          | ۲          | بر         | <b>,</b>   | ۳,         | ₩          | H          | ы          | H          | ₩          | ۳          | ۳          | ۳          | μ.                 | BB          |        |
| HV24_MOUSE         | HV27 MOUSE | HV40_MOUSE         | HV3D_HUMAN | HV3 I_HUMAN | HV05_CARAU         | HV41_MOUSE | HV25_MOUSE | HV02_CANFA         | HV32_MOUSE | HV26_MOUSE         | HV3B_HUMAN | HV37_MOUSE         | HV3F_HUMAN | HV3H_HUMAN | HV3A HUMAN | HV3C HUMAN         | HV35_MOUSE | HV3T_HUMAN | HV39_MOUSE | HV38_MOUSE | HV3J_HUMAN | HV53_MOUSE | HV3G HUMAN | HV59 MOUSE | HV3K HUMAN | HV56 MOUSE | HV58_MOUSE | HV54_MOUSE | HV16_MOUSE | HV55_MOUSE | HV57_MOUSE         | ID          |        |
| P01793 mus musculu | Bum        | P01810 mus musculu |            | -           | P19181 carassius a | Bum        |            | P01785 canis famil | ٠.         | P01795 mus musculu | -          | P01807 mus musculu | homo       | homo       | homo       | P01764 homo sapien |            | homo       | aus        | _          | home       | -          | home       | mus 1      | homo       | Bru        | Brum       | Bru        | Bru        | Bum        | P18528 mus musculu | Description |        |

60 60

01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
If heavy chain V region 345 precursor.

| 4 4<br>5 4   | 42                                       | 410        | 39                       | 37         | 35         | 34         |
|--------------|------------------------------------------|------------|--------------------------|------------|------------|------------|
| 384          | 385<br>384.5                             | 385<br>385 | 387.5                    | 388        | 390        | 390        |
| 59.7         | 59.9<br>59.8                             | 59.9       | 60.3                     | 60.3       | 60.7       | 60.7       |
| 119          | 123<br>122                               | 113<br>123 | 119<br>122               | 113        | 120        | 115        |
| <b>11</b> 11 | <b>,,</b> ,                              |            |                          |            | ب .        | ,_         |
| HV3L_HUMAN   | HV23_MOUSE                               | HV19 MOUSE | HV3M_HUMAN<br>HV20_MOUSE | HV31_MOUSE | HV3E HUMAN | HV33_MOUSE |
| home         | P01792 mus musculu<br>P01790 mus musculu | mus<br>mus | mus                      | mus<br>mus | hom        | mus        |

### ALIGNMENTS

| A D O D WHHAD                                                                        | 0 44200000000000000                                                                                                                                                                    | *******                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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|                                                                                      | T B C C C C C C C C C C C C C C C C C C                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 1 POYLEGGALANCOCKIAGOS PRETY 117 AA.  1 POSTRORFITSHDMANNILYIQUESIASBITANTYCTE 98  1 | encine S.G., Gearhart P.J.; en in immunoglobulin VH genes g) EBELONES TO THE WIT183 SUBFR UNOGLOBULIN-like domain. G-LIKE. G-LIKE. B8644F7F92F8F95B CRC64; R64, N6., 1.2e-40; T-7-1-1. | SULY 1  1852  HV57, MOUSE  FV57, MOUSE  1852  10.1 NOV-1990 (Rel. 16, Created)  10.1 NOV-1990 (Rel. 16, Last sequence update  15.5 SEP-2003 (Rel. 42, Last sequence update  15.5 SEP-2003 (Rel. 42) Last amountion update  16. Mouse of the sequence update  17. Mouse of the sequence update  18. Mouse of the sequence update  19. Mouse of the sequence |
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collaboration -

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RESULT 3
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 InterPro; IPR007110; IS
InterPro; IPR00306; IS
InterPro; IPR00396; IS
InterPro; IPR00396; IS
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
 HV16_MOUSE
P01783;
21-JUL-1986
21-JUL-1986
15-SEP-2003
 SEQUENCE FROM N.A.
MEDLINE-81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
 21-JUL-1986 (Rel. Ol. Last sequence update)
21-JUL-1986 (Rel. Ol. Last sequence update)
13-SEP-2003 (Rel. 42 Last amnotation update)
IG beavy chain V region MOPC 21 precursor (Fr
 DISULFID
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SEQUENCE
 Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
 MED;(NE=77100368, PubMed=401950;
Adetugbo K., Milstein C., Secher D.S.;
Molecular analysis of spontaneous som
Nature 255:299-304(1977);
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 DOMAIN
 DOMA.IN
 PROSITE; PS50835; IG LIKI Immunoglobulin V region;
 PIR; JT0502; HVMS34.
HSSP; P01810; 2FBJ.
 J. Exp. Med. 169:2007-2019(1989)
 MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque
"Early onset of somatic mutation in
 SEQUENCE OF 17-136.
 Cell 24:625-637(1981).
 antibodies:
 "Heavy chain variable region
 Baltimore D.;
 NCBI_TaxID=10090,
 DOMAIN
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 -!- MISCELLANEOUS: THIS SEQUENCE BELONGS
 SEQUENCE FROM N.A.
 NCBI TaxID=10090;
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 Similarity
 PDSVRGRETISRDNAKNTLYLQMSSLKSEDTAMYYCTR 98
 EVOLVESGGGLVKPGGSLKLSCAASGPAFSSYDMSWVRQTPBKRLEWVAYISSGGGSTYY 79
 117
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 somatic mutation
 Conservative
 4 6 6 5 5 5 6 9 5
 ĀΑ;
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 IG LIKE; 1
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 Rodentia;
 Chordata;
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 Ig_MHC.
 Chordata;
 72.5%;
 12902 MW;
 Signal
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 IG HEAVY CHAIN V REGION 345.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
 contribution to the NPb family evident in a gamma 2a variable
 Score 466;
Pred. No. 1
 Reth M., Imanishi-Kari T., Rajewsky
 FRAMEWORK-3
BY SIMILARI
 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
 Sciurognathi; Muridae; Murinae; Mus
 Craniata; Vertebrata; Euteleostomi;
 PRT;
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 the Buropean Highiformatics Institute. There are no restrictions use by non-posit institutions as long as its content is in modified and this statement is not removed. Usage by and for on antities requires a license agreement (See http://www.isb-sib.ch/ar antities requires a license agreement. (See http://www.isb-sib.ch/ar
PIR; JT0505; HVMS84.
HSSP; P01810; 2FBJ.
IntexPro; IPR007110; Ig_Nike
IntexPro; IPR003006; Ig_MHC.
 CHAIN
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 the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
-i- MISCELLANBOUS: THIS SEQUENCE
 MEDLINE=89279149; PubMed=2499654;
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
 Mus musculus (Mouse)
 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 PIR; E90809; G1MS21.
 EMBL; J00522; AAD15290.1; -.
 "Early onset of somatic mutation
 Levy N.S., Malipiero U.V.,
 STRAIN=BALB/CJ
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Ig heavy chain V region 5-84 precursor
 PROSITE;
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 121
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 ADTVKGRETISRDNPKNTLFLQNTSLRSEDTAMYYCARWGNYPY-YAMYDWGQGTSVTVS
 PDSVRGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
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 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 PS50835; IG LIKE;
 IPR007110;
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W -> H (IN REF. 2).
Y -> W (IN REF. 2).
 Score 462.5;
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 Query Match
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Ffam; Pe00047; 15; 1.
SNART; SM00406; IGV; 1.
PROSITB, P850835; IG LIKE; 1.
PROSITB, P850835; IG LIKE; 1.
 InterPro; IPR007110; Ig-like.
InterPro; IPR007506; Ig_MC.
InterPro; IPR003506; Ig_v.
Pfam; PF00047; ig; I.
SMART; SM00406; IGv; 1.
 "Early onset of somatic mutation the primary immune response."; J. Exp. Med. 169:2007-2019(1989)
 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Lat sequence update)
15-UUL-1999 (Rel. 38, Last amotation update)
1g heavy Chain V region 5-76 precursor.
1g heavy Chain V region 5-76 precursor.
Buharyota, Merasor; Chordata; Craniata; Vertebrata; Eutelsostomi;
Buharyota, Merasor; Chordata; Craniata; Vertebrata; Eutelsostomi;
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 PIR; JT0506; HVMS57.
HSSP; P01810; 2FBJ.
 STRAINSEALB/UJ PubMed=2499654;
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Levy N.S., Maliplero U.V., Lebecque
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 !- MISCELLANEOUS: THIS SEQUENCE
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 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 Similarity
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTR
 EVXLVESGGGLVQPGGSLKLSCAASGFTESSYTMSWVRQTPEKRLEWVAYISNGGGSTYY
 PDTVKGRFTISRDNAKNNLYLOMSSLKSEDTAMYYCAR
 1
20
20
50
55
69
86
41
117
 117
 Conservative
 Conservative
 1
20
20
50
55
69
69
86
41
117
 Ä
 Ā,
 STANDARD;
 49
54
68
85
117
 49
54
68
85
117
 71.7%;
 12991
 71.7%;
 12872 MW;
 MW;
 IG HEAVY CHAIN V REGION 5-76.
PRANSWORK. 1.
COMPLENSWIFARITY-DETERMINING-1.
FRAMSWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMSWORK-3.
BY SIMILARITY.
BY SIMILARITY.
 6
Score 461; DB
Pred. No. 4.3e
3; Mismatches
 Score 461;
Pred. No.
 IG HEAVY CHAIN V REGION 5-84.
FRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
 FRAMEWORK-3
BY SIMILARI
 PRT;
 93A04782B78B8FA0
 234055CB6A469861
 Mismatches
 SIMILARITY
 BELONGS
 S.G., Gearhart immunoglobulin
 117
 . 4.3e-39;
5;
 DB 1;
1.3e-39;
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 SHT
 Length 117;
 117
 VH7183 SUBFAMILY
 86
 CRC64;
 Length 117;
 CRC64;
 Indels
 Indels
 P.J.;
VH ge
 Murinae;
 genes
0;
 during
 0,
Gaps
 Gaps
 79
0
 0
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SAFE E SOOO SEE
 RESULT 7
HV3K_HUMAN
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 RESULT 6
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 Matches
 Query Match
Best Local
 HYAK HUMAN STANDARD, PRT, 126
PA1772;
21-UUL-1986 [Rel OI] Lett sequence upda
15-SEP-2003 [Rel 142 Let sequence upda
164 homo sepiens (Human)
 NON TER
SEQUENCE
SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=83289131; PubMed=6884994;
 NCBI_TaxID=9606;
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
 the primary immune response.";

J. Exp. Med. 189:2007-2019(1999).

1- MISCELLANBOUS: THIS SEQUENCE BELONGS TO THIS

1- SIMILARTY. Contains 1 immunoglobulin-like
PIR, J70504; HYMS91.
 MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecq
"Early onset of somatic mutation
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V region 914.
 HV56_MOUSE
P18527;
 MOUSE
 DOMAIN
 Mus musculus (Mouse)
 SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
 HSSP; P01810; 2FBJ
 STRAIN=BALB/CJ;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 60
 61
 80
 61
 20
 μ.
 ,..
 88;
 Similarity 89.1
88; Conservative
 PDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCAR
 PDSVRGRETISRDNAKNTLYLQMSSLKSEDTAMYYCTR
 EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASISSGGS-TYY
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 PDSVRGRFTISRDNAKUTLYLQMSSLKSEDTAMYYCTR 98
 EVHLVESGGGUVKPGGSLKLSCVVSGFTFNKYAMSWVRQTPEKRLEWVATISSGGLYTYY
 EVQLVESGGGLVKPGGSLKLSCAASGPTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 97 AA;
 97
 STANDARD;
 10661 MW;
 Primates;
 Chordata;
 71.2%;
 Lebecque
station in
 6,
 Score 457.5; DB 1; Length Pred. No. 7.8e-39; 6; Mismatches 3; Indels
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 IG-LIKE
 C23CB33FF55DA893 CRC64;
 PRT;
 update)
on update)
 S.G., Gearhart
immunoglobulin
 126
 97
 Å
 ₿
 THE VH7183
 97
 98
 domain
 P.J.;
VH genes during
 SUBFAMILY
 97;
 1;
 Gaps
 59
 60
 79
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S
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 Matches
 Query Match
 STRAND
NON_TER
SEQUENCE
 TURN
 STRAND
HELIX
STRAND
 DOMAIN
MOD_RES
DISULFID
 HELIX
STRAND
 TURN
 STRAND
HELIX
 TURN
 GO) GO:1008575; Cicetracellular; MAS.
GO; GO:1008525; F:amtigen binding activity; MAS.
GO; GO:1008525; F:amtigen tresponse; MAS.
InterPro; IPRO:1006; Ig.MEC.
InterPro; IPRO:1007; Ig.1.
SMART; SMO:106; IGV, I.
SMART; SMO:106; IGV, I.
SMART; SMO:106; IGV, I.
SMART; PRO:003; IG.I.I.
SMART; PRO:003; IG.I.I.
SMART; PRO:003; IG.I.I.
SMART; PRO:0047; Ig.I.
SMART; PRO:0047; Ig.I.
SMART; SMO:106; IG.I.I.
SMART; SMO:106; IG.I.
SMART; SMART; SMART; IG.I.
SMART; SMART; SMART; IG.I.
SMART; SMART; S
 "Cypetallographic refinement and atomic models of the intact immunoglobulin molecule kol and its antigen-binding fragment and atomic models of the intact immunoglobulin molecule kol and its antigen-binding fragment and a
 STRAND
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 STRAND
 PIR; A02055; G1HUKL.
PDB; 2FB4; 12-JUL-89
 J. Mol.
 Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; "Three-dimensional structure determination of antibodies. Prin structure of crystallized monoclonal immunogloukin 1961 KOL, Roppe-Sayler's Z. Physiol. Chem. 364:713-747(1983).
 STRAND
 DISULFID
 MEDLINE=81072295; PubMed=7441755;

 -!- SIMILARITY: Contains 1 immunoglobulin-like domain

 K-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 Local
 116
121
 21G2; 12-JUL-89
 61
 61
 Н
 84;
 Similarity
 Biol. 141:369-391(1980).
PVTVSS
 TLTVSS 121
 ADSVKGRFTISRDNSKNTLFLQMDSLRPEDTGVYFCARDGGHGFCSSASCFGPDYWGQGT
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSF-----DYWGQGT 115
 EVOLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 Conservative
126
 68.7%;
 13718 MW;
 16;
 Score 441.5;
Pred. No. 4.1e
16; Mismatches
 IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID
 E4D71B52B16F8776 CRC64;
 4.16-37;
 DB 1;
 21;
 Indels
 Length
 126;
 Primary
KOL, I.";
 5
 at 3.0 A
 Gaps
 60
 60
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HYS MOUSE
HYS MOUSE
TO THIS MOUSE
AC PLESSO,
TO 1. NOV.1990
TO 2.
 HV3G
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 S
 RESULT
 Matches
 Query Match
Best Local
 P18530;
01-NOV-1990
MEDILIME-81013859, PubMed=6714332;
Lehman D. W., Putnam F. W.
**Panino acid sequence of the variable region of a location of a possible JH segment. **/
Proc. Natl. Acad. Sci. U.S.A. 77:323-3243(1980)
 NON_TER
 NCBI_TaxID=9606;
 Bukaryota; Metazoa;
Mammalia; Eutheria;
 Homo sapiens (Human).
 21-JUL-1986
15-SEP-2003
 21-JUL-1986
 HV3G HUMAN
P01768;
 SEQUENCE
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
 PIR; JT0507; HVMS39.
 -1- MISCELLANEOUS: THIS SEQUENCE
 J. Exp. Med. 169:2007-2019(1989)
 the primary immune response."
 MEDLINE=89279149; PubMed=2499654;
 01-NOV-1990 (Rel. 16, La
15-JUL-1999 (Rel. 38, La
Ig heavy chain V region
Mus musculus (Mouse)
 HSSP; P01810; 2FBJ
 "Early onset of somatic mutation in
 STRAIN-BALB/CJ
 SEQUENCE FROM N.A.
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Eukaryota; Metazoa;
 SEQUENCE
 InterPro; IPR003006;
InterPro; IPR003596;
 InterPro; IPR007110;
 levy N.S., Malipiero U.V.,
 CBI_TaxID=10090;
 mmunoglobulin V region; Signal
 -JUL-1986 (Rel. 01, Created)
-JUL-1986 (Rel. 01, Last sequence update)
-SEE-2003 (Rel. 42, Last annotation update)
heavy chain V-III region CAM.
 80
 13
 20
 83;
 Similarity
 PDSVKGRFTISRDNAKNNLYLQMNSLTSEDTALYYCAR 117
 PDSVRGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCTR
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLFWVATISSGGSYTYY
 EVKWVESGGGSVKPGGSLKLSCEASGFTFSNYGMSWVRQTPEKRLEWVASISGGVSYTYY
 117
117 AA;
 Conservative
 46655020
 STANDARD;
 STANDARD

 Last sequence update
 Last annotation update

 49
68
68
117
115
 Chordata;
Primates;
 Ig_NHC.
 12972
 Chordata;
 84.7%;
 68.0%;
 Created)
 7-39 precursor.
 M.
 μ
 IG HEAVY CHAIN V REGION 7-39.

PRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.

PRAMEMORK-2.
COMPLEMENTARITY-DETERMINING-2.

PRAMEWORK-3.
 5
 Score 437; DB 1;
Pred. No. 1.1e-36;
 Craniata, Vertebrata; Euteleostomi, Catarrhini; Hominidae; Homo.
 Craniata; Vertebrata; Euteleostomi;
 PRT;
 PRT;
 DSCA4167D0F1774F CRC64;
 Mismatches
 BELONGS
 S.G., Gearhart
immunoglobulin
 122
 117
 update)
 A
 S
 À
 THE VH7183 SUBFAMILY
 10,
 a
 98
 Length
 human
 Indels
 P.J.;
VH genes during
 mu chain:
 0
 60
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RESULT 10
HV53_MOUSE
1D HV53_MOUSE
AC P18524,
AC P18524
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 Matches
 Query Match
Best Local :
 PIR, J70503 HWASER
HSEP, PORED, ZEBJ
INTERPRO, IFROOTHO, ISL, MR.
INTERPRO, IFROOTHO, ISL, MR.
INTERPRO, IFROOLSOS, ISL, MR.
INTERPRO, IFROOLSOS, ISL, MR.
PEAM, PEROOLY, ISL, 1.
PROSUTE, PSOSOSS, IG LIKE, 1.
IMMILTOSION, ISL, 1.
INTERPROSUMER, ISL, 1.
INTERPROSUMER, ISL, 1.
INTERPROSUMER, ISL, 1.
INTERPROSUMER, INTERPROSUMER, ISL, 1.
INTERPROSUMER,
 the primary immune response.";
J. Exp. Med. 169:2007-2019(1989)
-i- MISCELLANBOUS: THIS SEQUENCE
 NON TER
 inicerPro; PR007110; 19-11ke.
InicerPro; PR003106; 1g MrC.
InicerPro; PR003596; 1g WrC.
Pfam; PF00047; 149; 1
Pf0047; 1800406; 1Gv; 1.
Pf0047172; P$03035; 1d LIKE; 1.
Pf0047172; P$03035; 1d LIKE; 1.
Immunojobulin V region; Pyrrolidone carboxylic acid.
D00418
 MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque
"Early onset of somatic mutation in
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 Mus musculus (Mouse)
 Ol-NOV-1990 (Rel. 16, Created)
Ol-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last amnotation update)
Ig heavy chain V region RF precursor.
 SEQUENCE
 SEQUENCE FROM N.A.
 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
 -i- MISCELLANBOUS: THIS NU CHAIN WAS ISOLATED FROM THE PATIENT WITH MACROGLOBULINEWIA.

-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
FIR: A02051, MCHUM.
 NCBI_TaxID=10090;
 HSSP; P01772; 2FB4.
 120
 13
 61
 Similarity
 SS
 ABSVKGRFTISRDBSKBTLYLQMNSLKABBTAVYYCARDRPLXGBYRAFNYMGQGTLVTV 120
 SS
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGG-HGYGSSFDYWGQGTTLTV 119
 QVELVESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY
 EVQLVESGGGLVKFGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 122
122 AA;
 122
 121
 Conservative
 55001
55001
 STANDARD;
 132
13668 MW; A42D0F17D252F1C2 CRC64;
 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sclurognathi; Muridae; Murinae; Mus
 66.4%;
 SEQUENCE
 19,
IG HEAVY CHAIN V REGION RF. FRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
COMPLEMENTARITY-DETERMINING-2.
 Pred. No. 4.
 PYRROLIDONE CARBOXYLIC ACID
 PRT;
 Mismatches
 BELONGS
 Signal
 S.G., Gearhart immunoglobulin
 117
 4.9e-36;
 ö
 B
 DB 1; Length 122;
 H
 VH7183 SUBFAMILY
 Indels
 P.J.;
VH genes during
 PLASMA
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 Mus
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 Gaps
 60
 60
 RESULT 11

RESULT 12

RESULT 14

RESULT 15

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Query Match
Best Local &
Matches 80
 Query Match
Best Local S
Matches 83
 DOMAIN
DISULFID
NON TER
SEQUENCE
 MOD RES
 DOMAIN
 FIR, A02054; GHNUL.
HSSP, POLY72, Zewiracellular; NAS.
OG; GO:0003827; Cewiracellular; NAS.
OG; GO:0003827; Fantigen binding scrivity;
OG; GO:0003827; Fantigen binding scrivity;
OG; GO:0003807; Fantigen binding scrivity;
OG; GO:0003807; Fantigen binding scrivity;
Incerbo: 150003806; 161-M6C.
Incerbo: 150003806; 161-M6C.
Incerbo: 150003806; 161-M6C.
 MEDILINE-9124695; PubWed4409600;
Chiu Y.-Y.H., Oppez de Coatro J.A., Poljak R.J.,
"Makino acid sequence of the VH region of human myeloma
cryoimmunoglobuln 1gG HH.",
Blochemiatry 18:553-560(1979).
-- MIGGELLANGUS: THIS CHAIN WAS ISOLATED FROM AN IGG
 Nomo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 HUMAN
HV3J_HUMAN
 -1- SIMILARITY: Contains 1 immunoglobulin-like domain
 21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region HIL.
 SEQUENCE
 PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Pyrr
 SMART, SM00406, IGv, 1
 Pfam; PF00047; ig; 1.
 SEQUENCE
 NCBI_TaxID=9606;
 21-JUL-1986
 P01771;
121 S
 121
 61
 61
 80
 61
 20 DVKLVESGGGLVKLGGSLKLSCAASGFTFSSYYMSWVRQTPEKRLELVAAINSNGGSTYY
 80,
 83 /
 Similarity
 Similarity
 $ 121
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTR 98
 EVQ1/VESGGGLVK/PGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 GDSVKGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARDPDILTAFSFDYWGQGVLVTVS
 PDSVRGRETISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSEDYWGQGTTLTVS
 QVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYY
 PDTVKGRFTISRDNAKNTLYLQMSSLKSEDTALYYCAR 117
121
 86
41
117
117
 121
121 AA;
 Conservative
 Conservative
 B
 STANDARD;
 2
 13566 MW;
 65.9%;
 12866 MW;
 66.9%;
84.7%;
 Created
 Pyrrolidone carboxylic acid
 16;
 7;
 Score 424; DB 1;
Pred. No. 2.1e-35;
6; Mismatches 25
 Score 430;
Pred. No. 5.
 PYRROLIDONE CARBOXYLIC ACID
 FRAMEWORK-3.
BY SIMILARITY.
 IG-LIKE
 480FC53610EF5DAB CRC64;
 PRT;
 2CE3295F390F725B CRC64;
 Mismatches
 ISOLATED FROM AN IGG1
 121
 DB 1;
5.2e-36;
 B
 NAS
 Length 121;
 Length 117;
 Indels
 Indels
 MYBLOM
 0;
 0,
 Gaps
 Gaps
 120
 60
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RESULT 12
HV38 MOUSES
TD HV38 MOSS
PO1868
PO
 Query Match
Best Local S
Matches 81
 HSSP; PO1810; 2FBJ.
InterPro; IPR003006; InterPro; IPR003006; InterPro; IPR003006; InterPro; IPR003596; InterPro; IPR003596; InterPro; IPR003596; InterPro; IPR003596; InterPro; IPR003596; I
 p00800, 21.JUL-1986 (Rel. 01, Created)
21.JUL-1986 (Rel. 01, Last sequence update)
21.SEP-2003 (Rel. 42, Last amountation update)
19 heavy chain v region X24.
Mus musculaus (Mouse).
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene in
immunoglobulin heavy chains from anti-galacten myeloma proteins and
 MOUSE
 PROSITE: PS50835, IG LIKE; 1.
Immunoglobulin V region.
DOMAIN 1 112
NON TER 119 119
SEQUENCE 119 AA; 13169 MW;
 complementarity-determining regions,";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).
-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA
 21.-ULI-1986 (Rel. Ol. Last sequence update)
15-5EP-2003 (Rel. 42) Last annotation update)
15-5EP-2003 (Rel. 42) Last annotation update)
129 heavy chain V region T601.
Mus musculus (Movuse).
Mus musculus (Movuse).
Musmalla, Entherais Rodentia; Scurognath; Murides; Murinee; Mus
Musmalla, Entherais Rodentia; Scurognath; Murides; Murinee; Mus
 HV38 MOUSE
 SEQUENCE.
MEDLINE=79223895; PubMed=111245;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 HV39_MOUSE
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
 THAT BINDS GALACTAN.
-!- SIMILARITY: Contains 1 immunoglobulin-like
 Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene
immunoglobulin heavy chains from anti-galactan myeloma pa
its potential role in generating diversity in
 NCBI_TaxID=10090;
 MEDLINE=79223895; PubMed=111245;
 NCBI_TaxID=10090;
 21-JUL-1986
 118 S
 121 $ 121
 61
 61
 _
 Similarity
 TPSLKDKFIISRDNAKWTLYLOMSKVRSEDTALYYCARLGYYGY---FDVWGAGTTVTVS
 PDSVRGRFTISRDNAKVTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYMKSWVRQAPGKGLEWIGBINPDSSTINY
 118
 Conservative
 (Rel. 01, Created)
 STANDARD;
 STANDARD;
 64.6%;
 ig-like.
ig_MHC.
ig_v.
 Score 415.5;
Pred. No. 1.5e
l3; Mismatches
 IG-LIKE
 PRT;
 BC38CC84E6EA00E8 CRC64;
 118
 119
 .5e-34;
 B
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 DB 1;
 24;
 domain
 Indels
 Length 119;
 MYELOMA PROTEIN
 proteins
 3
 Gaps
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 120
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 STINGER
 RESULT 14
 Query Match
Best Local S
Matches 82
PRI AN2664 MEMOGL.

HSSP, PO17712, ZPBA.

OO, GO.10005576; Creatracellular; NAS.
OO, GO.10005576; Primmune response; NAS.
InterPro; INGOVILO; 91_Alke.
InterPro; INGOVILO; 91_Alke.
InterPro; INGOVISO6; 19_MC.

SMART; SMO4066; 10c; 1.

SMART; SMO4066; 10c; 1.
 MSSE; POISIÓ, 2FB1.
InterPro. IPBRO77110, Ig-like.
InterPro. IPBRO77110, Ig-like.
InterPro. IPBRO77106, Ig_wc.
InterPro. IPBR077106, Ig_v.
PEam; PF00047; ig_ 1.
SWART; SW00465; IG_JIXE; 1.
IMMITTGG1000111, V region.
DOMAIN 1 111
IG
 NEWDH
 its potential role in generating diversity in complementarity-determining regions; "194(1979). Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979). 1970. INTEGELLANDOUS; THIS CHAIN MAS IGOLATED FROM AN IGHTHAT BINDS GALACTAN.
 Submitted (JUN-1975) to
 Hilschmann N.;
 when we so, parnikol H.U., Horn J., Bertram J., Hilechmann N.; when primary seructure of a monocional 194-immunoglobulin (milechia) properties and a equation of the H-chain (milechia) J. Hiles and a equation of the H-chain (milechia) and a service complete 194-molecule.
 MEDLINE=75059123;
Watanabe S., Barni
 21-UU-1986 (Rel. O1, Created)
21-UU-1986 (Rel. O1, Last sequence update)
15-88P-2003 (Rel. 42, Last annotation update)
15 heavy Chain V-III region GAL.
Homo sepiens (Human)
 -!- SIMILARITY: Contains 1 immunoglobulin-like
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 HV3T HUMAN
 PIR; PT0394; AVMSX2.
 SEQUENCE
 NCBI_TaxID=9606;
 SEQÜENCE
 NON_TER
 EVISION TO 28-33.
 117
 121
 60
 61
 ,
 Similarity
 s
 တ
 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLGYYGY---FDYWGQGTTLTVS
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
 EVKLLESGGGLVQPGGSL-LSCAASGPDFSRYWMSWARQAPGKGQEWIGEINPGSSTINY
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSMVRQTPEKRLEWVATISSGGSYTYY
 117
 121
 118 AA;
 Conservative
 9123; PubMed=4803843;
Barnikol H.U., Horn J.,
 STANDARD;
 13105 MW;
 64.4%;
 the PIR data
MU CHAIN WAS
 12;
 Score 414;
Pred. No. 2
 IG-LIKE
 BB16A2DB677EF17F CRC64;
 ed. No. 2.1e-3:
Mismatches
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 116
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 DB 1;
 FROM A WALDENSTROM'S
 Length 118;
 AN IGA MYELOMA PROTEIN
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 4.
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Search completed: November 7, 2003, 07:28:08 Job time: 9.72363 secs

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经基础证明
 Query Match
Best Local Similarity
Matches 78; Conserv
 Query Match
Best Local Similarity
Matches 82; Conserv
 Hasir, Pol109, 1MCP.
InterPro; IPRO0710; Ig-11ke.
InterPro; IPRO03106; Ig-MSC.
InterPro; IPRO03506; Ig-MSC.
InterPro; IPRO03506; Ig-V.
Fiam; PP00047; Ig-1.
SMART; SMO046; IGV-J.
SMART; SMO046; IGV-J.
MNBURG; LOULIN V Region.
 DOMAIN
NON TER
SEQUENCE
 MyOUSE STANDARD, PRT, 111 AA.
PO1854; MOUSE STANDARD, PRT, 111 AA.
21-UUL-996 (Rel. 01, Created)
21-UUL-996 (Rel. 01, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
15-SBP-2003 (Rel. 42)
15-SBP-2003 (Rel. 42)
15-SBP-2003 (Rel. 43)
15-SBP-2003 (Rel. 43)
15-SBP-2003 (Rel. 43)
15-SBP-2003 (Rel. 44)
15-SBP-2003
 MEDILNE-gloil907; phbMcde55147;

Bernard O., Googh N.M.;

Muclectide sequence of immunoglobulin heavy chain joining segments between translocated W1 and mu constant regions genes.";

Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).

Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).

1-1 MICCELLANDOUS: THE SOURCE OF THE FIRST 19 TRESIDUES OF THE CRESION WAS ALSO DETERMINED & DIFFERS IN OULY 3 POSITIONS FROM THE CRESION WAS ALSO DETERMINED & DIFFERS IN OULY 3 POSITIONS FROM THE -1- SINLARITY: CONTAINS PROM THE MUSIS MOPE CLUST MU CHAIN.

1-1 SINLARITY: CONTAINS 1 Immunoglobulin-like domain.

FIR; A02074; MEMS76.
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Immunoglobulin V region.
DOMAIN 1 112
NON TER 116 116
SEQUENCE 116 AA; 12730
 NON TER
 NCBI_TaxID=10090;
 PROSITE; PS50835; IG_LIKE; 1.
 SEQUENCE FROM N.A.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 116 T 116
 121 S 121
 61
 65 RGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVSS 121
 61 VDSVKGRFTISRDNAKNSLYLQMMSLRVEDTALYXCARGWGGG-----DYWGQGTLVTVS 115
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 1 EVOLVESGODLVOPGRSLRLSCAASGFBFBBLGMTWVRQAPGKGLEWVANIKZBGSZZBY 60
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
KGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTRPGVP-----DYWGQGTTLTVSS 111
 ESGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVAEIRLKSGYATHYAESV 60
 ESGGGLVKPGGSLKLSCAASGFTFSTYTWSWVRQTPEKRLEWVATISSGGSY-TYYYPDSV 64
 111 AA; 12304 MW; 0EDE98EC7348056A CRC64;
 1 112 10-1165.
116 116
116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;
 63.4%; Score 407.5; DB 1; Length 111; ilarity 66.7%; Pred. No. 8.5e-34; Conservative 17; Mismatches 15; Indels 7
 Conservative
 63.8%; Score 410.5; DB 1; Length 116; 67.8%; Pred. No. 4.5e-34; Live 10; Mismatches 24; Indels 5
 IG-LIKE.
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Result
No.
 Database
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 Total number of hits satisfying chosen parameters:
 Scoring table:
 Sequence:
 Title:
Perfect score:
 Run on:
 OM protein -
 Fred. No. is the number of results predicted by chance to have a soore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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437.46.5
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1: sp_archea:*
2: sp_bacteria
 643
 November 7, 2003, 07:21:18; Search time 39.9025 Seconds [18] Search time 39.9025 Seconds 782.516 Willion cell updates/sec
 830525 segs, 258052604 residues
 BLOSUM62
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84.0
75.9
73.9
73.4
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71.9
70.3
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69.8
69.8
69.8
67.3
 Gapop 10.0 , Gapext 0.5
 1 EVQLVESGGGLVKPGGSLKL......HGYGSSFDYWGQGTTLTVSS 121
 US-09-661-992B-84_COPY_1_121
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
 sp_archea:*
sp_bacteria:*
sp_fungi:*
 sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 sp_organelle:*
sp_phage:*
 sp_mhc:*
 sp_mammal:*
 sp_invertebrate.*
 sp_human:*
 sp_plant:*
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Q91XE1
Q8TC77
Q8TC77
Q96K68
Q9UL93
Q96BB9
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Q9UL71
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Q920E7
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Q91WP5
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O91281 mus musculi
O91281 mus musculi
O96ka7 homo sapien
O90139 homo sapien
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O9139 homo sapien
O9139 homo sapien
O9139 homo sapien
 Description
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# ALIGNMENTS

| 유왕                                                               | M B Q                                                                                                                                                                              | A COCCOSS DE COCCOSS D | RESULT<br>Q99KA4 |
|------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------|
| 1 EVOLVESGGGLVKEGGSLKLSCAASGFTESTYNGSWINGCTERKILENYTISGGSYTTY 60 | Very Match  97.5%; Score 553.5; DB 11; Length 487;  Best Local Similarity 87.5%; Ered, No. 10-47; 8; Indels 3; Gaps 2  Matches 109; Conservative 4; Mismatches 8; Indels 3; Gaps 2 | 099KA; PRELIMINARY; PRT; 487 AA.  099KA; PRELIMINARY; PRT; 487 AA.  099KA; Created; 01-UN-2001 (TERBLIFEL 1.7), Last sequence update) 01-UN-2001 (TERBLIFEL 1.3), Last annotation update) 10-MAR-2003 (TERBLIFEL 1.3), Last annotation update) Mysolimetical S.c. Map sprotein.  10-MAR-2003 (TERBLIFEL 1.3), Last annotation update) Mysolimetical S.c. Map sprotein.  10-MAR-2003 (TERBLIFEL 1.3), Last annotation update) Mammalia, Enthreais Rodentia, Sciurognathi, Muridae, Musinae; Mus.  101-MAR-2003 (TERBLIFEL 1.3), Marianae, Musinae; Mus.  101-MAR-2003 (TERBLIFEL 1.3), MARIA (TERBLIFEL 1.3), MARIA (MAR-2003), To the EMBL/GenBank/DDBJ databases.  101-MAR-2003 (TERBLIFEL 1.3), MARIA (MAR-2003), MARA | 7J.T 1<br>CA4    |

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61 PDSVRGRETISRDNAKUTLYLQMSSLKSEDTAMYYCTRD-GGHGYG--SSFDYWGQGTTL 117

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 Query Match
Best Local S
Matches 104
 Submitted (SEP-2000) to the EME

EMBL, AF20737; ALMOSYL1.1; -

INTESPPO; IFR007101; IG-11ke.

INTESPPO; IFR003006; IG-MC.

INTESPPO; IFR003065; IG-MC.

INTESPPO; IFR003585; IG-MC.

SEARN; FR0047; IG-MC.

PROSTITE MSSGGG; IG-MCB; I.
 091207 PRELIMINARY, PRT; 486 AA.
091207.001 (TREMELICAL 19. Created)
01-DEC-2001 (TREMELICAL 19. Last sequence update)
01-DEC-2001 (TREMELICAL 29. Last annotation update)
01-MAR-2003 (TREMELICAL 29. Last annotation update)
Hypothetical 27. PKD protein.
Bytanyota, Mesanosilus (Mouse), Chordeta, Craniata, Vertebrata; E
Butanyota, Mesanosa, Kodentia, Sciunognathi; Moridae;
Strausberg R.;
Submitted (UIL-2001) to the EMBL/GenBank/DDBJ
EMBL, BC010224, AMH10324.1; -.
IncerPro; IPR007110; Ig-11ke.
InterPro; IPR003306; Ig_MRC.
InterPro; IPR003596; Ig_v.
 0920E7 PRELIMINAY PRT, 119 AA.
0920E7 PRT, 119 AA.
0920E7.201 (TrEMELrel. 19. Created)
01-DEC-2001 (TrEMELrel. 19. Last sequence update)
01-DEC-2003 (TrEMELrel. 23. Last ammodation update)
01-DEC-2003 (TrEMELrel. 23. Last ammodation update)
presin-mimickelmy anti-idiotoppe heavy Ondain variable
 Atkin J.D., Tape A., Jennings 1 "Definition of the Idiotope of in Mammalian Cells.";
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 SEQUENCE
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 Mus musculus (Mouse)
 (Fragment)
 121
 104;
 119 A 119
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 Similarity
 S 121
 PDSVRGRETISRDNAKUTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 TVSS
 PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCARHGDYDVG--FAYWGQGTLVTVS
 EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
 SSAL
 119
119 AA,
 Conservative
 143
 121
 84.0%;
 13025 MW;
 to the EMBL/GenBank/DDBJ databases
 6,
 Score 540; DB 1:
Pred. No. 4e-46;
6; Mismatches
 I.G., Horaitis O.,
E Pterin-Mimicking
 Craniata; Vertebrata;
Sciurognathi; Muridae;
 F6E904044381CA7C CRC64;
 DB 11;
 databases
 9
 Antibodies Expr
 Length 119;
 Indels
 ; Murinae; Mus
 Euteleostomi;
; Murinae; Mus.
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 Strumberg R.;

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ dat

BMBL; BC013666, AMB13656.1;

InterPro; IPR007110; Ig_like.

InterPro; IPR003196; Ig_MC.

R InterPro; IPR003196; Ig_MC.

R Pfam; PP00447; 3g; 4.

R Pfam; PP0144; 3g; 4.

R
 Matches
 Query Match
Best Local Similarity
Q91Z05;
 01-DEC-2001 (TYEMBLIE). 19, Created)
01-DEC-2001 (TYEMBLIE). 19, Last sequence update)
01-MER-2003 (TYEMBLIE). 23, Last annotation update)
Hypothesical 51.6 kDa protein.
 TISSUE=Colon;
 SEQUENCE FROM N.A.
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
 Mus musculus (Mouse).
 SAMT60
 PROSITE; PS50835; IG LIKE; 4. PROSITE; PS00290; IG MHC; 2. Hypothetical protein. SEQUENCE 486 AA; 52682 MW;
 Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
 NCBI_TaxID=10090;
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 134
 118
 121 8 121
 139
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 PDSVRGRFTISRDWAKWTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 TVSS
 SDIMKGRFTISRDNAKSTLYLQMSSLRSEDTAFYYCVR------GGYFDVWGAGTAVTVS
 EVQLVESGGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSPEKRLEWVAAINSNGGNTYY
 TVSS 121
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGY---GSSFDYWGQGTTL
 BVHLVBSGGGLVKPGGSLKLSCVVSGFSFTSYDMSWVRQTPERRLEWVAAITSGGN-TYY
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 PDNVKGRFTVSRDNAKYTLYLQMSSLKSEDTAMYYCVRPEIPIYYYSGSYFDSWGQGTTI
 73.7%;
ilarity 75.2%;
Conservative
 PRELIMINARY,
 Conservative
 PRELIMINARY;
 52682 MW; 4FEF835125DA870B CRC64;
 75.9%;
 10;
 9
 Score 488; DB
Pred. No. 3.2e
10; Mismatches
 Score 474; DB 11;
Pred. No. 7.8e-39;
9; Mismatches 15
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
 PRT,
 ECB2D0877748584F CRC64;
 473
 479
 DB 11;
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 DB 11;
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 14;
 Length 479;
 Length 486;
 Indels
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 Query Match
Best Local S
Matches 91
 Query Match
 01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
Hypothetical 51.9 kDa pro
 Strausberg R.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ
BMBL, BC010927, AMH10327 1;
MCD, MCI 2144657, AUMA491;
InterPro; IPR000345; CytC heme_bind.
InterPro; IPR000306; Ig_MCC.
InterPro; IPR000306; Ig_MCC.
InterPro; IPR003966; Ig_W.
InterPro; IPR003966; Ig_W.
 PROSITE;
 Strausberg R.,
Submitted (ULL-2001) to the EMBL/GenBank/DDBJ databases
BMBL, BC010798; AMH0798.1.1 -
IntexPro; IREOUTO10; 15-1lke.
IntexPro; IREOUTO06; 14_MEC.
INTEXPRO(128019366; 14_MEC.
INTEXPRO(128019366; 14_MEC.
SMART, SMOMAGE, 14_MEC.
SMART, SMOMAGE, 14_MEC.
SMART, SMOMAGE, 14_MEC.
 091XEI PRELIMINARY, PRT; 480 AA.
091XEI.0 (TrEMBLICAL 19 Created)
01-DEC-2001 (TREMBLICAL 19 Last sequence update)
01-DEC-2003 (TREMBLICAL 19 Last sequence update)
01-DEC-2003 (TREMBLICAL 19 Last ammoration (protein for INAGE:4224494) (Fragment).
Mus musculus (Mouse).
 PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 473 AA; 51946 MM; CF6
 Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 Mus muscullus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinæ; Mus
 FISSUE=Colon;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Pfam; PF00047; ig; 3. SMART; SM00406; IGv;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 121
 137 S
 80 ADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCARE---LWLRRIDYWGQGTTITVS
 61
 20
 н
 91,
 Similarity
 PS50835; IG_LIKE; 4.
PS00290; IG_MHC; 2.
 S 121
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 EVQLVESGGGLVKPGGSRKLSCAASGFTFSDYGMHWVRQAPEKGLEWVAYINSGSTTIYY
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 137
 480 AA;
 72.4%; Score 465.5; ilarity 75.2%; Pred. No. 5.4 Conservative 10; Mismatches
 kDa protein.
 51936 MW;
 72.2%;

 Created)
 Last sequence update)
 Last annotation update)

 Score 464;
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
 2089234EEF2B41ED CRC64;
 CF625F008932AF12 CRC64;
 ed. No. 5.46
Mismatches
 5.4e-38
 DB 11;
 DB 11; Length 473;
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Length 480;
 Indels
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 A Stramberg R.;

I Submitted (FBE 2002) to the EMBL/GenBank/DDBJ databases.

BMBL; BC022299, AMB4489.;;

R InterPro, IPR00710: 1g-like.

R InterPro, IPR007306; Ig-MiC.

R InterPro, IPR003506; Ig-MiC.

R InterPro, IPR003506; Ig-MiC.

R InterPro, IPR003506; Ig-MiC.

R Pfam, PF00047; 184.

R SMART; SM00465; IGV.

R SMART; SM00465; IGV.

R SMART; SM00465; IGV.

SB00ENCE: 471.AA; 51791 MM; 38897F4CF588660E CRC64;
 Query Match
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Matches 91; Conserv
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 01-DBC-2001 (TrEMELTe1. 19, Created)
01-DBC-2001 (TrEMELTe1. 19, Last sequence update)
01-MBC-2001 (TrEMELTe1. 23, Last amnotation update)
Ryporthetical potenin FUJ14473.
Bakaryota, Metason, Chordata, Craniata, Vertebrata, Mammala, Butherfa; Primetes, Gatarrhini; Hominidae
 Q96K68;
01-DEC-2001
 NCBI_TaxID=9606;
 Q96K68
 TISSUE=Spleen;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 æ
 Local Similarity
 117
 135
 121
 137 VIVSS
 80
 61 PDSVRGRETISRDNAKNTLYLQMSSLKSEDTAMYYCTRD----GGHGYGSSFDYWGQGTT 116
 20
 79
 5
 19
 1 BVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTFEKRLEWVATISSGGSYTYY
 99;
 1 BYQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 Ø
 S 121
 LTVSS 121
 ADSVXGRFTISRDNAKNSLYLQNNSLRAEDTAVYYCARDLRQLTSYNY--
 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMMVRQAPGKGLEWVSSMSSSSYIYY
 DVKLVESGGGLVKPGGSLRLSCAASGFIFSNSYMSWARQTPEKRLEWVATISNSGYATHY
 Conservative
 Conservative
 PRELIMINARY;
 141
 71.9%;
71.2%;
 75.2%;
 16; Mismatches
 13;
 Last sequence update)
Last annotation update)
 Created)
 Pred.
 Pred. No. 7.8e
3; Mismatches
 Score
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 PRT;
 No. 1.1
 No. 7.8e-38;
smatches 13;
 471
 494 AA
 1.1e-37
 8
 DB 4;
 13,
 Indels
 Length
 Indels
 471;
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 FDLWGRGTL
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 Query Match
Best Local S
Matches 89
 TidSUE-Mammary gland;
Isogai T. Otea T. Hayashi K., Sugiyama T., Oteaki T., Suzuki Y.,
Isogai T., Otea T., Hayashi K., Sugiyama T., Oteaki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shirattori A., Sudo H., Sugawara M.,
Hagatsuma M., Hesoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
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Watanabe S., Memura K., Murakami K., Ishii S., Kawai Y., Saito K.,
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Nisomario K., Takahasi T., Nakamura Y., Nagahari K., Mashbo Y.,
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Nisomario K., Nakanasi M., Nakamura Y., Nagahari K., Mashbo Y.,
Nisomario K., Nakanasi M., Nakamura Y., Nagahari K., Mashbo Y.,
Nisomario K., Nakanasi M., Nakamura Y., Nagahari K., Mashbo Y.,
Nisomario K., Nakanasi M., Nakanasi Y., Nakanasi M., Nakanasi M
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 01-MAY-2000 (TYEMBERE]. 13, Created)
01-MAY-2000 (TYEMBERE]. 13, Last sequence update)
01-MAY-2000 (TYEMBERE]. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
 Q9UL93;
01-MAY-2000
 Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
 "MEDD himman cDMN sequencing project.";
Submitted (MNY-2001) to the EMEL/GenBank/DDBJ databases.
SMBL; ANC27379; BABS5072.1;
- Interpro; 196001710; 1g-like.
Interpro; 196003006; 1g_MEC.
Interpro; 196003006; 1g_MEC.
Interpro; 196003006; 1g_MEC.
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50635; IG LIKE; 1.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 EMBL; AF035021; AAD56257.1; -. HSSP; P01772; 2FB4.
 fetus."
 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney Young D.C.;
 MEDLINE=98277139; PubMed=9614934;
 NCBI_TaxID=9606;
 Homo sapiens (Human)
 Q9UL93
 Hypothetical protein.
SEQUENCE 494 AA; 5
 [1]
SEQUENCE FROM N.A.
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 SEQUENCE FROM N.A.
 (Fragment).
 138
 118 TVSS 121
 Immunol. Immunopathol. 87:184-192(1998)
 80 RDSVKGRFTISRDNAKNSLYLQMNSLRVDDTAVYYCARDSCNGAICYG--FSPWGQGTLV
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHG---YGSSFDYMGQGTTL
 20 EVQLVESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWVSSISSRSDYIYY
 ,_
 89,
 Similarity
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSMVRQTPEKRLEMVATISSGGSYTYY
 TVSS 141
 116
116 AA,
 PRELIMINARY;
 Conservative
 Chordata;
 53088 MW;
 12434 MW;
 70.7%;
 ; Score 454.5; DB 4
; Pred. No. 7.1e-37;
13; Mismatches 17
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 9A1D7AEB5AEE4C0E CRC64;
 PRT;
 0DA0348154DD6061 CRC64;
 116 AA
 DB 4;
 17;
 Length 494;
 Indels
 region
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 Gaps
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RESULT 10
Q96BB9
ID Q96BB
 RESULT 11
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ID Q8WUI
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 Query Match
Best Local Similarity
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 Query Match
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 Pfam; PF00047; 19; 5.
SMART; SMO0406; IGV; 1.
PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; 3.
Hypothetical pxotein.
SEQUENCE 597 AA; 65039 MM;
 Strausberg R.;
Submitted (CCT-2001) to the BWBL/GenBank/DDBJ databases.
BWBL; BC015760, AAH15760.1; .
InterFro; IFR007101; Ig-11ke.
InterFro; IFR003106; Ig-18EC.
InterFro; IFR00356; Ig-v.
 Q96BB9
 Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
 01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Hypothetical protein. Homo sapiens (Human).
 01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
 NCBI_TaxID=9606;
 DSWUK1;
 Q8WUK1
 SEQUENCE FROM N.A.
 TISSUE=B-cell;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 139
 116
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 62
 ,..
 1 EVOLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEMVATISSGGSYTYY
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 Similarity
 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA
 VQLVBSQGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPBKRLEWVATISSGGSYTYYP
 ADSVXGRFTISRDNSRDTLXLQMNSLRAEDTAVYYCAKD-PRGYSASGNYTREDYWGQGT
 DSVRGRETISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVSS
 LVTVSS 144
 TLTVSS 121
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSS-----FDYWGQGT
 BVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYY
 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYCAGGGGLGLG---
 Conservative
 Conservative
 PRELIMINARY;
 PRELIMINARY;
 65039 MW;
 70.3%;
 70.3%;
68.3%;
 18;
 10;
 Created)
Last sequence update)
Last annotation updat
 Created)
Last sequence up
 Score 452;
Pred. No. 2
 Score 452; DB 4;
Pred. No. 1.6e-36;
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 PRT;
 4FCA3AD8ECE263D9 CRC64;
 Mismatches
 Mismatches
 613
 597
 DB 4;
2.2e-37;
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 DB 4; Length 597
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 16;
 Length 116
 Indels
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 -YWGQGTLVTVSS
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 4;
 Gaps
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 61
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 121
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TISSUE=Tonsil

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RESULT 12
Q9UL90
ID Q9UL9
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 IntesPro; IPB007110; Ig-11ke.
IntesPro; IPB003006; Ig_WC.
IntesPro; IPB003506; Ig_W.
Pfam; PF00471; Ig, S.
PF4m; PF00471; Ig, S.
PF004371E; ES50835; IG_URG; S.
PROSSITE; ES50835; IG_URG; S.
PROSSITE; ES50835; IG_URG; S.
 Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 1.
 Clin.
 SEQUENCE FROM N.A. MEDLINE=98277139; Pubmed=9614934;
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
 Q9UL90;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
 InterPro;
 InterPro; IPR007110;
 EMBL; AF035024; AAI
HSSP; P01772; 2FB4.
 fetus."
 Young D.
 (Fragment).
Homo sapiens (Human)
 Q9UL90
 InterPro; IPR003006;
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 Hypothetical protein.
SEQUENCE 613 AA; 6
 Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC020240; AAH20240.1; -
 Strausberg
 139 S
 121 8 121
 61
 Immunol. Immunopathol. 87:184-192(1998) AF035024; AADS6260.1; -.
 85;
 80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDWSEGV-ETFDIWGQGTMVTVS
 13
 20
 Liu B., Van
 ; 38
 Similarity
 Similarity
PDSVRGRETISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
 EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFTRYDGSNKYY
 EVQLVESGGGLVKPGGSLK1SCAASGFTFSTYTMSWVRQTPEKRLEWYATISSGGSYTYY
 PDSVRGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 IPR003006; Ig_MHC.
IPR003596; Ig_v.
 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
 113 AA;
 Conservative
 PRELIMINARY;
 Conservative
 113
 der Merwe P.L.,
 12437 MW; ED57FDD19086D07F CRC64;
 67296 MW;
 68.7%;
 69.8%;
 Ig-like.
 13;
 14;
 Created)
 Score 442;
Pred. No. ;
 Score 448.5; DB 4
Pred. No. 3.6e-36;
4; Mismatches 20
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 60C7F5950671E315 CRC64;
 Mismatches
 Kalis N.N., Berney S.M.,
 113
 2, DB 4,
2.1e-36;
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 DB 4; Length 613;
 15;
 Length 113,
 Indels
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RESULT 14
Q9UL91
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Q9Y509
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 Query Match
Best Local S
Matches 85
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
 Q9UL91
Q9UL91;
01-MAY-2000
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
USE_TaxID=9606;
 01-MAY-2000 (TREMBLrel. 13, Created)
01-MAY-2000 (TREMBLrel. 13, Last sequence update)
01-MAY-2000 (TREMBLrel. 13, Last sequence update)
01-MAR-2003 (TREMBLrel. 23, Last snnotation update)
Myosin-reactive immunoglobulin heavy chain variable region
 Q9Y509;
 Pfam; PF00047; ig; i. "
SMART; SM00406; IGV; I. TE
PROSITE; PS50835; IG_LIKE; 1.
NON TER
1 1 15768 MM;
 MEDLINE=96071149; PubMed=7475288; Cao J., Vescio R.A., Rettig M.B., Lichtenstein A.K., Berenson J.R.,
 Homo sapiens (Human).
 EMBL; $80860; AAD14339.1; -. HSSP; P01772; 2FB4.
 "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with pastient-specific immunoglobulin gene primers.", Leukemia 9:1948-1953 (1995).
 Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 01-NOV-1999
 (Fragment)
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 InterPro;
 NCBI_TaxID=9606;
 Homo sapiens
 VH3 protein
 01-MAR-2003
 01-NOV-1999
 SEQUENCE FROM N.A.
 13
 121
 116 TLTVSS 121
 113 S 113
 121 S
 61
 61
 5
 1 EVQLVESGGGLVKPGGSLKLSCAASGETESTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 85
 Similarity
 SSALAT
 AGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYYCAKDGNYFDSVGYYYAGIDYWGQGT
 PDSVRGRFTISRDNAKNTLYLQMS9LKSEDTAMYYCTRDGGH-----GYGSSFDYWGQGT
 QVHLVESGGGVVQPGKSLRLSCEASGFTFSTYGMSWVRQAPGKGLDWVALISYDGSTQYY
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD-----LNYWGQGTLVTVS 112
 147 AA; 15768 MW;
 (TrEMBLrel.
 Conservative
 PRELIMINARY;
 (Fragment).
 (TrEMBLrel.
 (Human)
 68 4%;
67 5%;
 12,
12,
23,
 14;
 Created)
Last sequence update)
Last annotation update)
 Score 439.5;
Pred. No. 5e-
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 PRT;
 8489FCAAA7BC925C CRC64;
 Mismatches
 Hong C.H., Kim A.,
 Kalis N.N.,
 118 AA
 147
 DB 4;
 22;
 Berney S.M.
 Length 147;
 Indels
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 Gaps
 115
 60
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Fri Nov 7 09:40:21 2003

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RESULT 15
Q9R1A4
 Query Match
Best Local Similarity
Matches 85; Conserva
 Query Match 67.3%;
Best Local Similarity 72.5%;
Matches 87; Conservative
 NON TER
NON TER
SEQUENCE
 SOURNCE FROM N. D. Ekzemoddoullab A.K.M., Misre S., wilde K.G. Y. N. J. Ekzemoddoullab A.K.M., Misre S., wilde K.G. Y. N. J. Ekzemoddoullab n. entropine blister rust monoclonal "Cloning of cDNNs smoothly for and heavy chains) and construction of a antibody (Mab 7, its light and heavy chains) and construction of a
 Q9R1A4;
 NON TER
 Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 23, Last senotation update)
03-WMR-2003 (TREMBLRel. 23, Last samotation update)
Gammal heavy chain of Mab7 (Fragment).
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
 SEQUENCE
 EMBL; AF152372; AAD40243.1; -. HSSP; P01842; 7FAB. MGD; MGI:95446; Igh-4.
 antibody (Mab 7, its light and heavy chains) and construsingle chain antibody (scPV).";
Simplited (MAY-1999) to the EMBL/GenBank/DDBJ databases
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Clin. Immunol. Immunopathol. 87:184-192(1998). EMBL; AF035023; AAD56259.1; -. HSSP; P01772; 2FB4.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 NCBI_TaxID=10090
 Mus musculus (Mouse).
 IGH-4
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
 tetus."
63 DSVRGRFTISRDNAKUTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVSS 121
 61 PISVICARFTISRDMAKNITYLOWSSLKSEDTAMYYCTREGGHGYGSSEDYMOGGTTLITVS 120
61 ADSVICARFTISRDMAKNISLYLOWNSLRAEDTAVYYCARGDS---SEAFDIMOGGTMVTVS 117
 2 VQLVESGGGLVKPGGSLKLSCAASGFTFSTYIMSWVRQTPEKRLEWVATISSGGSYTYYP 61
 VQLQESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASFSSGG-IIYYT 59
 437 AA;
 118 AA;
 118
 437
 1larity 70.8%; Score 437.5; DB 4; Length 118; 1larity 70.8%; Pred. No. 6.1e-36; Conservative 14; Mismatches 18; Indels 3
 PRELIMINARY;
 118
 437
 48142 MW; SC3A7BB3EE7D697C CRC64;
 12843 MW; D0633949F2AC149D CRC64;
 Score 432.5; DB 11; Length
Pred. No. 9.4e-35;
8; Mismatches 18; Indels
 437
 3
 DB 11; Length 437;
 7;
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 Gaps
 Gaps
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Search completed: November 7, 2003, 07:34:35
 문
 60 DSVKGRFTIYKDKDRNILSLQMSSLRSEDTAMYYCAR-----GDYSAYWGPGTLVTVSA 113
```

Job time : 41.0025 secs

```
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
```

| OM protein - pr                               | OM protein - protein search, using sw model                                                                    |
|-----------------------------------------------|----------------------------------------------------------------------------------------------------------------|
| Run on:                                       | November 7, 2003, 07:21:17 , Search time 52.1802 Seconds (without alignments) 36:.089 Million cell updates/sec |
| Title: US-Perfect score: 643<br>Sequence: 1 E | US-09-661-992B-84_COFY_1_121 643 1 BYQLVBSQGGLVKPGGSLKL                                                        |
| scoring table: BLOSIMGS                       | RI OSIMS)                                                                                                      |

Great

Minimum DB seq length: 0
Maximum DB seq length: 200000000 Total number of hits satisfying chosen parameters:

1107863 seqs, 158726573 residues Gapop 10.0 , Gapext 0.5

1107863

Database Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

| 22:                                  | 21:             | 20:             | 19;             | 18:            | 17:             | 16:             | 15:                          | 14:                     | 13:             | 12;                    | 11:              | 10:                            | 9:              | 80                   | 7:                     | 9                     | 'n                 | 4.             | 3:             | <i>ا</i> د     | <u>ب</u>       | A               |  |
|--------------------------------------|-----------------|-----------------|-----------------|----------------|-----------------|-----------------|------------------------------|-------------------------|-----------------|------------------------|------------------|--------------------------------|-----------------|----------------------|------------------------|-----------------------|--------------------|----------------|----------------|----------------|----------------|-----------------|--|
| /SIDSI/gcgdat                        | .<              | /SIDS1/gcgdata, | /SIDS1/gcgdata, | /SIDS1/gcgdata | /SIDS1/gcgdata, | /SIDS1/gcgdata, | 3                            | /SIDS1/gcgdat.          | /SIDS1/gcgdat   | /SIDS1/gcgdata         |                  | /SIDS1/gcgdat.                 | /SIDS1/gcgdata, | /SIDS1/gcgdata,      | /SIDS1/gcgdata         | /SIDS1/gcgdata        | /SIDS1/gcgdata     | /SIDS1/gcgdata | /SIDS1/gcgdata | /SIDS1/gcgdata | /SIDS1/gcgdata | Geneseq 19Jun03 |  |
| a/geneseq/                           | cgdata/geneseq/ | /geneseq        | /geneseq        | /geneseq       | /geneseq        | a/geneseq/      | a/geneseq/                   | cgdata/geneseq/geneseqp | cgdata/geneseq/ | a/geneseq/             | gcgdata/geneseq/ | a/geneseg/                     | /geneseq/       | /geneseq/            | /geneseq/g             | /geneseq/g            | /geneseq/geneseqp- |                | /geneseq/g     | /geneseq/g     | /geneseq/g     | *               |  |
| gcgdata/geneseq/geneseqp-emb1/AA2001 | /geneseqp-embl. | jeneseqp-embl   | /geneseqp-embl  | /geneseqp-embl | /genesegp-embl  | /geneseqp-embl  | cgdata/geneseq/geneseqp-embl | geneseqp-embl           | geneseqp-embl   | /geneseq/geneseqp-embl | /geneseqp-embl   | gcgdata/geneseq/geneseqp-embl, | eneseqp-emi     | geneseqp-embl/AA1987 | /geneseq/geneseqp-embl | geneseq/geneseqp-embl | eneseqp-embl       | geneseqp-embl, | geneseqp-embl, | geneseqp-em    | geneseqp-embl  |                 |  |
| D1/AA2001                            | b1/AA2000       | nb1/AA1999      | mb1/AA1998      | mb1/AA1997.    | mb1/AA1996      | `               | nb1/AA1994.                  | mb1/AA1993              | /AA1992         | /AA1991                | /AA1990          | nb1/AA1989.                    |                 | /AA1987              | 01/AA1986.I            | 01/AA1985.E           | 01/AA1984.I        | ol/AA1983.I    | 01/AA1982.I    | emb1/AA1981.I  | 01/AA1980.I    |                 |  |
| DAT: *                               | DAT: *          | .DAT:*          | DAT: *          | DAT: *         | DAT *           | DAT: *          | DAT: *                       | DAT: *                  | .DAT:*          | .DAT:*                 | DAT: *           | DAT                            | DAT: *          | DAT: *               | DAT: *                 | AT: *                 | AT:*               | AT: *          | AT: *          | AT:*           | YAT:*          |                 |  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

23:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

| 9070                                                     | 428407                                                                                                                | esult<br>No.                  |
|----------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------|-------------------------------|
| 545<br>545                                               | 5551<br>551<br>551                                                                                                    | Score                         |
| 888 B                                                    | 100.0<br>85.8<br>85.7<br>85.7                                                                                         | %<br>Query<br>Match           |
| 119<br>134<br>140                                        | 1440<br>1554<br>1555                                                                                                  | %<br>Query<br>Match Length DB |
| 2222                                                     | 222222                                                                                                                | BB                            |
| AAU72814<br>ABP60555<br>AAU76133                         | 100.0 249 22 AAB20434<br>85.8 140 23 AAU76122<br>85.7 144 23 ABB79730<br>85.7 155 24 ABP72295<br>85.7 165 24 ABP72294 | ID                            |
| Mouse mab 26-2F he Murine antibody 14 Mouse mab 26-2F he | Anti-FIX/FIXa anti Mouse monoclonal a Anti-Streptococcus Chimeric construct Chimeric construct                        | Description                   |

| 45   | 44    | 43   | 42   | 41   | 40       | 39   | 38           | 37     | 36    | 35   | 34   | 33   | 32   | 31   | õ    | 29   | 28   | 27   | 26   | 25       | 24   | 23   | 22   | 21   | 20   | 19   | 18      | 17   | 16  | 15   | 14   | 13  | 12   | H   | 10          |
|------|-------|------|------|------|----------|------|--------------|--------|-------|------|------|------|------|------|------|------|------|------|------|----------|------|------|------|------|------|------|---------|------|-----|------|------|-----|------|-----|-------------|
| μ    | ×     | -    |      | 52   | 522      | 23.  | 23.          | 23     | 23.   | 23.  | 23.  | 23.  | 23.  | 23.  | 23.  | 23.  | 23,  | 23.  | 23.  | 23.      | 23.  | •    | 23.  | 52   | 52   | 52   | ώς<br>• | •    | 53  | 4    | 44   | 4   | •    | 44. | 54          |
|      |       |      | e    | ۲    | 81.2     | ۲    | ۴            | ۳      | ï     | ۳    | ۳    | ۳    | ۳    | ۳    | ۳    | ۲    | ۳    | ۳    | ۳    | ۳        | ۳    | 81.4 | ۳    | ۳    | ö    | ö    | ü       | ü    | ü   | 4.   | 4    | 4   | ₹.   | Ä   | 4           |
| 4    | 4     | N    | N    | ø    | 119      | w    | w            | w      | w     | w    | w    | ω    | w    | -    | -    | 1    | ш    | -    | ,    | $\vdash$ | -    | -    | -    | -    | w    | N    | N       | 4    | N   | N    | w    | N   | ö    |     | o           |
| 24   | 22    | 22   | 22   | 22   | 23       | 24   | 23           | 22     | 22    | Ŋ    | 21   | 20   | 19   | 24   | 23   | 22   | 22   | 22   | 22   | 22       | 21   | 20   | 19   | 18   | 21   | 19   | 23      | 22   | 23  | 21   | 22   | 22  | 22   | 22  | 23          |
| 7424 | X4386 | 4893 | 9719 | 4893 | AAU72813 | 3666 | <b>B9520</b> | AG6477 | G6339 | 6710 | 7751 | 8962 | 5759 | 3664 | 9519 | 7691 | 7689 | 7688 | 6476 | 6338     | 7750 | 962  | 5757 | 2999 | 324C | 6609 | 1839    | 2043 | 642 | 5126 | 2043 | 043 | 2044 | 043 | <b>7280</b> |
|      |       |      |      |      |          |      |              |        |       |      |      |      |      |      |      |      |      |      |      |          |      |      |      |      |      |      |         |      |     |      |      |     |      |     |             |

reptide seq ID No.
Amino acid sequence
Mouse anti-FFHFP
mouse
Human FFHFP mouse
Human FFHFP mouse
Human FFHFP mouse
Mouse joint diseas
Anglogenesis inhib
Chineric antibody
Mouse humanised an
Mouse anti-Mouse
Amino acid sequenc
Amino acid sequenc
Mouse anti-FFHFP m

Anti-FIX/FIXa anti Murine CBE11 heavy anti-CD22 monoclon Mouse anti-verotox Heavy Chain variab Chimeric H chain S Mouse humanised an

TRA-8 heavy chain.
Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Anti-FIX/FIXa anti

Monoclonal antibod Mouse antibody 2A4

# ALIGNMENTS

Anti-TrkA single c Murine anti-PI-3,4 Anti-TrkA murine m Heavy chain (VH) g Mouse antibody MB3

Mouse joint diseas Angiogenesis inhib Humanised mouse TR

AAB20434 standard; Protein; 249 AA

AAB20434;

21-JUN-2001 (first entry)

Anti-FIX/FIXa antibody 193/K2 scFv.

RESULT 1
ARE20434
ARE20434
ID ARE2
XX XX
AC ARE2
XX 21-J
XX 21-J
XX Ant1
XX Pact
XW Fact
XW Fact
XW Fact
XW haem
OS Chim Factor IX, FIX, Factor IXa; FIXA; serv; antibody; procequiant; Factor VIII codector; blood cosquiation disorder; heemophilia h, haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

Chimeric - Mus musculus. Chimeric - Synthetic.

| g X          | PN              | X I          | 3      | 13         | ΡŢ      | 17             | PT       | FT           | F      | FT         | FF      | H                   | × |  |
|--------------|-----------------|--------------|--------|------------|---------|----------------|----------|--------------|--------|------------|---------|---------------------|---|--|
| 22-MAR-2001. | WO200119992-A2. |              | Region |            | Protein |                | Peptide  |              | Region |            | Protein | Key                 |   |  |
|              |                 | /label= CDR3 | 230238 | /label= VL | 136249  | /label= Linker | 122.,135 | /label= CDR3 | 98110  | /label= VH | 1121    | Location/Qualifiers |   |  |

```
ID AAUT6122
ID AAUT6127
XX AAUT XX AAUT XX AAUT XX AAUT XX XX XX MOULU XX XW MOULU XX XW KW CULU XXW KW KAPK XX KW CULU XXW CULU XXW KW Sicl XX XXX W OSLL XXX XXX W MYSEX XXX MYSEX XX MYSE
 in present sequence is that of a single chain by (serby) derivative of antiboly 193/KZ, comparising the heavy (W1) and 154mt (V1) chain (v2) chain and the sequence of 193/KZ yoined by an artificial, flexible linker peptide. The scriv was obtained by FCR smplification of cDNMs for 193/KZ W1 and W1 regions and cloning in vector phAP2. 193/KZ 18 and strangle of smi. human factor, 17 FEYN/SECTIVE (FIXA) occurred factor 11 (FIXA) and the sequence of smi. human factor 11 FEYN/SECTIVE (FIXA) occurred factor 12 (FI
 Matches
 Query Match
Best Local Similarity
 WH, sngiogenin, 26-2F, angiogenesis; tumour; cancer; retinopathy, coular neovascular disease; vitamin A deficiency; spyhlis, Raposi's sarcoma; rhoumatoid arthritis; macular depeneration; slockie cell anaemia, Paget of disease; mycobactorial infection; osteoarthritis; graft versus host disease; autoimmune disease; type i diabetes; multiple colerosis; systemic hupus erythematosus type i diabetes; multiple colerosis; systemic hupus erythematosus
 08-MAY-2002
 AAU76122 standard; Protein; 140 AA
 Sequence
 Claim 10; Fig 15; 138pp; English.
 coagulation disorders such as haemophilia A and haemorrhagic diathesis
 New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood
 Mouse; monoclonal antibody; heavy chain variable region;
 Mouse monoclonal antibody 26-2F heavy chain variable region.
 N-PSDB; AAF30724.
 WPI; 2001-290358/30
 Scheiflinger F,
 13-SEP-2000; 2000WO-EP08936
 121 S
 121 S 121
 61
 61
 BAXTER AG
 PDSVRGRETISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTFEKRLEWVATISSGGSYTYY
 121
 249 AA
 Conservative
 (first entry)
 99AT-0001576
 Kerschbaumer R,
 100.0%; Score 643; DB 22;
100.0%; Pred. No. 1.7e-52;
tive 0, Mismatches 0;
 sclerosis; systemic lupus erythematosus
 Falkner F,
 Dorner F;
 Indels
 Length 249;
 0
 Gaps
 120
 60
 60
```

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```
Peptide
Claim 6; Page 14; 20pp; English.
 N-PSDB; ABK15270.
 05-APR-1999;
 05-APR-1999;
 US2002010320-A1.
 Region
 Region
 Region
 Proteir
 Key
 New antibody immunologically reactive to angiogenin useful for the thinking angiogenesis and for treating conditions associated aphormal angiogenesis e.g. cancer, ocular neovascular disease.
 WPI; 2002-187790/24
 (FETT/)
 ds snw
 FETT J W.
 9905-0286240
 99US-0286240
 Location/Qualifiers
 /label= Complementarity_determining_region
/note= "This region is specifically_claimed
 /label= Complementarity_determining_region
/note= "This region is specifically claimed
 /label= Mature_VH
 /label= Signal_peptide
 'Label=
 118..129
 "This region is specifically claimed
 'n
 ä
 in claim
 with
 claim
 claim
```

abnormal angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid arthritis

The invention relates to an antibody immunologically reactive to candidecin or a frequent of angiogenia courising light and heavy chain endologenia or a frequent of angiogenia relative production with human captured complementarity determining regions having a binding caffinity to the angiogenia or its fragment in combination with human captured polypeptide regions (e.g. mouse monoclonal antibody 62-2F). Also included are an expression vector comprising a nucleic acid encoding the antibody and a host cell transformed with the vector. The antibody or its fragment is useful for inhibiting the angiogenia captured the prohibiting reducing or elaminating a tumour in manney by inhibiting prohibiting, reducing or elaminating a tumour in growth, or inhibiting the ability of circulating tumour cell to form a vacularised tumour meas. The antibody is useful for treating a tumour growth, or inhibiting the ability of circulating tumour cell to form a vacularised tumour meas. The antibody is useful for treating a tumour growth, or inhibiting the ability of circulating tumour cell to form a vacularised tumour meas. The antibody is useful for treating a tumour growth, or inhibiting the ability of circulating cuncer, and other staces are considered tumour meas. The antibody is useful for treating a tumour growth, or inhibiting the ability of circulating cuncer, and other staces are considered tumour meas. The antibody is useful for treating a tumour growth, the second of the constant of the con antibody

Sequence

DB 23;

Length 140;

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 8
 Matches
 Query Match
Best Local
 The present sequence is the procein sequence of the heavy chain variable region (W1) of the murine monoclonal antibody SMLA3 (193), which binds specifically to the surface antigens of cartogenic type of streptococcus mutans (ARCC 25175). The monoclonal antibody is produced by SMLA3 (ARCC HB 12558) hybridoma cells. In an example from the invention, chimeric monoclonal antibody TEFF was produced comprising SMLA3 variable regions and human antibody constant regions. Such chimeric monoclonal antibodies can be used to prevent or treat dental cartes in humans. The antibodies engage the effector apparetus of the human insume system when they bind cartogenic organisms, resulting in their destruction. The chimeric antibodies may be produced, in eably be plants, in transgenic animals,
 Streptococcus mutans; monoclonal antibody, Mab; mouse; chameric antibody; therapy; therapy;
 Treatment and prevention of dental caries in mammals, in particular humans by orally administering genetically engineered or purified antibodies that hind to surface antigens of cariogenic organisms -
 Claim 14; Fig 3B; 30pp; English.
 N-PSDB; ABN84611.
 20-AUG-1999;
 15-JUN-2001; 2001US-0881823
 06-JUN-2002.
 US2002068066-A1
 Mus musculus
 Anti-Streptococcus mutans surface antigen
 29-0CT-2002
 ABB79730 standard; Protein; 144 AA
 (ANDE/
 (/SWIM)
 (TRIN/)
 (MORR/)
 (/MIHS
 Local Similarity
 2002-565838/60.
 121 $ 121
 140 S 140
 104;
 80
 61
 20
 Morrison SL,
 CHEN
 WIMS L.
 TRINH K.
 ANDERSON M
 MORRISON
 PDSVKGRFTISRDIAKNTLYLQMSSLRSEDTALYYCTRLGDYGYAYTMDYWGQGTSVTVS
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGGNTYY
 Conservative
 (first entry)
 99US-0378577
 တ
 Ξ
 85.8%;
 Trinh
 ×
 Score 552; DB 2
Pred. No. 3e-44;
 Wims
 Mismatches
 ۲
 Chen
 MAD SWLA3 VH
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 9
 Anderson MH
 Indels
 ç
 Gaps
 139
 120
 79
 60
 0
```

or in chicken eggs

for oral ingestion

A composition comprising a targeting molety and an anti-microbial peptide moiety useful for treating microbial infections, e.g. on mucosal surfaces, caused by bacteria, rickettsia, fungi, yeasts, protozoa, or parasites

N-PSDB; ABZ58398

2003-229542/22.

Example 1; Fig 4; 53pp; English.

The present sequence is that of a chimeric conscribed via the attimicrobial peptide divari (see also ABP7291) joined via a peptide linker to the heavy chain variable region of SNLA3, a monoclonal antibody made sgisinst the cariogenic expanism such a terperococcus mutans. The chimeric construct shows antimicrobial activity toward 8. mutans strains ATCC 25170; LM 2nd 062779, but not expanism consistency toward 8. mutans strains ATCC 25170; LM 2nd 062779.

```
RESULT 4
ABP72295
ID ABP
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 S
 SX
 Matches 105;
 Best Local
 Query Match
 Shi W,
 19-JUL-2001; 2001US-0910358
14-FEB-2002; 2002US-0077624
 17-JUL-2002; 2002WO-US22695
 WO2003007989-A1
 Protein
 Peptide
 Unidentified
 Dhvar1; SWLA3;
 Chimeric construct comprising dhvarl fusion to SWLA3 VH
 08-MAY-2003
 ABP72295;
 ABP72295 standard; Protein; 155 AA.
 Sequence
 REGC
 30-JAN-2003
 Peptide
 139 TVSS 142
 118 TVSS 121
 80
 61
 20
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 Morrison SL,
 UNIV CALIFORNIA
 WASHINGTON DENTAL SERVICE
 Similarity
 PDSVRGRPTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGS---SFDYWGQGTTL
 DVKLVESGGGLVNPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVASISSGGTYTYY
 PDSVKGRFTISRDNAKNTLYLQMTSLKSEDTAMYYCSRDDG-SYGSYYYAMDYWGQGTSV
 144
 Conservative
 (first entry)
 ₽
 antibody; antimicrobial; antibacterial; anticaries
 /label= Linker
31..155
 Location/Qualifiers
 /label= SWLA3_VH
 /label= Dhvarl
 85.7%; Score 551; DB 23;
84.7%; Pred. No. 3.9e-44;
 11;
 Wims
 Mismatches
 ۲
 Chen
 23;
 ۲
 Length 144;
 Indels
 Anderson
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 4
 p.
 'n
 138
 117
 79
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RESULT ABPTZ294
ABPTZ294
YOU ABPT ABPTZ294
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YOU ABPT ABPTZ294
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 S
 Query Match
Best Local S
Matches 105
 example of chimeric constructs of the invention which generally comprise a target microorganism, and an antimicrobial paptide. Claimed compositions comprising the chimeric constructs are useful for treating microbial infections or diseases, e.g. on mucosal surfaces such as mouth, vagina gattonitestinal tract, or oscophageal tract, coased by bacteria, ticketteia, fingi, years, proboroa or parasites.
 (WASH-)
 Histatin 5;
anticaries.
Example 1; Fig 3; 53pp; English
 ps domposition comprising a textering motolsty and an infection, e.g. on ps domposition comprising a text material pagital maisty, caused by bacteria, ricketteia, fungi, yeasts, protozoa, or parasites
 N-PSDB; ABZ58397.
 WPI; 2003-229542/22.
 19-JUL-2001; 2001US-0910358.
14-FEB-2002; 2002US-0077624.
 17-JUL-2002; 2002WO-US22695
 30-JAN-2003.
 WO2003007989-A1
 Protein
 Peptide
 Unidentified
 Chimeric construct
 08-MAY-2003
 ABP72294 standard;
 Sequence
 Peptide
 150
 118
 91
 61
 31
 105;
 1 EVQLVESGGGLVXPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 WASHINGTON DENTAL SERVICE.
 Similarity
 Morrison SL,
 UNIV CALIFORNIA.
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGS---SFDYWGQGTTL 117
 TVSS 153
 TVSS 121
 PDSVKGRFTISRDNAKNTLYLQMTSLKSEDTAMYYCSRDDG-SYGSYYYAMDYWGQGTSV 149
 DVKLVESGGGLVNPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVASISSGGTYTYY 90
 155 AA;
 SWLA3; antibody; antimicrobial; antibacterial;
 Conservative
 (first entry
 41..165
/label=
 /label= Linker
 /label= Histatin-5
 Location/Qualifiers
 comprising histatin 5 fusion to SWLA3 VH
 Protein; 165 AA.
 85.7%;
 Trinh K,
 SWLA3_VH
 Score 551; DB 24;
Pred. No. 4.2e-44;
1; Mismatches 4
 Wims L,
 Chen
 ŗ
 Length 155;
 Anderson MH,
 Indels
 4:
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 $868686868688888
 The present seguence is that of a chimeric construct composed of the antimicrobial peptide histain 5 (see also ABP7229) joined va a peptide linker to the heavy chain variable region of SWLA), a consolonal antibody made against the cariogenic organism. Streptococcus mutens. The chimeric construct shows antimicrobial catrivity toward 8. mutens eracine AVC 2515, LW7 and OWZ175, but not against a range of other oxal bacterial etrains. It is an extivity toward 8. mutens eracine AVC 2515, LW7 and OWZ175, but not peptide of chimeric constructs of the invention which generally comprise a targeting molety that recognises a target microorganism, and an antimicrobial peptide. Claimed compositions comprising the chimeric constructs are useful for treating motorbial infections or diseases, e.g. on mucosal surfaces such as mouth, waghin, constructs of safety of the control of the constructs of the control o
 Matches 105;
 Query Match
Best Local
 Sequence
 61
 41
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 Similarity
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGS---SFDYWGQGTTL
 DVKLVESGGGLVNPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVASISSGGTYTYY
 165 AA;
 Conservative
 85.7%;
 11,
 Score 551; DB
Pred. No. 4.5e
11; Mismatches
 No. 4.5e-44;
 Length 165;
 Indels
 4
 Gaps
```

### 160 TVSS 163 118 101 PDSVKGRFTISRDNAKNTLYLØMTSLKSEDTAMYYCSRDDG-SYGSYYYAMDYWGQGTSV TVSS 121 60 159 100

# RESULT 6

片 ð

```
AAU76132
ID AAU
08-MAY-2002
 AAU76132;
 AAU76132 standard; Protein; 140 AA
(first entry)
```

Mouse mAb 26-2F heavy chain variable region mutant M100Y.

coular neovascular disease; vitemin A deficiency; syphilis; Kapod's sarcona; rheumatorid arthritis; macular degeneration; sickle cell anaemia; Pager's disease; mycobacteria infection; osteoarthritis; graft versus bost disease; autoimum disease; type I diabetes; multiple sclerosis; systemic lupus erythemator wyasthenia gravis; mutant; mutelin; monocional antibody; 26-27; heavy chain variable region; MiOOV; Mouse; angiogenin; angiogenesis; tumour; cancer; retinopathy; lupus erythematosus;

```
Mus sp.
Synthetic.
 05-APR-1999;
 05-APR-1999;
 24-JAN-2002
 US2002010320-A1
 Misc-difference
 Key
 Protein
 Peptide
 99US-0286240
 100
 /note= "Wild-type Met substituted by Tyr'
 1..19
/label= Signal_peptide
20..140
 Location/Qualifiers
 /label= Mature_VH
```

FETT

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AXB
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 8
 can have included are an expression vector comprising a nucleic acid."

Centroding the antibody of the transment is useful for inhibiting the antibody of centroling and a base cell transferend with the vector.

Centricty of angiogenin The antibody is useful for tracking a tumour in humans, by inhibiting, prohibiting, reducing or eliminating tumour in the antibody is useful for tracking a tumour of the second of the control Query Match
Best Local S
Matches 103
AAU72814
 AAU72814 standard; Protein; 119 AA
 The invention relates to an antibody immunologically reactive to anaptogenin or a fragment of angiogenin comprising light and heavy chain nonhuman-derived complementarity determining regions having a binding affinity to the angiogenin or its fragment in combination with human derived polypeptide regions [6.5], mouse monopolanal antibody %5.28).
 Sequence
 Claim 10; Page -; 20pp; English
 New antibody immunologically reactive to anglogenin useful for inhibiting anglogenesis and for treating conditions associated with abnormal anglogenesis e.g. cancer, ocular neovascular disease,
 WPI; 2002-187790/24
 Fett JW;
 (FETT/)
 140 S 140
 121 $ 121
 61
 20
 103;
 Similarity
 PDSVKGRFTISRDIAKNTLYYQMSSLRSEDTALYYCTRLGDYGYAYTMDYWGQGTSVTVS
 PDSVRGRPTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGGSFDYWGQGTTLTVS 120
 EVMLVESGGGLVKPGGSLKLSCAASGPTFSSYTMSWVRQTPEKRLEWVATISSGGGNTYY
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPBKRLEWVATISSGGSYTYY 60
 140
 Conservative
 AA;
 85.1%;
 Score 547; DB 23;
Pred. No. 8.9e-44;
8; Mismatches 10
 23;
 10,
 Length 140;
 Indels
 0
 Gaps
 79
```

```
'Unmour necrosis factor-related apoptosis-inducing ligand receptor;
URALI, 'TRALI receptor M5, cytostatic, apoptosis, cell proliferation;
autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
rhematoid atthitis; sjogren's syndrome; Chron's disease; anaemia;
Addison disease; scleroderma; docepasture's syndrome; sterility;
myasthenla gravis; multiple sclerosis; Basedow's disease; diabetes;
allesgy; arteriospiarosis; myocarditis; cardiomyopathy;
glomerular nephritis; ancer; antibody; chromesome 8p21-22; 7RA-8.
 02-MAY-2000; 2000US-201344P
 02-MAY-2001; 2001WO-US14151
 W0200183560-A1
 Synthetic
 Humanised mouse TRA-8 anti-human DR5 antibody #4
 26-FEB-2002
UAB RES FOUND
 (first entry)
```

Novel antibody specific for tumour apoptosis-inducing ligand, useful f r necrosis factor-related for inhibiting cell proliferation in

WPI; 2002-049338/06

Ichikawa K,

Kimberly RP,

Koopman WJ

Example 26; Page 212-213; 229pp; English

conservais factor (TWN) related appprosis inducing ligand (TWN1) receptor to the St (located on chromosome Sp21-29. The antibody has appropriate inducing cattivity to a cell expressing DRS in vivo. It is also useful for the control of the property of the state of the control of the property of the control of the control of the property of the control of the contro Sequence The invention describes a novel antibody which recognizes a tumour 119 Ä

```
밁
 Ş
 Db
 Query Match
Best Local S
Matches 106
121 8 121
 61
 61
 ш
 Similarity
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
 EVMLVESGGGLVXPGGSLKLSCAASGFTFSSYVMSMVRQTPEKRLEMVATISSGGSYTYY
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCARRGDSMI--TTDYWGOGTTLTVS
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKKLEWVATISSGGSYTYY
 Conservative
 84.8%;
 4
 Pred. No. 1.1e-43;
 Mismatches
 Indels
 2;
 Gaps
 60
 60
```

Length 119;

밁

119

တ

119

```
Query Match
Best Local Similarity
 Sequence
 134
84.8%;
Score
Pred.
545; DB 24;
No. 1.3e-43;
 Length
```

The invention relates to an antibody immunologically reactive to augiogenin or a fragment of angiogenin comprising light and heavy chain menhuman-derived complementarity determining regions having a binding affinity to the angiogenin or its fragment in combination with human derived polypeptide regions (e.g. mouse monoclonal antibody 26-27). Also included are an expression vector comprising a nucleic ocid encoding the antibody and a host cell transformed with the vector.

New antibody immunologically reactive to angiogenin useful for inhibiting angiogenesis and for treating conditions associated abnormal angiogenesis e.g. cancer, ocular neovascular disease,

with

cheumatoid arthritis

English

WPI; 2002-187790/24

05-APR-1999;

99US-0286240

(FEIT/) FEIT J

```
identifying characteristics of, or that is a monoclonal antibody 1483. An antibody of the invention has estepachtic, antithewastic, antitalentic, antitalentic, antitalentic, antitalentic, antitalentic, antitalentic, and neuroprotective activity. The polymoclectides encoding the antibodies and polymoclatic are useful for treating or preventing estepachtic diseases, such as rheumatoid archititis, estepaceous, metastatic and primary bone cancer, wear debris induced osreolysis or outerantitis, and amune diseases such as psoriasis, inpulin-dependent diseases, and amune diseases such as psoriasis, inpulin-dependent esquance represents the heavy chain variable region of the murine monoclonal antibody 143 of the invention. The sequence contains three complementary determining regions
 03-MAY-2002;
 antiarthritic, antinflammatory, cytostatic, antispoziatic, antidabetic, neuroprotettive, gene therapy, rhematoid arthritis, osteopozosis, bone cancer, osteolypsis, osteoarthritis, immune disease; psoriasis; bone cancer, osteolypsis, osteoarthritis, immune disease; psoriasis;
 Mouse; monoclonal antibody; 14F3; osteopathic; antirheumatic;
 Murine antibody 14F3 heavy chain variable region.
 21-MAR-2003
 ABP60555;
 ABP60555
 Disclosure; Page 8; 51pp; English.
 psortasts,
 New monoclonal antibody having the characteristics of a monoclonal antibody 14F3, useful for treating or preventing osteopathic diseases, e.g. rheumatoid arthritis, or osteoporosis, and immune diseases e.g.
 Sweet RW,
 (SMIK)
 18-MAY-2001; 2001US-292031P
 WO200295012-A1.
 Region
 Region
 Region
 Mus musculus
 complementary
 insulin-dependent diabetes; inflammatory bowel disease; multiple sclerosis; heavy chain variable region;
 The invention relates to a novel monoclonal antibody having the
 2003-156758/15.
 SMITHKLINE
 SMITHKLINE
 ABV99887
 standard; protein;
 or diabetes
 Tornetta MA,
 2002WO-US14246
 (first entry)
 determining region; CDR.
 99..110
 /label= CDR1
 Location/Qualifiers
 /label= CDR3
 /label= CDR2
 BEECHAM PLC
 BEECHAM CORP
 Wattam TA
 134
AUT/6133

AUT/61
 먉
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 밁
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Matches
 osteoarthritis; graft vērsus host diseasē; autoimmune diseasē;
type I dabetes; multiple sclerosis; systemic lupus erythematosus;
myasthenia gravis; mutant; muteli; monoclonal antibody; 26-28;
heavy chain variable region; 259%.
 Mouse; angiogenin; angiogenesis; tumour; cancer; retinopathy, coular neovascular disease; vitamin A deficiency; syphilis; Kaposi's sarcoma; rheumatoid arthritis; macular degeneration; sickle cell anaemia; Paget's disease; mycobacterial infection;
05-APR-1999;
 US2002010320-A1
 Misc-difference
 Mus sp.
Synthetic
 Mouse mAb 26-2F heavy chain variable region mutant E59Y
 08-MAY-2002
 AAU76133;
 AAU76133 standard; Protein; 140
 24-JAN-2002
 Protein
 Peptide
 121 8 121
 121 $ 121
 105;
 61
 61
 ,..
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 EVQLVESGGDLVKPGGSLKLSCAASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSYTYY
 PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCARLDGYNYRWYFDVWGTGTTVTVS
 PDSVRGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
 Conservative
 (first entry)
9905-0286240
 Location/Qualifiers
1..19
 /label=
 /label= Signal_peptide
 note= "Wild-type Glu substituted by
 Mature_VH
 4.
 Mismatches
 12;
 Indels
 0
 Gaps
 120
 60
```

```
AUT2801
ID AAUT
XX AAUT
XX AAUT
XX AAUT
AC AAUT
XX TRA
XX
 continity of antibody or its fragment is useful for inhibiting the angiogenic cartivity of angiogenin me antibody is useful for training a useful for training and the manana by inhibiting, prohibiting, reducing or siminating a tumour in commans, by inhibiting, prohibiting, reducing or siminating a tumour in comman or inhibiting the shifty of circulating tumour call to form a crassing and the comman or unwanted angiogenesis, including only the comman or unwanted angiogenesis, including only and other calcaled by angiogenesis, including only and other reducing only an extraording of the reducing of th
 Matches
 Query Match
Best Local
 'unmour necrosis factor-related apoptosis-inducing ligand receptor:
TRALI, 'TRALI receptor MES, cytostatic, apoptosis, oll proliferation,
autoimmune disease, systemic lupus erythematosus; Hashimoto's disease,
rhaumatoid arthritis; Signera's syndrome; Chron's disease; namemia,
Addition disease, scieroderma; doodpasture's syndrome; Sterility;
myestbania graybis, multiple scierosis; Basedow's diteases; diabetes)
 Mus musculus
 glomerular nephritis; cancer; antibody; chromosome
 allergy; arteriosclerosis; myocarditis; cardiomyopathy;
 26-FEB-2002
 AAU72801;
 AAU72801 standard; Protein, 464 AA
 Sequence
 140
 121 8 121
 103;
 80
 13
 20
 H
 Similarity
 S 140
 PDSVRGRETIERDNAKWTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 EVQLVESGGGLVXPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 PDSVKGRFTISRDIAKNTLYLQMSSLRSEDTALYYCTRLGDYGYAYTMDYWGQGTSVTVS
 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQYFEKRLEWVATISSGGGNTYY
 140 AA;
 Conservative
 (first entry
 the claims.
 Score 545; DB 23;
Pred. No. 1.4e-43;
 Mismatches
 10,
 Length 140;
 Indels
 0,
 139
 79
```

õ 멼 ş В S

```
The invention describes a novel antibody which recognizes a tumour
 Claim 26; Page 198-199; 229pp; English.
 Novel antibody specific for tumour necrosis factor-related apoptosis-inducing ligand, useful for inhibiting cell proliferation
 WPI; 2002-049338/06
 02-MAY-2000; 2000US-201344P
 02-MAY-2001; 2001WO-US14151
 UAB RES FOUND
 Kimberly RP,
 Koopman WJ
 5
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888888888888888888888888888888888888

CC mecrosis factor (TMP)-related apoptosis-inducing ligand (TRAIL) receptor CC DRS (located an chromosome Bp21-2). The antibody has apoptosis-inducing cactivity to a cell expressing PRS in vivo. It is also useful for cactivity to a cell expressing PRS in vivo. It is also useful for comparing a therapsuto for selective apoptosis of abnormal or comparing a therapsuto for selective apoptosis of abnormal or preferably a human breast, owary colon, haematopoiseis, prostate. Comparing producing producing producing producing and for liver cancer cell. A therapsutio agent may calso be administered e.g. pacitives, taxol or cytchostatide. The cantibody is used to treat an autoimmune disease, systemic upus comparing producing the production of the producing comparing the producing comparing producing the producing comparing producing producing comparing producing comparing producing comparing producing comparing producing producing comparing producing comparing producing comparing producing comparing producing producing comparing producing comparing producing comparing producing producing producing comparing producing producing comparing producing producing producing comparing producing producing producing producing comparing producing pr glomeriular nephritis, hypoplastic anaemia, rejection after cogan transplantation, and numerous malignamancies of lung, posstate, liver, ovary, lymphatic or breast tissue. Peptides used to design primers for isolating heavy and light chain 100MA of the mouse TRAIL (ANI/280) and ANI/2802], TRAF are shown in ANI/2799 and ANI/2800.

```
Matches 106;
 121
138 S 138
 20
 1 BYOLVESGGGLYKPGGSLKLSCAASGFTFSTYTMSWYROTPEKRLEWVATISSGGSYTYY
 $ 121
 EVMIVESGGGUVKPGGSLKISCAASGFTFSSYVMSWVRQTPEKKLEWVATISSGGSYTYY
 Conservative
 4.
 Mismatches
 Indels
 <u>۲</u>
 79
 60
```

밁 Ś 몆

Query Match

Local

Similarity

84.8%;

Score 545; DB 23; Pred. No. 5.3e-43;

DB 23;

Length 464;

Sequence

464 AA;

```
RESULT 11
AAB20436
ID AAB2
```

멼

AAB20436 standard; Protein; 249 AA.

21-JUN-2001 (first entry)

Anti-FIX/FIXa antibody 198/A1 scfv

8X222X2X2X2X Factor IX, FIX, Factor IXa, FIXa, scPv, antibody, procoagulant, Factor VIII cocactory blood coagulation discorder, haemophilia A, haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

Chimeric - Mus musculus

Chimeric

Synthetic.

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 or The present sequence is that of a single chain PV (scPV) derivative of antiboly 198/AL comparising the heavy (VI) and 19th (VI) chain variable regions of 199/AL joined by an artificial, flexible linker comparising the heavy (VI) and 19th (PC) chain for 199/AL is a solution by PCR emplification of cDNs for 199/AL is a few and the regions and cloning in vector pbPa 20. 199/AL is a comparison of anti-human sacron the FIDYDY constituted for the FIDYDY control of the FIDYDY control
 Query Match
Best Local Simi
Matches 107;
 New factor IX/factor IXa antibodies and their derivatives useful for increasing andolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
 Misc-difference
 Misc-difference
 Sequence
 Example 10; Fig 17; 138pp; English.
 Scheiflinger F,
 14-SEP-1999;
 13-SEP-2000;
 22-MAR-2001
 WO200119992-A2
 Region
 Protein
 Peptide
 Region
 Protein
 ě
 (BAXT)
 Local Similarity
 2001-290358/30.
121 ·SS 122
 120
 61
 61
 ,
 AAF30726
 BAXTER
 SS
 PDSVKGRFTISRDNAKNTLYLOMSSLKSBDTAMYHCTREGGGYYVNWYFDVWGAGTTLTV
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTANYYCTRDGGHGYGS-SFDYWGQGTTLTV
 EVQLQESGGGLVKPGGSLKLSCAASGFIPSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 249
 121
 Conservative
 2000WO-EP08936
 Ã
 Ä
 99AT-0001576
 224
 Location/Qualifiers
 Kerschbaumer
 /note= "encoded by GCN"
 labe
 note= "encoded by
 label= CDR3
 label= Linker
 label= CDR3
 abel= VL
 84.7%;
 .249
 HV =1
 UI
V
 Score 544.5;
Pred. No. 2.5
 æ
 Mismatches
 Falkner F,
 ACN"
 .9e-43;
 DB
 9
 22;
 Dorner
 Indels
 Length
 249
 Ļ
 Gaps
 119
 60
 60
```

```
RESULT 1
ANAZO142
XX
ANAZO142

 Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII coffector; blood coagulation disorder; haemophilia haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
 New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic disthesis
 N-PSDB;
 13-SEP-2000; 2000WO-EP08936
 WO200119992-A2
 Peptide
 Protein
 Peptide
 Misc-difference
 Protein
 Chimeric
 Chimeric
 Chimeric
 myc-tag.
 Anti-FIX/FIXa antibody 198/B1-myc-tag fusion
 21-JUN-2001
 AAB20442 standard; Protein; 294
 Scheiflinger F,
 14-SEP-1999;
 22-MAR-2001.
 Peptide
 Peptide
 Region
 Region
 Protein
 Peptide
 (BAXT) BAXTER
 2001-290358/30.
DB; AAF30732.
 Mus musculus.
Synthetic.
Escherichia coli
 (first
 AG.
 99AT-0001576
 287..288
 /label= Mature_protein
 /label= Signal_peptide
 Location/Qualifiers
 Kerschbaumer R,
 /label= His_tag
 /label=
 /note= "encoded
 /label=
 'label= VL
 label= VH
 label=Myc_tag
 iabel=
 label= Linker
 entry)
 159
 SCFV
 Spacer
 Spacer
 S
 ķ
 Falkner
 GGN"
 'n
 Dorner
 Ψ,
```

The present sequence is that of a fusion proceth comprising: a PelB leader; a single chain FW (sePW) derivative of antibody 198/BU comprising the heavy (WH) and light (WL) chain variable regions of 198/BU joined by an artificial. Heavible linker applie; a spacer; as My-eag peptide; a spacer; and a C-terminal GMB affinited as 189/BU is an example of anti-human factor X (FIX)/activated Factor X (FIX) antibodies of the invention. Anti-FIX/FIX antibodies of the sinvention.

Example 18;

Fig 34; 138pp; English.

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ARBOULT 13
ARBOUT 13
ARBOUT 13
ARBOUT 21-UT

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 Best Local Sin
Matches 106;
 Query Match
 their derivatives, including serv fragments, have FVIII a cofactor activity or FIXa activating activity. Administration leads to an increase in the procoagalant activity of FIXa, even in the presence of FVIII a inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII or FVIIIa, and in the case of FVIII with the presence patients. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, sepecially hearopoilia a had haemorrhagic distribution for the servence of the
 Misc-difference
 Peptide
 Paetor IX, FIX, Factor IXa, FIXa, miniantibody, procoagulant, Paetor VIII ocactor; blood coagulation disorder, haemorphilia h, haemorrhagic disthesis; haemostatic; anidolytic; therapy; mouse; bivalant antibody; plasnid pEIp:198802#102.
 Misc-difference
 Misc-difference
 Region
 Proteir
 Chimeric -
 Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody.
 21-JUN-2001
 AAB20438 standard; Protein; 325 AA
 Peptide
 Protein
 Chimeric
 Chimeric
 Sequence
 119
 142
 83
 61
 23
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYIMSWVRQTPEKRLEWVATISSGGSYTYY 60
 Similarity
 PDSVRGRFTISRDNAKNTLYLCMSSLKSEDTAMYYCTRDGGHGYGSS--FDYWGQGTTLT 118
 VSS 144
 VSS 121
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGG-GFTVNWYFDVWGAGTSVT
 EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 82
 Mus musculus.
 Escherichia coli.
 294 AA;
 Conservative
 (first entry)
 /label= Spacer
275..284
/label= Hinge
 Location/Qualifiers
 'note= "encoded by
 /label= Linker
 'note= "encoded
 /label= Mature_protein
 /label= Signal_peptide
/note= "PelB leader"
 note=
 label= VL
 'label= VH
 label= scfv
 84.7%;
 .271
 "encoded
 9
 Score 544.5; DB 2
Pred. No. 3.5e-43;
 Š
 ş
 Mismatches
 90
 ď
 DB 22;
 Ģ
 Indels
 Length 294;
 υ
••
 Gaps
 2
```

```
RESULT 14
AAB20437
XXXXXXX
 멹
 S
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 Б
 The present sequence is that of a bivalent miniantibody comprising can tillody 199/H1 (subblone H2), an amphipathic helical Extricture and a C-terminal fidis tag. The protein was expressed in Escherichia coli from plaemid polipishability sequences and a C-terminal fidis tag. The protein was expressed in Escherichia coli from plaemid polipishability (see ANF30788). Cantibody 199/H1 is an example of anti-human Protor IX (FIXA) antibodies and that derivatives have PVIIIa cofactor activity of FIXA antibodies and that derivatives have PVIIIa cofactor activity of FIXA antibodies and that derivatives have PVIIIa cofactor activity of FIXA, even in the presence of FVIII in this procession at a contract of FVIII in this presence of FVIII or FVIIIa, and in the case of FVIII called the composition for treating patients with blood calmed phaemaceutical composition for treating patients with blood calmed phaemaceutical composition for treating patients with blood calmed phaemaceutical manufacturity and the theory of the case Best Loc
Matches
 Query Match
 AAB20437 standard; Protein; 732 AA
 New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as beemophilla A and haemorrhagic disthesis
 Sequence
 Example 16; Fig 28; 138pp; English.
 N-PSDB;
 Scheiflinger F,
 14-SEP-1999;
 13-SEP-2000; 2000WO-EP08936
 22-MAR-2001
 WO200119992-A2
 Peptide
 Protein
 (BAXT) BAXTER
 Local
 2001-290358/30.
 142 VSS
 119 VSS 121
 106;
 83
 61
 23
 Similarity
 AAF30728
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSS--FDYWGQGTTLT
 EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGG-GFTVNWYFDVWGAGTSVT
 325 AA;
 Conservative
 144
 99AT-0001576
 285..319
/label= Helix
320..325
 Kerschbaumer R,
 /label= His_tag
 84.7%;
 9
 Score 544.5; DB 22
Pred. No. 3.9e-43;
9; Mismatches 5;
 Falkner F,
 DB 22;
 Dorner
 Indels
 Length
 325;
 ω
 Gaps
```

Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion

21-JUN-2001

(first entry)

AAB20437;

118 82 N

```
The present asquence is that of a fusion procesh comprising: PPIB readers in a process of the pr
 Key
 Factor IX; FIX; Factor IXa; FIXa; scPv; antibody; procagulant; Factor VIII cofactor; blood cosgulation disorder: haemophilia A; haemorrhagic diathesis; heemostatic; amidolytic; therapy; mouse;
 New factor IX/factor IXa antibodies and their derivatives useful for
increasing amidolytic activity of factor IXa, and for treating blood
coagulation disorders such as haemophilia A and haemorrhagic diathesis
 WPI; 2001-290358/30.
N-PSDB; AAB30727.
 Scheiflinger F,
 13-SEP-2000; 2000WO-EP08936
 WO200119992-A2
 Protein
 Peptide
 Region
 Peptide
 Misc-difference
 Region
 Protein
 Protein
 Peptide
 Chimeric
 Chimeric
 Chimeric
 Example 16; Fig 26; 138pp; English
 14-SEP-1999;
 (BAXT) BAXTER AG
 phosphatase.
 Mus musculus.
 Synthetic.
Escherichia coli.
 99AT-0001576
 726..732
/label= His_tag
 /label= Mature_protein
 /label= Signal_peptide
 Location/Qualifiers
 Kerschbaumer R,
 /label= Alkaline_phosphatase
 /label= Linker
 145..159
 /note= "encoded by
 /label= VH
 /label= scFv
 Labe.
 abel= Spacer
 .271
= VL
 .275
 Falkner F,
 GGN
 Dorner F;
```

Sequence

732 AA

ş g

S 맑

PDSVKGRFTISRDNAKNNLYLOMSSLKSEDTAMYYCARDKAYYGNYGDAMDYWGQGTSVT PDSVRGRETISRDNAKNTLYLQWSSLKSEDTAMYYCTRDGGH--GYGSSFDYWGQGTTLT

60 60

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RANSIZIAG SANSIZIAG SANSIZ
 묽
 S
 片
 S
 밁
 Ş
 S
 Query Match
Best Local S
Matches 106
 Query Match
Best Local Simi
Matches 104;
 This invention describes novel peptides derived from a framework region of the variable domain of an antibody for detection, immunocheanpy or detect analytes in a sample by aliminating interference in the sample that a fact that a sample of the first analytes in a sample by aliminating interference in the sample. ANES1264-Y51267 represent peptides derived from the framework regions of the variable domain of an antibody which are used to illustrate the
 Unidentified
 Framework region; monoclonal antibody; variable domain; detection; immunotherapy; MAK 33.
 14-APR-2000
 AAY51266;
 AAY51266 standard; peptide; 123 AA
 Sequence
 Disclosure; Page 18; 20pp; German.
 suppressor
 WPI; 2000-107255/10
 Nussbaum S,
 26-JUN-1998;
 26-JUN-1998;
 30-DEC-1999
 DE19828466-A1
 (HOFF) ROCHE DIAGNOSTICS GMBH
 142
 119 VSS 121
 106;
 83
 61
 23
 of.
 Similarity
 Similarity
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGG-GFTVNWYFDVWGAGTSVT
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSS--FDYWGQGTTLT
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTNSWVRQTPEKRLEWVATISSGGSYTYY
 VSS 144
 EVKLVESGGGLVKFGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
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 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 the invention.
 peptides derived from antibodies for use in immunoassays
 antibody MAK 33 heavy chain variable region peptide
 Conservative
 123 AA;
 Conservative
 Moessner E,
 (first entry
 98DE-1028466
 98DE-1028466
 84.7%;
 84.6%;
 Lenz H,
 9;
 Score 544.5; DB 2
Pred. No. 9.8e-43;
 Score 542; DB 21;
Pred. No. 2.3e-43;
5; Mismatches 12
 Mismatches
 Praast
 a
 22;
 12;
 Length 123;
 Indels
 Length
 Indels
 ů,
 2
 Gaps
 Gaps
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Page 11

В

121 VSS 123

Search completed: November 7, 2003, 07:27:02 Job time: 53.1802 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on:
 OM protein -
 protein search, using sw model
November 7, 2003, 07:30:19, Search time 106.138 Seconds (withbout alignments) 195.799 Willion cell updates/sec
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| 121 | GTTLTVSS | ОБМХС | GSSFE | HGY | : | : | :   | :  | 1 EVQLVESGGGLVKPGGSLKLHGYGSSFDYWGQGTTLTVSS 121 |       | equence        |
|-----|----------|-------|-------|-----|---|---|-----|----|------------------------------------------------|-------|----------------|
|     |          |       |       |     |   | - | 123 | ¦- | ttle: US-09-661-992B-84_COPY_1_121             | score | tle:<br>erfect |
| -   |          |       |       |     |   |   |     |    |                                                |       |                |

Se Pr

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Scoring table:
 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters:
 644079
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644079 segs, 171749292 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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| Database :                                                      | Post-processing: Minimum Match 0%<br>Maximum Match 10<br>Listing first 45 |
|-----------------------------------------------------------------|---------------------------------------------------------------------------|
| Published Applications AA:* : /cgn2_6/ptodata/2/pubpaa/US07_PUB | Minimum Match 0%<br>Maximum Match 100%<br>Listing first 45 Bummaries      |

| Published Applications AA:  1/0912_6/Dodae.2/2/Dubpas/USO7_EUROOMS.pep:  1/0912_6/Dodae.2/2/Dubpas/USO5_EUROOMS.pep:  1/0912_6/Dodae.2/2/Dodae.2/2/Dodae.2/2/Dodae.2/2/Dodae.2/2/Dodae.2/2/Dodae.2/2/Doda |               |                             |                           |                          |                          |                          |                                      |                                      |                          |                          |                           |                           |                             |                              |                                |                         |                         |                                   |             |  |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|-----------------------------|---------------------------|--------------------------|--------------------------|--------------------------|--------------------------------------|--------------------------------------|--------------------------|--------------------------|---------------------------|---------------------------|-----------------------------|------------------------------|--------------------------------|-------------------------|-------------------------|-----------------------------------|-------------|--|
| JABPI KORLIONE AA.*  (FORCERS L.) FUNDAME (USD. PURDONE PEP:  (FORCERS L.) FUNDAME (USD. PURDONE)  (FORCERS L.) FUNDAME (U | 18:           | 17:                         | 16:                       | 15:                      | 14:                      | 13:                      | 12:                                  | 11:                                  | 10:                      | 9:                       |                           | 7:                        |                             |                              |                                |                         | 2                       |                                   | Pub         |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | _6/ptodata/2/ | 6/ptodata/2/pubpaa/US60_NEW | 6/ptodata/2/pubpaa/US10 N | 6/ptodata/2/pubpaa/US10C | 6/ptodata/2/pubpaa/US10B | 6/ptodata/2/pubpaa/US10A | 6/ptodata/2/pubpaa/US09 NEW PUB.pep: | 6/ptodata/2/pubpaa/US09C_PUBCOMB.pep | 6/ptodata/2/pubpaa/US09B | 6/ptodata/2/pubpaa/US09A | 6/ptodata/2/pubpaa/US08_P | 6/ptodata/2/pubpaa/US08_N | n2_6/ptodata/2/pubpaa/PCTUS | n2_6/ptodata/2/pubpaa/US07_N | /ptodata/2/pubpaa/US06_PUBCOMB | 6/ptodata/2/pubpaa/US06 | /ptodata/2/pubpaa/PCT_N | /ptodata/2/pubpaa/US07_PUBCOMB.pe | d_Applicati |  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

# SUMMARIES

| 14               |                  | -             | 13               | 7.7              | 3             | 11               | 10                |                   | · œ               |                   | 10                | , U               | 1 🕰             |                 | , ,              | J         | ,                | No.         | Result |
|------------------|------------------|---------------|------------------|------------------|---------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-----------------|------------------|-----------|------------------|-------------|--------|
| 523.5            | 22.5             | 3 1           | 523.5            | 020.0            | 2             | 532.5            | 545               | 545               | 4.0               | 54.5              | 045               | 545               | 100             | 195             | 10               | 199       | 552              | Score       |        |
| 81.4             | 01.4             | 2             | 81.4             | 8.18             | 3 1           | 82.8             | 84.8              | 84.8              | 84.8              | 84.8              | 84.8              | 84.8              | 85.7            | 85.7            | 10.              | 9         | 85.8             | Match       | Ouerv  |
| 118              | PTT              | : !           | 118              | 118              |               | 118              | 464               | 462               | 462               | 119               | 119               | 119               | 165             | 155             | 1                |           | 140              | Length      |        |
| 15               | 1                |               | 10               | T O              |               | ;                | 12                | 12                | 12                | 12                | 12                | 12                | 12              | 12              |                  | ,         | φ                | 80          |        |
| US-10-182-018-46 | US-10-337-981-46 | 10 00 000 000 | US-09-423-800-46 | US-U9-144-886-62 | 20 00 111 000 | US-09-144-886-63 | US-10-275-180A-23 | US-10-286-132A-23 | US-10-281-479A-23 | US-10-286-132A-61 | US-10-275-180A-61 | US-10-281-479A-61 | US-10-077-624-4 | US-10-077-624-7 | 05-09-881-823-12 | 10 00 001 | US-09-286-240-4  | ID          |        |
| 46               | Sequence 46, Ap  | ٦             | 'n.              | •                | ٠             | 3                | 23                | 23,               | •                 | •                 | Sequence 61, App. | Sequence 61, Ap   | Sequence 4, App | Sequence 7, App | Sequence 12, App |           | Segmence 4 Appli | Description |        |

S 8 Ś 밁

61 DSSYGGRETISEDMANTLYLOWSSLKSEDTMAYYCTRLGGGHGYGSSPDYWGQCTTLTVS 120 | 80 PDSYKGRETISEDIANATLYLOWSSLKSEDTMAYYCTRLGGHGYAYTDWGYGCTTLTVS 139

0

RESULT 2 US-09-881-823-12 ; Sequence 12, Application US/09881823

| ų.<br>Ui         | 44               | 43   | 42                | 1                 | 40                | 39                | 8               | 37               | 36                | 35                | 34                | 33                | 32                | 31                | 30               | 29                | 28               | 27                | 26               | 25                | 24              | 23              | 22               | 21                | 20                | 19                | 18               | 17               | 16                |
|------------------|------------------|------|-------------------|-------------------|-------------------|-------------------|-----------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|------------------|-------------------|------------------|-------------------|-----------------|-----------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|
| 498              | 498              | 499  | 500               | 500               | 500               | 500               | 502.5           | 502.5            | 503               | 503               | 503               | 505               | 505               | 505               | 506              | 507               | 508.5            | 511               | 512              | 513.5             | 516             | 518.5           | 521              | 522               | 522               | 522               | 523.5            | 523.5            | 523.5             |
| 77.4             | 77.4             | 77.6 | 77.8              | 77.8              | 77.8              | 77.8              | 78.1            | 78.1             | 78.2              | 78.2              | 78.2              | 78.5              | 78.5              | 78.5              | 78.7             | 78.8              | 79.1             | 79.5              | 79.6             | 79.9              | 80.2            | 80.6            | 81.0             | 81.2              | 81.2              | 81.2              | 81.4             | 81.4             | 81.4              |
| 125              | 98               | 117  | 121               | 119               | 119               | 119               | 443             | 118              | 119               | 119               | 119               | 119               | 119               | 119               | 123              | 119               | 118              | 121               | 121              | 120               | 140             | 124             | 123              | 119               | 119               | 119               | 137              | 137              | 118               |
| 12               | 10               | 12   | 12                | 12                | 12                | 12                | 9               | 10               | 12                | 12                | 12                | 12                | 12                | 12                | 10               | 15                | 10               | 12                | 12               | 12                | 14              | ;               | 10               | 12                | 12                | 12                | 12               | 5                | 15                |
| US-10-169-351-31 | US-09-840-459-39 |      | US-10-300-215-113 | US-10-286-132A-31 | US-10-275-180A-31 | US-10-281-479A-31 | US-09-917-410-4 | US-09-144-886-65 | US-10-286-132A-59 | US-10-275-180A-59 | US-10-281-479A-59 | US-10-286-132A-56 | US-10-275-180A-56 | US-10-281-479A-56 | US-09-144-886-61 | US-10-305-268-2   | US-09-144-886-64 | US-10-300-215-133 | US-10-300-215-90 | US-10-229-335-3   | US-10-006-773-4 | US-09-518-737-2 | US-09-144-886-60 | US-10-286-132A-60 | US-10-275-180A-60 | US-10-281-479A-60 | US-10-337-981-76 | US-09-423-800-76 | US-10-169-003-46  |
| 31,              |                  | 56,  | Sequence 113, App | 31                | 31,               |                   |                 | _                | 59                |                   | 59                | 56                |                   | 56                | 61               | Sequence 2, Appli | 64               | 13                | 9                | Sequence 3, Appli | 4               | N               | 60               |                   | 60,               | 60,               | 76,              | 76               | Sequence 46, Appl |

# ALIGNMENTS

```
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 RESULT 1
US-09-286-240-4
 Matches
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 y Match 85.8%;
Local Similarity 86.0%;
nes 104; Conservative
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Pred. No. 8.6e-44;
8; Mismatches 9; Indels
 0
 Gaps
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US20020068066A

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; OTHER INFORMATION: Synthesized using squential PCR techniques US-10-077-624-7
 밁
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 밁
 US-10-077-624-7
 US-09-881-823-12
 Query Match
Best Local Similarity
 GENERAL INFORMATION
 SEQ ID NO 7
 Sequence 7, Application US/10077624 Publication No. US20030143234A1
 SEQ ID NO 12
LENGTH: 144
 Patent No.
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 APPLICANT: Nims, Lettia
APPLICANT: Opt. Lid.
APPLICANT: Opt. Registry
APPLICANT ON HOWER, US /10/077,624
CURRENT APPLICANTON HOWER, US 09/310,358
PRICE APPLICATION HOWER: US 09/310,358
PRICE APPLICATION HOWER: US 09/318,577
PRICE APPLICATION HOWER: US 09/378,577
 APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA APPLICANT: WASHINGTON DENTAL SERVICE
 Matches 105;
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 Query Match
 APPLICANT:
 CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-68-15
PRICAR APPLICATION NUMBER: US 07/378,577
PRICAR FILING DATE: 1999-08-20
NUMBER OF ESQ 1D DAS: 12
SOFTMARE: RetentIn version 3.0
 APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MI
APPLICANT: MORRISON, SH
 FILE REFERENCE: 22851-032
 APPLICANT:
 APPLICANT:
 APPLICANT:
 TYPE: PRT ORGANISM: Artificial sequence
 TITLE OF INVENTION: Method for the Treatment
 FEATURE:
 ORGANISM: Murine
 TYPE: PRT
 LENGTH: 155
 INFORMATION
 139 TVSS 142
 118 TVSS 121
 61
 80 PDSVKGRFTISRDNAKNTLYLQMTSLKSEDTAMYYCSRDDG-SYGSYYYAMDYWGQGTSV 138
 20 DVKLVESGGGLVNPGGSLKLSCAASGFTESSYTMSWVRQTPEKRLEWVASISSGGTYTYY
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 PDSVRGRETISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGS---SFDYWGQGTTL 117
 Anderson, Maxwer
Morrison, Sherie
 Shi, Wenyuan
 WIMS, LETITIA
CHEN, LI
 Trinh, Kham
 ANDERSON, MAXWELL MORRISON, SHERIE
 TRINH, RYAN
 Conservative
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 85.7%;
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 Mismatches
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 Indels
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 Gaps
 79
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Sequence 61, Application US/10281479A
Publication No. US20030133932A1
GENERAL INFORMATION:
APPLICANT: The UNB Research Foundation
APPLICANT: Lobo, Tong
APPLICANT: Inhikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
 S
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 US-10-281-479A-61
 RESULT 5
 ; OTHER INFORMATION: Synthesized using sequential PCR techniques US-10-077-624-4
 US-10-077-624-4
 밁
 S
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 밁
 PILOR IPPLICATION INDUBRE: US 00/210,358
PILOR IPPLICATION WINDER: US 00/278,577
PILOR PELLOR INDUST: 1999-08-20
REPLICATION WINDER: US 00/278,577
PILOR PELLOR DI NOS: 31
SOUTHARE: PATENTIN VETSION 3.1
SEQ ID NO 4.
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 Sequence 4, Application US/10077624
Publication No. US20030143234A1
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 APPLICANT: 01, FERSKIA
TITHE DE INVENTION: ANTI-MICROBIAL TRRGETING CHIMERIC PHARMACEUTICAL
FILE REFERENCE: 110136: 991200
GURRENT APPLICATION UNMERS: US/10/077,624
GURRENT ZILING DATE: 2002-02-14
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 TYPE: PRT
ORGANISM: Artificial sequence
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 ENGTH: 165
 160
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 150 TVSS 153
 118 TVSS 121
 105; Conservative
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 91
 61
 31 DVKLVESGGGLVNPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEMVASISSGGTYTYY
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 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGS---SFDYWGQGTTL 117
 THE REGENTS OF THE UNIVERSITY OF CALIFORNIA WASHINGTON DENTAL SERVICE
Zhou, Tong
Ichikawa, Kimihisa
Kimberly, Robert P
 PDSVKGRFTISRDNAKNTLYLQMTSLKSEDTAMYYCSRDDG-SYGSYYYAMDYWGQGTSV 149
 Trinh, Kham
Wims, Letit
 Shi, Wenyuan
Anderson, Maxwell
Morrison, Sherie
 Chen, Li
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 85.7%; Score 551; DB 12;
84.7%; Pred. No. 1.3e-43;
ative 11; Mismatches 4;
 11; Mismatches
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 Length 165,
 Indels
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 4
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 Gaps
 117
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2

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PRIOR HEPLONITION NUMBER: 60/3014.402
PRIOR PLIANE DATE: 2001-11-0.1
PRIOR PRIOR PRIOR DATE: 2001-15-0.2
PRIOR PLIANED DATE: 2001-05-02
PRIOR REPLICATION NUMBER: 60/201.344
PRIOR PLIANED DATE: 2000-05-02
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PRIOR PRIOR DATE: 3000-05-02
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PRIOR DATE:
 US-10-275-180A-61
 US-10-275-180A-61
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 US-10-281-479A-61
Query Match
Best Local Similarity
 GENERAL INFORMATION:
 Sequence 61, Application US/10275180A
Publication No. US20030190687A1
 Matches 106; Conservative
 Query Match
Best Local Similarity
 APPLICANT: Zhou, Tong
APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Robert P.
APPLICANT: Komberly, Robert P.
APPLICANT: Komberly, ROBERT P.
APPLICANT: KOMPANIA HILIAM J.
TITLE OF INVENTION: AND ANTIBODY SELECTIVE FOR A TUNOR NECROSIS FACTOR-RELATED APOPTOR
TITLE REFERENCE: 2105.0029US
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILMO DATE: 2002-10-31
LUMBER OF SEQ ID MOS: 102
 SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
LENGTH: 119
 APPLICANT: The UAB Research Foundation APPLICANT: Zhou, Tong APPLICANT: Ichikawa, Kimihisa
 APPLICANT: BUCHSHAUM, DONALD J.

TITLE OF INVENTIONS COMMENTIONS OF ANTIBODIES SELECTIVE FOR A TUMOS NECESISS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
FILE REFERENCE: 21085.002016
 CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
 APPLICANT:
 TYPE: PRI
ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687Ale = OTHER INFORMATION: Synthetic Construct
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932Ale = Synth
 ORGANISM: artificial sequence
 FEATURE:
 119 S 119
 121 $ 121
 61
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSEDYWGQGTTLTVS 120
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCARRGDSMI - - TTDYWGQGTTLTVS 118
 EVMLVESGGGLVKFGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY 60
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 LoBuglio, Albert S.
Buchsbaum, Donald J
 Koopman,
 nur
 William
 84.8%;
84.8%;
Score 545; DB 12;
Pred. No. 3.2e-43;
 Score 545; DB 12;
Pred. No. 3.2e-43;
 Mismatches
 Length 119;
 Length 119
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RESULT 8
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Publication No. US20030133932A1
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APPLICANT: The Unb Research Foundation
 ; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637Ale \approx US-10-286-132A-61
 US-10-286-132A-61
 SOFTWARE: P
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 Query Match
Best Local :
 Sequence 61, Application US/10286132A
Publication No. US20030198637A1
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 CURRENT PAPLICATION NUMBER: US/10/286,132A
CURRENT FILING DATE: 200-01-22
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PRIOR PAPLICATION NUMBER: US 60/346,402
PRIOR PAPLICATION NUMBER: ECT/US01/14151
PRIOR PAPLICATION NUMBER: ECT/US01/14151
PRIOR PAPLICATION NUMBER: 050-050
PRIOR PAPLICATION NUMBER: US 60/201,344
WHOMER FILING DATE: 200-05-02
 MPELICANT: Zhou, Tong
APELICANT: Kinhelly, Robert P.
APELICANT: Kinhelly, Robert P.
APELICANT: Koopman; William J.
APELICANT: Koopman; William J.
APELICANT: Moughain, Donald J.
APELICANT: MOUGhain, Moug
 Matches
 APPLICANT:
 APPLICANT
 APPLICANT:
 NUMBER OF SEQ ID NOS: 102
 TYPE: PRT ORGANISM: artificial sequence
 FEATURE:
 LENGTH: 119
 Local Similarity 87.
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 121 $ 121
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 119 S 119
 121 S 121
 61 PDSVRGRFTISRDNAXNTLYLQMSSLKSBDTAMYYCTRDGGHGYGSSFDYMGQGTTLTVS
 61
 61
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 1 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTESTYINSWVRQTPEKRLEWVATISSGGSYTYY
Zhou, Tong
Ichikawa, Kimihisa
Kimberly, Robert P.
Koopman, William J.
 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY
 PatentIn version 3.0
 BVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
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 PDSVRGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 84.8%;
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 Score 545; DB 12;
Pred. No. 3.2e-43;
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 Length 119;
 Indels
 Indels
 2,
 2;
 Gaps
 120
 60
 60
 60
 60
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```
APPLICAME. BUCINGSON, DORALG J.

TITLE DO INVENTION. COMENNATIONS OF ANTHODIES SELECTIVE FOR A TUNOR NECROSIS

TITLE DO INVENTION. FACTOR-SELATED AFORTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER

TITLE OF INVENTION. AGENTS

FULL REFERENCE: 21005-001-0206

CURRENT PAPLICATION MUMBER: US/10/281,479A

CURRENT PELLATION MUMBER: 05/240,402

FRIOR APPLICATION MUMBER: 05/344,402

FRIOR APPLICATION MUMBER: 05/344,40
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 US-10-286-132A-23; Sequence 23, Application US/10286132A; Publication No. US20030198637A1
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 ; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-23
 Query Match
Best Local Similarity
Matches 106; Conserv
 GENERAL INFORMATION
 SEQ ID NO 23
 APPLICANT: Zhou, Toog
APPLICANT: Khahelly. Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Koopman, William J.
APPLICANT: Koopman, William J.
APPLICANT: Benchsamn, Donald J.
APPLICANTON: MURER: PROPERTY OF A TUMOR NECESTREE PROPERTY PILLAGE AND SOUTH J.
APPLICANTON NUMBER: US 60/346, 402
ARIOR APPLICANTON MURER: PCT/MSO1/14451
ARIOR APPLICANTON MURER: US 60/201, 344
BRIOR FILMS DATE: 2001-05-02
BRIOR APPLICANTON MURER: US 60/201, 344
 SOFTWARE: PatentIn version 3.0
 PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
 TYPE: PRT
ORGANISM: artificial sequence
 FEATURE:
 ORGANISM: artificial sequence
 LENGTH: 462
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637Ale = Synthe
 LENGTY: 462
 138 S 138
 121 S 121
 106; Conservative
 80 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMI--TTDYWGQGTTLTVS 137
 61 PDSVRGRETISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 20 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKKLEWVATISSGGSYTYY 60
 LoBuglio, Albert S.
 84.8%;
 Score 545; DB 12; Length 462;
Pred. No. 1.4e-42;
 Mismatches
 Indels
 2;
 Gaps
 79
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y Sequence 63, Application Us/9144896
Patent No. USS/0201551401/9144896
Patent No. USS/02015514149
GENERAL INFORMATION:
APPLICANT: AMERICANT SHORT SHO
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 US-09-144-886-63
 US-10-275-180A-23
 US-10-275-180A-23
 US-10-286-132A-23
 GERSEAL IMPORMATION
APPLICANT: ED UMA Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Chou, Tong
APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Robert P.
APPLICANT: Koppman, William J.
TITLE OF INVENTION: AN ANTIBOD SELECTIVE FOR A TUNOR NECROSIS PACTOR-RELATED
TITLE OF INVENTION: AN ANTIBOD INVENTION OF AND USES THEREOF
FILE REPERENCE: 21065.002915
CURRENT APPLICATION NOBER: US/10/275,180A
 SEQ ID NO 23
 Best Local Similarity
Matches 106; Conserv
 Matches 106; Conservative
 Query Match
 Sequence 23, Application US/10275180A
Publication No. US20030190687A1
 CURRENT FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
 OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e = OTHER INFORMATION: Synthetic Construct
 FEATURE:
 TYPE: PRT
ORGANISM: Artificial Sequence
 LENGTH: 464
 Local Similarity
 138 S 138
 121 $ 121
 138 & 138
 121 S 121
 80
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 80
 20
 20 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
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 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
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 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCARRGDSMI--TTDYWGQGTTLTVS
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 Conservative
 84.8%;
87.6%;
 84.8%;
 Score 545; DB 12;
Pred. No. 1.4e-42;
4; Mismatches 9;
 Score 545; DB 12;
Pred. No. 1.4e-42;
4; Mismatches 9
 Length 464;
 Length 462
 Indels
 2;
 2:
 60
 60
 79
 137
 79
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CURRENT APPLICATION NUMBER: US/09/144,886

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RESULT 13
US-09-423-800-46
; Sequence 46, Application US/09423800
; Patent No. US20020165363A1
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 US-09-144-886-62
 US-09-144-886-62
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 US-09-144-886-63
 Sequence 62, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
 SEQ ID NO 62
 Query Match 82.8
Best Local Similarity 84.3
Matches 102; Conservative
 Matches 101; Conservative
 Best Local Similarity
 Query Match
 SEQ ID NO 63
 APPLICANT: Marks, James D.
APPLICANT: Marchadrier, Peter
ITITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
ITITLE OF INVENTION: Devolitum Neurocoxins
FILE REFERENCE: 100. NOMERS: US/09/144,886
CURRENT APPLICATION NOMERS: US/09/144,886
CURRENT FILING DATE: 1398-08-31
UNDERC OF SRQ ID NOS: 98
00/THARE: PARCHAIN VM. 7.9
 CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN VET. 2.0
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: C39 region VH epitope 2
 OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: C25 region VH epitope 2
 FEATURE:
 ORGANISM: Artificial Sequence
 ENGTH: 118
 118 S 118
 121 S 121
 118 $ 118
 121 S 121
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 61 PDSVRGRETISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 61
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 QVQLQESGGSVKFGGSLKLSCAASGFTFSDYYMSWVRQTPEKRLEWVATISDGGSYTYY 60
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 EVQLVESGGGLVXEGGSLXLSCAASGETFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 81.9%; Score 526.5; DB 10;
83.5%; Pred. No. 1.6e-41;
ktive 5; Mismatches 12;
 82.8%; Score 532.5; DB 10;
84.3%; Pred. No. 4.6e-42;
tive 6; Mismatches 10;
 DB 10;
 DB 10;
 Indels
 Indels
 Length
 Length 118;
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 Gaps
 Gaps
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1 BVQLVESGGDLVXPGGSLKLSCAASGFTFSSYGMSWIRQTPDKRLEWVATISSGGSYTYY

60

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CURRENT APPLICATION INDESE: US/13/37,981
CURRENT FILTURE DATE: 2003-01-08
PRIOR FALLANTON INDESE: ECT/PD89/02116
PRIOR PELICATION INDESE: ECT/PD89/02116
PRIOR PELICATION INDESE: LP 125505/1997
PRIOR PELICATION INDESE: JP 194445/1997
PRIOR PELICATION DATE: 13997-07-18
PRIOR PELICATION DATE: 13997-07-18
PRIOR PELICATION DATE: 13997-07-18
PRIOR PELICATION DATE: 13997-07-18
PRIOR PELICATION INDESE: JP 194445/1997
PRIOR PELICATION DATE: 13997-07-18
PRIOR PE
 US-10-337-981-46
 US-10-337-981-46
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 APLICANT: ISHII, KIMLE
TITLE OF INVENTION CACHEXA REMEDY
FILE REFERENCE. 04853-0036
CURRENT PILLING INTE. 1999-11.12
ERICE APPLICATION UNDER: US/09/423,800
CURRENT PILLING INTE. 1999-11.12
ERICE APPLICATION UNDER: CT 12505/1997
ERICE APPLICATION UNDER: CT 125445/1997
ERICE APPLICATION UNDER: CT 124445/1997
ERICE ERILING INTE: 197-07-18
ENUMER: CT 580_ID NOS: 87
ENUMER: ENEGATION UNC. 2.1
 US-09-423-800-46
 GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: TSUNENAR
 Matches 101; Conservative
 Query Match
Best Local Similarity
 Sequence 46, Application US/10337981
Publication No. US20030138424A1
 SEQ ID NO 46
LENGTH: 118
 Matches
 Query Match
 APPLICANT: ISHII, KIMIE
TITLE OF INVENTION: CACHEXIA REMEDY
FILE REPERENCE: 04853-0036
 APPLICANT:
APPLICANT:
 GENERAL INFORMATION:
 ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
 TYPE: PRT
 Local Similarity
 121 S 121
 118 A 118
 61 PDSVKGRETISRDNAKNTLYLOMSSLKSEDTAMEYCARQTTMTY---FAYWGQGTLVTVS
 61
 101;
1 BVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 EVQLVESGGDLVKPGSSLKLSCNASGFTFSSYGMSWIRQTPDKKLEWVANISSGGSYTYY
 PDSVRGRETISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSEDYWGQGTTLTVS 120
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 TSUNENARI,
 SATO, KOH
 TSUNENARI, TOSHIAK
 Conservative
 81.4%;
 81.4%;
 TOSHIAKI
 7; Mismatches
 Pred. No. 3.1e-41;
 7; Mismatches
 Score 523.5; DB 1
Pred. No. 3.1e-41;
 DB 10; Length 118;
 10;
 Indels
 Indels
 Length 118;
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 Gaps
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Search completed: November 7, 2003, 08:16:53 Job time: 107.138 secs
 Ouery Match 81.4%; Score 53.5; DB 15; Length 118; Best Local Similarity 83.5%; Pred. Mo. 3.1e-41; Matches 10; Conservative 7; Mismatches 10; Indels 3;
 118 A 118
 118 A 118
 121 S 121
 121 S 121
 61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMFYCARQTTMTY---FAYMGQGTLVTVS 117
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 1 BYOLVESGGGLYKFGGSLKLSCAASGFTPSTYTISHVRQTPEKRLEWYATISGGSYTYY 60
 10; Indels 3; Gaps
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compagen Ltd.
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OM protein -
 protein search, using sw model
November 7, 2003, 07:21:18 Search time 17.7704 Seconds (without alignments) 288.098 Willion cell updatos/sec
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| Scoring table: BLOSUM62             | Perfect score: 643                                                          |
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| BLOSUM62<br>Gapop 10.0 , Gapext 0.5 | US-09-661-992B-84_COPY_1_121 1 EVQLVESGGGLVKPGGSLKLHGYGSSFDYWGQGTTLTVSS 121 |

Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: 328/1/ seqs, 42310858 residues 328717

Post-processing: Minimum Match 0% Maximum Match 100%

Database Issued\_patents\_A1:
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// G972\_6/pscdate/l/lias/68\_COMB.pep:\*
// G972\_6/pscdate/l/lias/backfiles/pep:\*
// G972\_6/pscdate/l/lias/backfiles/pep:\* Listing first 45 summaries

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| Result NO. | SCOTE 531.52 531.52 531.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551.52 551 | Queaty Qu |                   | BQ 4 6 4 4 4 4 7 8 8 4 8 8 7 8 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9 | US-01-44-597-13 US-01-44-597-13 US-01-44-597-13 US-01-74-759-14 US-01-75-744-1 | Description  Sequence 1  Sequence 2  Sequence 3  Sequence 3  Sequence 3  Sequence 1  Sequence 2  Sequence 2  Sequence 4  Sequence 4  Sequence 4  Sequence 4  Sequence 1  Sequence 1  Sequence 1  Sequence 2  Sequence 3  Sequence 4  Sequence 4  Sequence 1 |
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| 4001       | 542<br>531.5<br>526                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 84.3<br>82.7<br>79.9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 123<br>135<br>119 | 4.04                                                           | US-09-344-587<br>US-08-579-378<br>US-08-875-674                                                                                                                                                                                                                                                                                                                             | 1-16                                                                                                                                                                                                                                                        |
| υ a        | 510.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 79.4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 123               | <u>ش</u> س                                                     | US-08-435-516<br>US-08-356-272                                                                                                                                                                                                                                                                                                                                              | ٺ ٺ                                                                                                                                                                                                                                                         |
| · თ        | 507                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 78.8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 247               | ы                                                              | PCT-US94-0765                                                                                                                                                                                                                                                                                                                                                               | 9-2                                                                                                                                                                                                                                                         |
| · •        | 505.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 78.6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 159               | ٠ <b>د</b>                                                     | US-08-653-402                                                                                                                                                                                                                                                                                                                                                               | 8-2                                                                                                                                                                                                                                                         |
| wω         | 505                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 78.5<br>78.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 119<br>239        | 4 0                                                            | US-08-875-674<br>US-08-553-497                                                                                                                                                                                                                                                                                                                                              | A-18                                                                                                                                                                                                                                                        |
| 10         | 503.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 78.3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 118               | s                                                              | PCT-US93-0843                                                                                                                                                                                                                                                                                                                                                               | 5-10                                                                                                                                                                                                                                                        |
| 12         | 502.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 78.2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 121               | ω <u>μ</u>                                                     | US-08-339-582                                                                                                                                                                                                                                                                                                                                                               | 2                                                                                                                                                                                                                                                           |
| 13         | 502.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 78.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 443               | IJ                                                             | PCT-US96-1315                                                                                                                                                                                                                                                                                                                                                               | 2-4                                                                                                                                                                                                                                                         |
| 14         | 500.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 77.8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 118               | μ                                                              | US-08-326-362                                                                                                                                                                                                                                                                                                                                                               | -2                                                                                                                                                                                                                                                          |
| 15         | 496                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 77.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 138               | N                                                              | US-08-379-057                                                                                                                                                                                                                                                                                                                                                               | -14                                                                                                                                                                                                                                                         |
| 16         | 496                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 77.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 158               | Ŋ                                                              | US-08-653-402                                                                                                                                                                                                                                                                                                                                                               | 8-6                                                                                                                                                                                                                                                         |
| 17         | 496                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 77.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 158               | N                                                              | US-08-653-402B-10                                                                                                                                                                                                                                                                                                                                                           | B-10                                                                                                                                                                                                                                                        |
| 18         | 400                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 77.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 117               | w                                                              | US-08-752-693A-                                                                                                                                                                                                                                                                                                                                                             | 3                                                                                                                                                                                                                                                           |
| 20         | 4 4 9 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 77.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 125               | y H                                                            | US-08-331-398A-65                                                                                                                                                                                                                                                                                                                                                           | 2 65                                                                                                                                                                                                                                                        |
| 21         | 495                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 77.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 125               | N                                                              | US-08-759-804A-64                                                                                                                                                                                                                                                                                                                                                           | A-64                                                                                                                                                                                                                                                        |
| 22         | 495                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 77.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 136               | 4                                                              | US-08-976-183A-                                                                                                                                                                                                                                                                                                                                                             | A-31                                                                                                                                                                                                                                                        |
| 23         | 495                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 77.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 136               | 4.                                                             | US-08-976-183A-32                                                                                                                                                                                                                                                                                                                                                           | A-32                                                                                                                                                                                                                                                        |
| 4 6        | 495                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 77.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 136               | 4.                                                             | US-08-976-183A-33                                                                                                                                                                                                                                                                                                                                                           | A-33                                                                                                                                                                                                                                                        |
| 3 6        | 495                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 77.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 3 H               | 4 C                                                            | US-08-976-183A-34                                                                                                                                                                                                                                                                                                                                                           | A-34                                                                                                                                                                                                                                                        |
| 27         | 495                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 77.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 245               | 4                                                              | US-09-069-821-                                                                                                                                                                                                                                                                                                                                                              | 5                                                                                                                                                                                                                                                           |
|            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                   | ,                                                              |                                                                                                                                                                                                                                                                                                                                                                             | •                                                                                                                                                                                                                                                           |

US-08-579-378A-16

Sequence 16, Application US/08579378A
Ratent No. 6210671
GENERRAL INFORMATION:
APPLICANT: Co. Man Sung
TITLE OF INVENTION: Humanized Ant
TITLE OF INVENTION: L-Selectin

NUMBER OF SEQUENCES:

L-Selectin 20

Humanized Antibodies Reactive with

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| 76.8 1107 4 US-09-339-922A-6 76.8 140 3 US-08-836-561-23 76.8 1217 5 US-08-836-561-23 76.8 217 5 US-08-836-761-23 76.8 217 5 US-08-262-789-16 76.8 237 2 US-08-262-789-16 76.8 237 2 US-08-262-789-18 76.8 241 2 US-08-262-789-18 76.8 241 2 US-08-262-789-18 76.9 264 4 US-08-262-789-18 76.7 119 2 US-08-462-798-16 76.7 119 2 US-08-462-798-16 76.7 119 2 US-08-462-798-16 76.7 119 2 US-08-481-798-16 76.7 119 2 US-08-481-798-17 76.1 120 5 US-08-481-508-17 76.1 120 5 US-08-262-877-78 76.1 120 5 US-08-262-877-78 76.1 121 US-08-262-877-78 76.1 122 5 US-08-262-877-78 76.1 122 5 US-08-262-877-78 76.1 122 5 US-08-482-184-502 76.1 122 5 US-08-482-184-502 76.1 122 5 US-08-482-184-502 76.1 122 5 US-08-482-184-502                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 117 4 US-09-339-922A-6 110 3 US-09-339-922A-3 110 3 US-09-339-922A-3 110 4 US-09-341-122-23 Sequence 23, 1217 5 PCT-1939-14105-29 Sequence 23, 1217 5 PCT-1939-14105-29 Sequence 16, 1217 5 US-08-224-591-16 Sequence 16, 1217 10 US-08-224-591-18 Sequence 16, 1218 10 US-08-225-291-18 Sequence 16, 1219 10 US-08-225-291-18 Sequence 16, 1219 10 US-08-236-279-28 Sequence 16, 1219 10 US-08-338-378-38 Sequence 16, 1219 10 US-08-438-3191-16 Sequence 16, 1219 10 US-08-438-391-16 Sequence 16, 1219 10 US-08-238-3770-59 1216 10 US-08-238-3770-59 1216 10 US-08-238-38-39 122                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 489.5             | Ü                 |                   |                   |                  | 93               |      |                  | 5                 |                  |                  |                  |                  |                  |                   |                  |                  |                  |
| A W A D G G G G G G G G G G G G G G G G G G                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 4 US-09-319-922A-6 sequence 6, 3 US-08-316-512.3 sequence 2, 3 US-08-316-512.23 sequence 2, 3 E-CT-US94-141.12-23 sequence 2, 3 E-CT-US94-141.05-19 sequence 2, 3 E-CT-US94-141.05-19 sequence 5, 3 US-08-216-799-16 sequence 1, 2 US-08-216-799-18 sequence 1, 3 E-CT-US94-141.09-16 sequence 2, 3 E-CT-US94-141-199-16 sequence 2, 3 E-CT-US94-196-11 sequence 1, 3 US-08-415-1199-16 sequence 3, 1 US-08-415-1199-16 sequence 3, 1 US-08-415-1199-16 sequence 5, 7 E-CT-US94-08435-42 sequence 5, 7 E-CT-US94-08435-43 sequence 6, 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 76.1              | 76.1              | 10.2              | 2 6               | 76.4             | 76.7             | 76.7 | 76.7             | 76.7              | 76.8             | 76.8             | 76.8             | 76.8             | 76.8             | 76.8              | 76.8             | 76.8             | 76.8             |
| 4 (03-09-039-9922A-6 3 (03-08-05-651-2) 3 (03-08-05-651-2) 4 (03-09-034-110-59 5 (07-1093-110-59 2 (03-08-204-591-16 2 (03-08-204-591-16 2 (03-08-204-799-16 2 (03-08-204-799-16 3 (03-08-204-799-16 4 (03-09-16)-799-16 2 (03-08-407-199-16 2 (03-08-407-796-16 4 (03-09-16)-796-11 4 (03-09-16)-796-11 4 (03-09-16)-796-11 5 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 2 (03-08-452-1470-57) 3 (03-08-452-1470-57) 3 (03-08-452-1470-57) 3 (03-08-452-1470-57) 3 (03-08-452-1470-57) 4 (03-08-452-1470-57) 4 (03-08-452-1470-57) 4 (03-08-452-1470-57) 4 (03-08-452-1470-57) 4 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452-1470-57) 5 (03-08-452- | 108-385-561.23 Sequence 6, 7 108-434-122-23 Sequence 23 7-1094-11102-23 Sequence 23 7-1094-11102-23 Sequence 24 1-108-282-191-16 Sequence 16, 7 1-1094-191-18 Sequence 16, 7 1-1094-191-191-191-191-191-191-191-191-191-1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 122               | 122               | 100               | 1 3 6             | 167              | 119              | 119  | 119              | 354               | 265              | 241              | 241              | 237              | 237              | 217               | 140              | 140              | 117              |
| US-09-339-922A-6 US-09-345-512-3 US-09-344-112-3 PCT-US94-14106-59 US-09-224-591-16 US-09-224-591-16 US-09-224-591-18 US-09-224-591-18 US-09-226-799-18 US-09-236-7312-8 US-09-2 | 108-385-561.23 Sequence 6, 709-439-922A-6 Sequence 23, 7-1094-1110-2-23 Sequence 23, 7-1094-1110-2-23 Sequence 23, 7-1094-1110-2-23 Sequence 24, 7-1094-1110-2-23 Sequence 25, 7-1094-1110-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Ŋ                 | S                 | 1 1               | ) <u> </u>        | 4                | N                | N    | N                | 4                 | 4,               | N                | N                | N                | N                | s                 | 4.               | w                | 4                |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 115571156668 THE STATE OF THE S | PCT-US93-08435-43 | PCT-US93-08435-12 | US-US-452-154A-57 | US-08-253-877C-57 | US-09-318-786-31 | US-08-484-508-16 | 90   | US-08-475-000-16 | US-09-393-627B-28 | US-09-420-592A-5 | US-08-926-789-18 | US-08-224-591-18 | US-08-926-789-16 | US-08-224-591-16 | PCT-US94-14106-59 | US-09-434-122-23 | US-08-836-561-23 | US-09-339-922A-6 |
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| mn 1 1 1 m u u u u u . a a u u a n n .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Appl              | App1              | Appl              | Appl              | App1             | App1             | Appl | App1             | App1              | Appli            | App1             | Appl             | Appl             | Appl             | Appl              | Appl             | App1             | Appli            |

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# ALIGNMENTS

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 ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-344-587-13
 RESULT 1
US-09-344-587-13
 APPLICANT: PRASE; Gerald
APPLICANT: MOBBANN, SABING
APPLICANT: MOBBANN, SABING
APPLICANT: HOBBANN, SABING
APPLICANT: LAUR HOMBANN, SABING
APPLICANT: LAUR, Helmut
APPLICANT: LAUR, Helmut
APPLICANT: LAUR, Helmut
APPLICANT: LAUR, Helmut
APPLICANTION: REDUCTION OF INTERPERENCE OF INMUNOASSAYS BY SUBSTANCES
ITILB MERG ANDERTON HOMBEN: MS/00/44, S07
CURRENT PLIAU DATE: 199-06-25
EARLIER APPLICATION NUMBER: MS 19828466.7
EARLIER PLIAUR DATE: 199-06-25
EARLIER PLIAUR DATE: 199-06-26
EARLIER PLIAUR DATE: 199-06-25
EARLIER PLIAUR DATE: 199-06-26
EARLIER PLIAUR D
 Sequence 13, Application US/09344587
Patent No. 6331402
GENERAL INFORMATION:
 Ouery Match 84.3%; Score 542; DB 4; Length 123;
Best Local Similarity 84.6%; Bred, No. 4.5e-59;
Matches 104; Conservative 5; Mismatches 12; Indels
121
 119 VSS 121
 61 PDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCARDKAYYGNYGDAMDYWGQGTSVT 120
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGH--GYGSSFDYWGQGTTLT
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
VSS 123
 EVQGVESGGGLVKPGGSLKLSCAASGFTFSDYYMYMVRQTPEKRLEMVATISDGGSYTYY
 2
 Gaps
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ORRESPONDENCE ADDRESS

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 US-08-875-674A-1
 US-08-579-378A-16
 Sequence 1, Application US/08875674A
Patent No. 6572857
 Matches
 GENERAL INFORMATION:
APPLICANT: MONTERO CASIMIRO, J.
APPLICANT: LOMBARDERO VALLADARE
APPLICANT: PREZ RODR GUEZ, R.
APPLICANT: SIERRA BL ZQUEZ, P.
 Query Match
Best Local Similarity
 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
 APPLICANT:
 MOLECULE TYPE: protein
 APPLICATION NUMBER: BP 95112895.8
FILIKE DATE: 17-AUG-1195
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 95114696.8
FILIKE DATE: 19-SBP-1395
ATTORNEY/AGENT IMPORMATION:
ANTER 1/ABPCHANTION:
 PRIOR APPLICATION DATA
APPLICATION UNUBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-BGC-1992
PRIOR APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-BGC-1992
PRIOR APPLICATION DATA: 1992
PRIOR A
 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEBLUM TYPER: Ploppy disk
COMPUTER: IBM FC COMPALLA
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTMANE: Retentin Release #1.0, Version #1.25
NUMBER OF SEQUENCES:
 TITLE OF INVENTION:
 TELEPHONE: 415-326-2400
 APPLICATION NUMBER: US/0 FILING DATE: 27-DEC-1995 CLASSIFICATION: 424
 TOPOLOGY:
 NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,50
REFERENCE/DOCKET NUMBER: 1
 COUNTRY:
 STREET: One Marketpy
CITY: San Francisco
 LENGTH:
 ADDRESSEE:
 135 S 135
 121 $ 121
 103;
 61 PDSVRGRFTISRDNAKWTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSPDYWGQGTTLTVS 120
 20 EVKLVESGGGLVKPGGSLKLACAASGFTFSTYAMSWVEQTPEKRLEWVASISTGGS-TYY 78
 1 EVQLVESGCGLVKPGGSLKLSCAASGFTPSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 94105
 PDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCARD----YDGYFDYWGQGTTLTVS 134
 amino acid
 California
 SE: Townsend and Townsend and Crew
One MarketPlaza, Steuart Tower, Suite 2000
 SIERRA BL ZQUEZ; P.
TORMO ERANO, B. R.
VENTION: Anti-CD6 monoclonal antibodies and their uses
 Conservative
 USA
 82.7%; Score 531.5; DB 3; Length 135;
85.1%; Pred. No. 6.4e-49;
ative 7; Mismatches 6; Indels 5
 US/08/579,378A
 37,505
 VALLADARES, J
 11823-002220
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 Gaps
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 RESULT 4
US-08-435-516-3
 밁
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 , Sequence 3, Application , Patent No. 6500931
 US-08-875-674A-1
 OTHER INFORMATION: Sequence corresponding to the variable region Patent No. 687384TON: Sequence corresponding to the variable region OTHER INFORMATION: of the heavy chain of the monoclonal antibody recognity OTHER INFORMATION: designated as sub-clone for tlA.
 Matches 105; Conservative
 Query Match
Best Local Similarity
 GENERAL INFORMATION:
 ZIF: 10583

COMPUTER READALS PORM:
MEDITM TYPE: Flogby disk 3.5'/ (1.4 MB).
COMPUTER: Compatible PC IBM (80486, 8 M Ram).
OPERATING SYSTEM. Windows 95.
SOFTMARE: Mord Perfect 5.0 for Mindows 95.
URRENT APPLICATION DATA:
URRENT APPLICATION DATA:
 ORGANISM: Mice Balb/C
INDIVIDUAL ISOLATE: ior tla
TISSUE TYPE: Murine hibridoma
IMMEDIATE SOURCE:
 FRAGMENT TYPE: -N Terminal fragment. ORIGINAL SOURCE:
 MOLECULE TYPE: P:
HYPOTHETICAL: NO
ANTI-SENSE: NO
 TITLE OF INVENTION:
 FEATURE:
 APPLICANT
 APPLICATION NUMBER: US/08
FILING DATE: 17-July-1997
 CLONE: Sub-clone for tlA
 TYPE: Amino acid.
STRANDEDNESS: Unknown.
 CLASSIFICATION: 530
 STATE: New York COUNTRY: U.S.A.
 IDENTIFICATION METHOD: Experimental.
OTHER INFORMATION: Sequence corresponding to the variable region
 TOPOLOGY: Unknown.
 LENGTH:
 CITY: Scarsdale
 ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.
 118 $8 119
 120 SS 121
 61 PDSVKGRFTISRDNVKNTLYLQMSSLRSEDTAMYYCARRDYDLDY-
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCT-RDGGHGYGSSFDYWGQGTTLTV 119
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 EVQLVESGGGLVKPGGSLKLSCAASGFKFSRYAMSWVRQTPEKRLEWVATISSGGSYIYY
 119 Amino acid residues
 One Chase Road
 Protein
 81.8%; Score 526; DB 4; Length 119; 86.1%; Pred. No. 2.1e-48;
 US/08435516
HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
 PCT/CU96/00004
 US/08/875,674A
 Mismatches
 11; Indels
 4.
 Gaps
 60
 117
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 US-08-356-272-3
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 В
 US-08-435-516-3
 Sequence 3, Application US/08356272
Patent No. 5766946
GENERAL IMFORMATION:
 Matches
 Query Match
Best Local Similarity
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
 COMPUTER READBAGE FORM:
MEDIUM TYPES: Floppy disk
COMPUTER: IBM PC Compatible
COMPATER: DAY COMPATIBLE
OPERATING SYSTEM: PC-DOS/M9-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/356,272
FILIKE DAYE: 1.5-DEC-1994/356,272
 APPLICANT: Cianfriglia Dr., Maurizio
TITLE OF ENVENTION: Monoclonal Antibodies to glycoprotein
NUMBER OF ENCENTES: 4
CORRESPONDENCE ADDRESS:
 MOLECULE TYPE: peptide FRAGMENT TYPE: internal
 SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
 COUNTRY: U.S. A. ZIP: 07936
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
 PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
 TITLE OF INVENTION:
 STREET: 59 Route 1
CLASSIFICATION:
 TYPE; amino acid
TOPOLOGY: linear
 ADDRESSEE:
 ADDRESSEE: Patent and Trademark Department, Sando:
 CLASSIFICATION: 424
 FILING DATE:
 120 S 120
 121 8 121
 61 PDSVKGRFTISRDNÁKNNLYLÓMSSLKSEDTAIYYCAR-GYYRYEGAMDYWGQGTSVTVS 119
 61 PDSVRGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYIMSWVRQTPEKRLEWVATISGGGSYTYY
 99;
 EVQLVESGGGLVKPGGSLRLSCVASGFIFSDNYMYWVRQTPEKRLEWVATISDGGSYTYY 60
 59 Route 10
 120 amino acids
 Conservative
 linear
 79.9%;
 IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
 US/08/435,516
 7; Mismatches
 Pred. No. 4.5e-47;
 DB 4;
 14; Indels
 Length 120;
 1;
 60
```

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 RESULT 6
PCT-US94-07659-2
 US-08-356-272-3
 Sequence 2, Application PC/TUS9407659 GENERAL INFORMATION:
 Matches 103; Conservative
 Query Match
Best Local Similarity
OMPUTER READABLE FORM.

MEDIUM TWEE, Floppy disk
COMPUTER: ITMN FC compatible
OMERATING SYSTEM: FC-DOS/MS-DOS
SOFTMARE: BACENTIN BA-BASE #1.0, V
APPLICATION BATA:
APPLICATION MATHER: FOT/US94/07659
 TELEX: 240867
INFORMATION FOR SEQ ID NO: 3:
 ARTOKNAL/A-
NAME: Battle, Carl m. 0,731
REGERENTATION NUMBER: 30,731
REFERENCE/DOCKET NUMBER: 110-(
TELECOMMUNICATION INFORMATION:
""": REPERENCE (201) 503-8177
 APPLICANT: Young, Peter APPLICANT: Gross, Mitchell APPLICANT: Jonak, Zdenka L. APPLICANT: Theisen, Timothy APPLICANT: Hule, Mark APPLICANT: Jackson, Jeffrey FRIEDONT: Jackson, Jackson, Jeffrey FRIEDONT: Jackson, Jackson
 CORRESPONDENCE ADDRESS:
 APPLICANT: Jackson, Jeffrey R.
TITLE OF INVENTION: Recombinant and Humanized I1-1 beta
TITLE OF INVENTION: Anthodies for Treatment of I1-1 Mediated Inflammatory
TITLE OF INVENTION: Disorders in Man
WINDOWN CO. 1975-1975
 NUMBER OF SEQUENCES:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PAPPLICATION NUMBER: WO PAPPLICATION INFORMATION:
 MOLECULE TYPE: protein
 SEQUENCE CHARACTERISTICS
 CLASSIFICATION: A61K
PRIOR APPLICATION DATA:
 ZIP: 19406-2799
 COUNTRY:
 CITY: King of Prussia
STATE: PA
 ADDRESSEE: SmithKline Beecham Corporation - Corp
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road
 TOPOLOGY:
 APPLICATION NUMBER: IT REFILING DATE: 17-JUN-1992
 CLASSIFICATION:
CLASSIFICATION:
 LENGTH:
 CLASSIFICATION:
 119 VSS 121
 120 VSS 122
 61 FPDSVKGRFTISRDNAKVTLYLQVSSLKSEDTAMYYCARPAEFRGY-SWFAYWGQGTTVT 119
 60 YPDSVRGRETISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGG-HGYGSSFDYWGQGTTLT 118
 f: 123 amino acids
amino acid
 USA
 linear
 G01N33/574
G01N33/577
 79.4%; Score 510.5; DB 1; 83.7%; Pred. No. 9.6e-47;
 A61K39/295
 C12N5/20
 Disorders in Man
21
 PCT/US94/07659
 WO PCT/EP93/01533
 IT RM92A000457
 6; Mismatches
 118-8040
 Version #1.25
 11,
 Indels
 Length 123;
 u
 Gaps
```

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Ś
 PCT-US94-07659-2
 Sequence 2, Application US/08653402B Patent No. 5969107
 Query Match 78.8%;
Best Local Similarity 82.0%;
 Matches 100; Conservative
 -08-653-402B-2
 GENERAL INFORMATION:
 TELEFAX: (610) 270-5090 INFORMATION FOR SEQ ID NO: :
 MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-POS/NS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
 APELICATION NUMBER: EP 95107967.2
FILING DATE: 26-MAY-195
ATTORNEY/AGENT IMPORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 17
 APPLICATION NUMBER: US/08/653,402B
FILING DATE: 24-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 TITLE OF INVENTION: immune response against epidermal growth factor receptor.
 APPLICANT: CARCELLER, Ana APPLICANT: ROSELL, Elisabet APPLICANT: GOMEZ, Alicia APPLICANT: ADEN, Jaume
 MOLECULE TYPE: protein
 REFERENCE/DOCKET NUMBER: P50171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5024
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
 CORRESPONDENCE ADDRESS:
ELECOMMUNICATION INFORMATION:
 NUMBER OF SEQUENCES:
 APPLICANT:
 ZIP: 22201
 COUNTRY:
 CITY: Arlington
 ADDRESSEE: Millen, White, Zelano & Branigan, P.C STREET: 2200 Clarendon Boulevard, Suite 1400
 NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
 CLASSIFICATION
 137 SS 138
 120 SS 121
 80 PDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYHCARGGVRRGY---FDVWGAGTTVTV 136
 61
 20 EVHLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTPEKRLDWVAYISSGGGGTYY 79
 1 EVQLVESGGGLVXPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 Virginia
Y: U.S.A.
 PDSVRGRFTISRDNAKOTLYLQMSSLKSEDTAMYYCTRDG-GHGYGSSFDYWGQGTTLTV 119
 PIULATS, Jaume
 linear
 US 08/090,534
 MERCK 1781
 6; Mismatches
 Score 507; DB 5;
Pred. No. 5.3e-46;
 Version #1.30 (EPO
 DB 5; Length 247;
 12;
 Indels
 4
 Gaps
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 RESULT 8
US-08-875-674A-3
 8
 US-08-653-402B-2
 APPLICATION NUMBER: PCT/CU96/00
PILINEO DATE: 18-NOV-1966
APTORNEY/AGRAY IMPORMATION:
NAME: HERRY A MASTALLO, JR.
PREGISTRATION NUMBER: LO, 310
PREFERENCE/DOCKET NUMBER: LO, 310
PREFERENCE/DOCKET NUMBER: LO, 310
PREGISTRATION IMPORMATION:
TELEPRAN (914)-723-4301
IMPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 Patent No.
 Query Match
Best Local Similarity
 Matches
 GENERAL INFORMATION:
 TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 159 amino acid
TOPOLOGY: UP
MOLECULE TYPE:
HYPOTHETICAL:
 COMPUTER READMELE FORM:
MEDIUM TYRE: Eloppy disk 3.5' (1.4 MB).
COMPUTER: Compatible Po IBM (80486, 8 M Ram).
OPERATING SESTEM: Mindows 95.
SOPTHAIRS: MODIT Derifect 5.0 for Windows 95.
CUREENT APPLICATION DATA:
APPLICATION MUMBER: US/08/875.674A
PTLIANG DATE: MIT-DIMY-1958.
 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
 APPLICANT: MONTERO CASIMIRO, J.
APPLICANT: LOMBARDERO VALLADARE
APPLICANT: PREZ RODR GUEZ, R.
 MOLECULE TYPE: protein
 CORRESPONDENCE ADDRESS:
 APPLICANT: SIERRA
APPLICANT: TORMO
TITLE OF INVENTION:
 NUMBER OF SEQUENCES:
 STREET:
 TYPE: amino acid
TOPOLOGY: linear
 STRANDEDNESS:
 COUNTRY:
 STATE:
 ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C
 TELEPHONE:
 LENGTH:
 138 GTSVTVSS 145
 114
 80 PDSLKGRFTISRDNAKONLYLQMSSLKSEDTAMYFCARDGAARTSSQVYYYG--MDYWGQ 137
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGG-----HGYGSSFDYWGQ 113
 20 BVQLVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWFRQHPGKRLEWVATISDAGTYTYY
 99;
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 10583
 , Application US/08875674A
6572857
 Scarsdale
 Amino acid.
EDNESS: Unknown
 GITLIVSS 121
 New York
 119 Amino acid residues.
 One Chase Road
 159 amino acida
 Conservative
 Unknown.
 703-243-6333
 Protein
 BRAVO, B. R.
V: Anti-CD6 monoclonal antibodies and their uses
 BL ZQUEZ,
 78.6%;
 PCT/CU96/00004
 VALLADARES,
 N
 Score 505.5; DB 2;
Pred. No. 4.4e-46;
 Mismatches
 Length 159;
 Indels
 9;
 Gaps
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US-08-553-497A-18
 S
 US-08-875-674A-3
 Patent No. 6572857
OTHER INFORMATION:
OTHER INFORMATION:
 Sequence 18,
 Matches 101;
 Query Match
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9
 APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
 tent No.
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: ANTI-EGER SINGLE-CHAIN FVS AND ANTI-EGER
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
 APPLICANT:
 APPLICANT:
 APPLICANT:
 ORIGINAL SOURCE:
TISSUE TYPE: Animal cells
CELL LINE: NSO " SP 2/0 "
 IMMEDIATE SOURCE:
 FRAGMENT TYPE
 ANTI-SENSE:
 STREET:
 ADDRESSEE:
 IDENTIFICATION METHOD:
OTHER INFORMATION: Seq
 Local Similarity
 CLONE: Sub-clone for tlA
 118 SS 119
 120 SS 121
 INFORMATION:
 61
 22201
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTESTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 ARLINGTON
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va
 5844093
 PDSVKGRPTISRDNVKNTLYLQMSSLRSEDTAMYYCARRDYDLDY---PDSWGQGTLVTV 117
 PDSVRGRFTISRDNAKNTLYLOWSSLKSEDTAMYYCT-RDGGHGYGSSFDYWGQGTTLTV 119
 EVQLVESGGGLVKFGGSLKLSCAASGFKFSRYAMSWVRQAFGKRLEWVATI6SGGSYIYY 60
 Application US/08553497A
 MITJANS, FRANSESC
ROSELL, ELISABET
BLASCO, FRANCESC
PIULATS, JAUME
 2: MILLEN, WHITE, ZELANO & BRANIGAN, P.C
2200 CLARENDON BLVD. SUITE 1400
 ANSELL, KEITH H.
GUSSOW, DETLEF
ADAN, JAUME
 Conservative
 BENDIG, MARY M.
 No

 N Terminal fragment.

 78.5%;
 EP 94118970.6
 variant of sub-clone ior tlA recognizing human CD6, particul to the variable region of its heavy chain.
 DD: By similarity with known sequence.
Sequence corresponding to the humanized

 Mismatches 14; Indels

 Score 505; DB 4; Length 119;
Pred. No. 3.5e-46;
 4,
 RESULT 10
PCT-US93-08435-10
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 US-08-553-497A-18
 Matches
 REFERENCE/DOCKET NUMBER: SETELSCOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEPAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 10:
 Query Match
 GENERAL INFORMATION
 TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
 MEDIUM TYPE: Floppy
 APPLICANT:
 APPLICANT: the Army
TITLE OF INVENTION:
 APPLICANT:
 APPLICANT:
 MOLECULE TYPE: protein
 SEQUENCE CHARACTERISTICS
 ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
 CLASSIFICATION:
 FILING DATE
 COUNTRY:
 Local Similarity 82.0
 LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
 TELEPHONE: 703-243-6333
 FILING DATE:
 119 8 119
 121 $ 121
 Spring House
3: PA
fRY: USA
 19477
 the Navy
 02-DEC-1994
 78.5%;
82.6%;
 18:
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ARTOENEY, AGRET INFORMATION:

NAME: HAME-YLING, DIANN.

REGISTRATION INFORMATION:

REGISTRATION INFORMATION:

TELEPONET: 703-243-6410

INFORMATION: 703-243-6410

REGISTA: 23 mains acids

TOPOLOGY, AND ACID: 703-243-10

REGISTA: 23 mains acids

TOPOLOGY, AND ACID: 703-243-10

REGISTA: 23 mains acids

TOPOLOGY, AND ACID: 703-243-10

INFORMATION: 703-243-10

INFORMATION: 703-243-10

INFORMATION: 703-243-10

REGISTA: 104

INFORMATION: 703-243-10

REGISTA: 104

REPLICANT: SMILKNI INE Bescham. Corporation

APPLICANT: SMILKNI INE Bescham. Corporation

APPLICANT: SMILKNI INE Bescham. Corporation
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INGS-0445-10

INGS-0445-10

REPLICAM: Shrinkline Beecham, Corporation

APPLICAM: IntroRATINI

APPLICAM: Into Navy

APPLICAM: Into Navy

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 US-08-339-582-2
 RESULT 11
US-08-339-582-2
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 PCT-US93-08435-10
 Patent No. 5558852
 Matches 101; Conservative
 Query Match
Best Local (
 Query Match
Best Local :
 Matches
 TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
 GENERAL INFORMATION:
 LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
 APPLICANT: Bigner, Darell D.
APPLICANT: Zalutsky, Michael
APPLICANT: Carrel, Stefan
TITLE OF INVENTION: METHOD O
NUMBER OF SEQUENCES: 4
 SEQUENCE CHARACTERISTICS
 NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-89
TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
BYLING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 CORRESPONDENCE ADDRESS
 MOLECULE TYPE: protein
 TELEPHONE: 919-73175
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Match 78.3%; Score 503.5; DB Local Similarity 80.5%; Pred. No. 5e-46;
 CLASSIFICATION: 424
 FILING DATE:
 APPLICATION NUMBER:
 ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Drawer 34009
 TOPOLOGY: linear
61 PDSVRGRFTISRDNAKWTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 61 TGRFTISRDNAKWTLYLEMSSLRSEDTAMYYCASLIYYGYDGYAMDYWGQGTSVTVSS 118
 65 RGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGY-GSSFDYWGQGTTLTVSS 121
 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 28234
 1 LESGGGIVKPGGSLKISCAASGFTFSSYAMSWVRQSPEKRLEWVAEISDGGSYTYYPDTV 60
 5 VESGGGIVKPGGSIKISCAASGFTFSTYTMSWVRQTPEKRIEWVATISSGGSYTYYPDSV 64
 95; Conservative
 Similarity
 Charlotte
 : 118 amino acids
amino acid
 EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKSLEWVASISSGDS-TYY 63
 No. 5558852th Carolina
 919-420-2200
 78.2%;
 METHOD OF TREATMENT
 Michael R
 US/08/339,582
 11; Mismatches
 Score 503; DB 1;
Pred. No. 5.8e-46;
6; Mismatches 10
 , S 8d
 11,
 10; Indels
 Length 121;
 Length 118;
 Indels
 4.
 ļ,
 Gaps
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 S
 US-08-579-378A-20
 RESULT 12
US-08-579-378A-20
 밁
 S
 밁
 Patent No. 6210671
GENERAL INFORMATION:
APPLICANT: Co, Ma
 Sequence 20, Application US/08579378A
Patent No. 6210671
 Matches
 Query Match
 IELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
 FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATE: EP 95112895.8
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATE: EP 95114696.8
APPLICATION NUMBER: EP 95114696.8
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/160,074
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
 STREET: One space CITY: San Francisco STATE: California
 NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One MarketPlaza, Steuart Tower, Suite 2000
 MOLECULE TYPE: protein
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
 FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA: US 07/983,946
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized.
TITLE OF INVENTION: L-Selectin
 Local Similarity
 TYPE: amino acid
TOPOLOGY: linear
 NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220
 TELEPHONE:
 FILING DATE:
 FILING DATE: 27-DEC-1995
 APPLICATION NUMBER:
 COUNTRY:
121 $ 121
 121 S 121
 121 $ 121
 79
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 20
 64 PDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCARGGWLHY---FDYGGQGTTLTVS 120
 1 EVQLVBSQGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 97;
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 135 amino acids
 Conservative
 PatentIn Release #1.0, Version #1.25
 30-NOV-1993
 78.1%; Score 502.5; DB 3
80.2%; Pred. No. 7.5e-46;
 Humanized Antibodies Reactive with
 US/08/579,378A
 20
 10; Mismatches
 DB 3;
 Length 135;
 Indels
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 Gaps
 78
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 US-08-326-362-2
 RESULT 14
 8
 Sequence 2, Application US/08326362
Patent No. 5730981
GENERAL INFORMATION:
 PCT-US96-13152-4
 PCT-US96-13152-4
 Matches
 Query Match
 Sequence 4, Applicati
GENERAL INFORMATION:
 APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-59
APPLICATION NUMBER: EP 95 112 895.8
APPLICATION NUMBER: EP 95 114 895.9
APPLICATION NUMBER: EP 95 114 969.9
APPLICATION THE 19-Sep-95
APPLICATION THE PERSON OF THE 19-SEP-95
APPLICATION THE PERSON OF THE 19-SEP-95
APPLICATION THE 19-SEP-95
APPLICATIO
 TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
APPLICANT:
 TOPOLOGY: linear
MOLECULE TYPE: protein
 REFERENCE/DOCKET NUMBER: BO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
 SOFTWARE: ASCII
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
 PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 APPLICANT: Martin, Ulrich,
TITLE OF INVENTION: Anti-so
 NUMBER OF SEQUENCES:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OFFWARE: ASCII
 Local Similarity
 TYPE: amino acid
 STRANDEDNESS
 LENGTH:
 REGISTRATION NUMBER: 30,946
 CLASSIFICATION:
 APPLICATION NUMBER: PCT/US96/13152
FILING DATE:
 ZIP: 10022
 STATE: New York
 COUNTRY:
 STREET:
 ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D, Hanson
 116 $ 116
 121 S 121
 60 PDSVKGRETISRDNAKNTLYLQNNSLRAEDTAVÝÝČARD----ÝDGYFDÝMGQGTLVTVS 115
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLIVS 120
 1 EVOLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAFGKGLEWVASISTGGS-TYY 59
 Application PC/TUS9613152
 New York
 805 Third Avenue
 Conservative
 U.S.A.
 double
 78.1%; Score 502.5; DB 5
80.2%; Pred. No. 3.3e-45;
 Anti-selectin antibodies for prevention of multiple organ fai
 4:
 10; Mismatches
 BOER 1059-PCT-PFF/NDH
 et al.
 DB 5;
 Length 443;
 Indels
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 Gaps
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 US-08-379-057-14
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 RESULT 15
 US-08-326-362-2
 Sequence 14, Application US/08379057 Patent No. 5876950
 Matches
 Query Match
 GENERAL INFORMATION: Sladak, Anthony W. APPLICANT: Sladak, Anthony W. APPLICANT: Hollenbaugh, Diane APPLICANT: Gilliland, Lisa K. APPLICANT: Gordon, Marcia L.
 TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
 PILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Binaudi, Garol P.
REGISTRATION NUMBER: 33,220
REFERENCY/DOCKET NUMBER: 0240
TELECOMMUNICATION IMPORMATION:
APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Outro
APPLICANT: Artifo, Alejandro A.
APPLICANT: Artifo, Alejandro A.
TITUS OF INVENTION: Different Epicopes of human gp39 and Methods For Their
TITUS OF INVENTION: Different Epicopes of human gp39 and Methods For Their
TITUS OF INVENTION: In Diagnosis and Therapy
 MOLECULE TYPE:
 CLASSIFICATION: 435
PRIOR APPLICATION UNDER: US 0
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: DE P
 COMPUTER READMANE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC Compatible
COMPATINE: IBM PC Compatible
OPERATURG WISTEN: PC-COSE/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CUREBUT APPLICATION DATA:
 APPLICANT: Seeman, Gerhard
APPLICANT: Dippold, Molfgang
TITLE OF INVENTION: Honoclonal Anti-Ganglioside Antibody,
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
NUMBER OF SEQUENCES: 4
CORRESSONDENCE ADDRESS: 4
CORRESSONDENCE ADDRESS: 4
 TYPE: ami
 Local Similarity 81.8 hes 99; Conservative
 LENGIH:
 TELEPHONE:
 FILING DATE:
 APPLICATION NUMBER:
 STREET: 1300 I St
CITY: Washington
 ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700
 COUNTRY:
 118 S 118
 121 $ 121
 61 RDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCAR-GGSRY--AMDYWGQGTTVTVS
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
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 20005-3315
 amino acid
 QVQLQQSGGGLVKPGGSLTLSCAASRFTFSTYAMSWVRQTPAKRLEWVAYISSGGASTYY
 Ð.C.
 118 amino acide
 Hollenbaugh, Diane L.
Gilliland, Lisa K.
 USA
 202-408-4000
 peptide
 81.8%;
 DE P 42 08 795.3
 US 08/032,863
 US/08/326,362
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 7; Mismatches
 02481-1276-00000
 Score 500.5; DB
Pred. No. 1e-45;
 DB 1;
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 Indels
 Length 118;
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 Gaps
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COMPUTER READABLE FORM:
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PROBLEM TIPE: M PORPY disk
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MEDIUM DATE: AS -13N-195
MEDIUM TON MURBER: UN/08/379,057
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Search completed: November 7, 2003, 07:30:10 Job time: 18.7704 secs
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Best Local Similarity 90.3%; Fred. No. 3.8e-45;
Matches 98; Conservative 9; Mismatches 11; Indels
 NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS
STREET: 3005 First Avenue
CTYY: Seattle
STATE: Washington
COMPREY: USA
COMPREY: USA
 137 SS 138
 120 SS 121
 79 PDSVRGRFTISRDNARNILYLOMSSLRSEDTAMYYCARH--YDYDSYAMDYWGOGTSVTV 136
 61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGS-SFDYWGQGTTLTV 119
 1 BYOLVESGOGLIKEPOSELKISCASCOFTENTYMENTROPERKLEWATISSGOSTTYY 60 EVKLYESGOGLIVEPOSELKISCASCOFTENTANIANSWYNGTERKELEWATISSGOSTTY 78 20 EVKLYESGOGLIVEPOSELKISCTTSGETENNYANSWYNGTERKELEWASISSGOSTTY 78
 4.
 Gaps
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Result
No.
 Database
 Minimum DB seq
Maximum DB seq
 Post-processing: Minimum Match 0%
 Total number of hits satisfying chosen parameters:
 Scoring table:
 Perfect score:
 OM protein -
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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55699
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554
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 283308 segs, 96168682 residues
 Maximum Match 100%
Listing first 45 summaries
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
 Length
 DB
 $53750
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$41940
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D27887
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C27887
 ij
 PL0203
 B39276
 SUMMARIES
 283308
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 g
gr
 anti-DNA autoantib
Ig kappa chain - m
 Description
 chain (mo
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| 516    | 516     | 517      | 518    | 520       | 525     | 525     | 525     | 525     | 525     | 526     | 526    | 527    | 527     | 527    | 528         |
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| 131    | 121     | 113      | 103    | 131       | 132     | 115     | 113     | 112     | H       | 219     | 111    | 131    | 115     | 112    | 131         |
| N      | N       | N        | N      | N         | N       | N       | ,,,     | N       | N       | N       | N      | N      | N       | N      | N           |
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|        |         |          |        |           |         |         |         |         |         |         |        |        |         |        |             |
|        | Ig kapp | anti-DN  | H      | Ig kapp   | Ħ.      | Ig kapp | _       | Ig kapp |         | Ig kapp | ž      | ፠      | Ig kapp | Ξ.     | Ig kapı     |
| kappa  | kappa   | ti-DNA a | light  | kappa     | ti-digo | kappa   | kappa   | _       | kappa o | kappa   | kappa  | kappa  | kappa   | kappa  | Ig kappa ch |
| kappa  | kappa   | ti-DNA   | light  | kappa cha | ti-digo | kappa   | kappa c | _       |         | kappa   | kappa  | kappa  | kappa   | Ξ.     | _           |

# ALIGNMENTS

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AjMoleuie types mäkä
AjMoleuie types mäkä
AjResidues 1219 VUAN
AjCross-references SMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337
C;Superfamily: Lamunoglobulin v region; immunoglobulin homology
C;Superfamily: Lamunoglobulin bomology cIVM>
F;16-95/Domain: immunoglobulin bomology cIVM>
 Ig kappa chain mouse
Cispace: O'.May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
Cipace: O'.May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
Cipacesion: S5208
Ryan Engelen, F., Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schosubmitted to the EMBL Data Libbary, August 1994
Alpsecription: Coordinate expression of antibody subunit genes yields high level
Alpsecrence number: S52028
Alpsecrence number: S52028
 A; Molecule type: mana A; Middecule type: mana A; Molecule type: mana A; Molecule type: mana A; Molecule type: mana Middecule type: man
 anti-DNA autoantibody BNJ7-31, kappa chain V region - mouse (fragment)
CiSpecies; Mus muschius (house mouse)
CiDate: 20-Feb-1995 #8equence_revision 20-Feb-1995 #text_change 21-Jan-2000
CiAccession: PD203
Rismith, R.G.; Voss Ur., E.W.
Mol. Immunol. 27, 463-470, 1990
Mol. Immunol. 27, 46
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 A;Status: preliminary
 F;101-113/Region: D region
 Matches 107;
 Query Match
 Local Similarity
 62
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 2 VVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRPS
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 Conservative
 95.4%;
 4; Mismatches
 Score 566; DB 2;
Pred. No. 2.8e-45;
 Length 113;
 Indels
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 Gaps
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61 61

0

| RESULT 7 PT0359 Ig kappa chain V region (P4A.12) - mouse (fragment) C.Species: Mus musculus (house mouse) C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000                                                                                                                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| CY  2 INTOSPISLIPVILODASI SCRESOSI VISINARYTLARYLOZROZROZLIZYKYSIRRES 6:  Db 2 "INTOSPISLIZVILODASI SCRESOSI VISINARYTLARYLOZROZROZLIZYKYSIRRES 6:  CY AMOZTELSIZVILODASI SCRESOSI VISINARYTLARYLOZROZROZLIZYKYSIRRES 6:  CY OVEDKI SOSOSI DETIKI SKVENEDLAVYYCE QOSIVPYTE 9007KLE 110  Db 62 GYEDRESOSOSI DETIKI SKVENEDLAVYCE QOSIVPYTE 9007KLE 110 | StS313; ND:9198095; PID:ANA63385.1; PID:9198096 bbllin V region; immunoglobulin homology (100) bbllin homology (100) bbllin homology (100) blblin homology (100) 93 88; Score 556; DB 2; Length 131; 93 78; Excel No. 276-44; Troology (100)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| Query Match<br>Best Local :<br>Matches 10                                                                                                                                                                                                                                                                                                             | A; Reservation number: Asyz/o, Mull:slowssa0, PMID:2263605 A; Reservation size/s A; Rese |
| A;Molecule type: mRNA A;Mesidnes: 1.110 <str.\ 1.110="" <imm="" <str.\="" a;cross-references:="" a;residnes:="" c;keywords:="" c;supertamily:="" emblx59183;="" heteorotetramer;="" homology="" immunoglobulin="" nid:g52314;="" pid:g1334062="" pidn:caa41893.1;="" vegicn;=""> F;16-95/Domain: immunoglobulin homology <imm></imm></str.\>          | Ig light chain precursor V-D-7 region (6-19) - mouse C.Species: Mse musculus (house mouse) (C.Dates: 18-0ct-1991 #sequence_revision 18-0ct-1991 #text_change 21-Jan-2000 C.Maccession: 193276 C.Maccession: 193276 R.Meininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S. Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990 A.; Title: Cryoglobulineia induced by a murine 1933 rheumatoid factor: skin vasculitis ar                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| K;Stark, S.E.; Caton, A.J., 1991 J. Bxp. Med. 174, 613-624, 1991 A;Tille: Antibodies that are specific for a single amino acid interchange in A;Feference number: S26309; MUID:91341421; PMID:1908510 A;Accession: S26335 A;States:                                                                                                                   | Db 62 GVPDRESGSGSGTDFTLKISKVERNDLGVTYCCGGSKVPRTTGGGTYLEIKR 113  RESULT 4  BJ9276                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| S26335  Ig kappa chain V region - mouse C:Species: Mus musculus (house mouse) C:Datte: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000 C:Accession: 526335                                                                                                                                                                        | TPLSLPVSLGDQASISCRS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| Db 62 GYPDRETNSSSSGTDFTLKISKVERAEDLEVYYCHQOSHVPYTFGGGTKLEIK 112 RESUL7 6                                                                                                                                                                                                                                                                              | Query Match 94.3%; Score 559; DB 2; Length 219; Best Local Similarity 93.8%; Pred. No. 2.5e-44; Matches 105; Conservative 6; Mismatches 1; Indels 0; Gaps                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Qy 2 IUTQOSEISLPWSIADQASISCRSSQS:IVSRNSWTYLBWIQKRSQSEXLLYYKNSNERS Db 2 IUTQOFFUSLPWSIADQASISCRSSQS:IVSRNSWTYLBWIQKRGQSFULLIYKNSNERS 6 Qy 62 QYFDXF9GGGGGTDFTLKISRVDAEDLGYYYCFQGSHVPWTFGGGFKLSIK 112                                                                                                                                                   | A;cross-references: GHIU9147; NID:G1594225; FIDM:AGS2821.1; DIS:G1594236 C;Comment: This protein is specific for human plasma mpolipoprotein A-I of high-density C;Superfamily: immunoglobulin V region; immunoglobulin homology F;I-112/Domain: V region #status Predicted vRGb F;I13-219/Domain: C region #status predicted vCRGb                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| Overy March 93.4%; Score 554, DB 2; Length 112;<br>Best Local Similarity 92.8%; Pred. No. 3.5-44;<br>Marches 103; Conservative 8; Mismatches 0; Indels 0; Gaps                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1.112 < TNA C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin P; 16-95/Domain: immunoglobulin homology < IMM>                                                                                                                   | Cypectes non-measure number mouse, proceedings from the control of places 31-pec-1398 #sect-1398 #s |
| J. Bloi. Chem. 264, 259-265, 1989  A/Fitle: A monoclonal antibody against the platelet fibrinogen receptor cont A;Reference number: A31807; MUID:89079661; PMID:2909518 A;Accession: A31807 A;Status: pealininary A;Status: pealininary                                                                                                               | <pre>(abA34) - mouse (fragment)</pre>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| C.; Decreas: Mus macrulus (nouse mouse)<br>C; Date: 20-101-1989 #sequence_revision 20-Jul-1989 #fext_change 21-Jan-2000<br>C; Accession: A31807<br>R, Taub, R.; Gould, R.J.; Gareky, V.M.; Ciccarone T.M.: Hoxie, J.: Priedman.                                                                                                                       | Qy 62 GPPDKF86868GTDFTLKISRVEARDLGVYYCFQGSHVEWTFGGGTKLEIKR 113                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| RESULT 5<br>A31807<br>Ig kappa chain V region (PAC1) - mouse                                                                                                                                                                                                                                                                                          | Qy 2 IVINGERSILPVSLODQASISCESSGSIVESKURTYLENYLQKEGGSPLLITYKISKRES 61 2 VANTQSPLSILPVSLODQASISCESSGSIVESKURTYLENYLQKEGGSPLLITYKISKRES 61 2 VANTQSPLSILPVSLODQASISCESSGSIVESKURTYLENYLQKEGGSPLLITYKISKRES 61                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| Qy 62 GVPDKESGSGSGTDFTLK1SRVEAEDLGVTYCFQGSHVPWTFGGGTKLEIK 112                                                                                                                                                                                                                                                                                         | Overy Match 94.8%; Score 562; DB 2; Length 219;<br>Best Local Similarity 95.5%; Pred. No. 1.3e-44;<br>Matches 107; Conservative 3; Mismatches 2; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |

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sesion: $2635 ... The control of the
 ppa chain V region (PAC1) - mouse
is: 20-7ul-1809 #sequence_revision 20-7ul-1989 #text_change 21-Jan-2000
sesion: A31807
 e references: EMBL:X59183, NID:952314, FIID:CAM41893.1, FID:93334062
rfamily: immunglobulin v region; immunglobulin homology
ords: heteroterramer; immunglobulin
's/Domain: immunglobulin
 us: preliminary
cule type: mRNA
dues: 1-110 <STA>
 pa chain V region - mouse mouse)
ides Wha musculus (house mouse)
ii 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 y Match
 y Match
 hes 103; Conservative
 cule type: mRXA
dues: 1-112 cTAU>
rtanily: immunoglobulin V region; immunoglobulin homology
ords: heterotetramer; immunoglobulin
 ssion: A31807
 , R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.
d. Chem. 264, 259-265, 1989
e: A monoclonal antibody against the placelet fibrinogen receptor contain
rence number; AJ1807, MUT199079661; PWTD:2090516
 nes 103; Conservative
 5/Domain: immunoglobulin homology <IMM>
 us: preliminary
 Local Similarity
 Local Similarity
62 GVPDKESGSGSTDFTLKISKVBAEDLGVYYCFQGSHVPWTFGGGTKLE 110
62 GVPDKFSGSGSGTDFTLKISKVBAEDLGVYYCFQGSHVPYTFGGGTKLE 110
 62 GVEDEREGGGGGTDFTLK1SRVEARDLGVYYCFQGGHVHATGGGTKLEIK 112
62 GVEDRETGGGGGTDFTLK1SRVEARDLGVYYCFQGGHVHTFGGGTKLEIK 112
63 GVEDRETGGGGGTDFTLK1SRVEARDLGVYYCFQGGHVPYTFGGGTKLEIK 112
 2 IVLTOSPISI, PVSLODO, ASISCESSOS IVERNANTYLENYLO, CEGOS PKLLLYKVSNIRES
2 IVLTOSPISI, PVSLODO, ASISCESSOS IVERNANTYLENYLO, CEGOS PKLLLYKVSNIRES
2 VLATOTELSLIPVSLODO, ASISCESSOS IVERNANTYLENYLO, CEGOS PKLLLYKVSNIRES
2 VLATOTELSLIPVSLODO, ASISCESSOS IVERNANTYLENYLO, CEGOS PKLLLYKVSNIRES
 28
 62
 2 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIYKVSNRFS
 93.3%; Score 553; DB 2;
94.5%; Pred. No. 4.3e-44;
 93.4%;
 6; Mismatches
 8; Mismatches
 Score 554; DB 2;
Pred. No. 3.5e-44;
 0
 Length 110;
 Length 112,
 Indels
 Indels
 o,
 0
 Gaps
 Gaps
 61
 61
 61
 61
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0;

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A.NStatus; preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A.Molecule type: mRWA
A.Residucs: 1-114 c.EEV>
A.Cross-cetero.ces: GB:N30481, NID:g197157; PIDM:AAA38935.1; PID:g197158
C.Superfamily: immunoglobulin V region; immunoglobulin homology
 Ig kappa chain V-II region TE33 - mouse
C:Species: Mus musculus (loose mouse)
C:Species: Mus musculus (loose mouse)
C:Date: 29-Jan-1990 #equance_revision 29-Jan-1990 #text_change 21-Jan-2000
C:Accession: A3267
C:Accession: A3267
Biochemistry 29- Tide-7175, 1989
Biochemistry 29- Tide-7175, 1989
A:Title: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
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A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
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A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
A:Tette: Probling antibody diversity by 2D MMR: comparison of amino acid sequences,
A:Tette: Probling antibody diversity acid acid acid acid acid acid acid
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 (;Superfamily: immunoglobulin v region; immunoglobulin homology C;Reywords: immunoglobulin F;16-95/Domain: immunoglobulin homology <1MM>
 Ig light chain V region mouse
C:Species Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
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 C;Comment: This protein is an anti-double-stranded DNA antibody.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;19-98/Domain: immunoglobulin homology -IPM>
 C.Accession: P70359
R.Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
W.Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.;
Diamond, B.
J. Exp. Med. 173, 287-296, 1991
A;Title: A novel class of anti-DNA anribodies identified in BALB/c mice.
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 A. Kisacus; proliminary
A. Kisacus; proliminary
A. Residues; i-112 cCIN;
A. Krosse-references: EMBL, X7,6021; NID:g416112; PIDN:Chac3608.1; PID:g1334264
 A;Reference number: S38713
A;Accession: S38719
 R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
 C; Accession:
 A;Molecule type: mRNA
A;Residues: 1-118 <SHE>
A;Experimental source: strain BALB/c
 A;Reference number: PT0352; MUID:91108325; PMID:1988536
A;Accession: PT0359
 S38719
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 Query Match
 Matches
 Query Match
 Local
 Local
 104;
 62
 102;
 62 GVPDRFSGSGSGTDFTLKIGRVEAEDLGVYYCFQGSHVPLTFGAGTKLELK 112
 62 GVPDKRSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
 65 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGTKLEIKR 116
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
 2 IVMTQTPLSLPVSLGDQASISCRSSQSIVYSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 2 IVLTQSPLSLFVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
 5 VVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFS 64
 Similarity
 S38719
 Similarity
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 Conservative
 Conservative
 92.9%;
91.1%;
 92.4%;
 Mismatches
 7; Mismatches
 Score 551; DB 2;
Pred. No. 7.1e-44;
 Score 548; DB 2; Length 112;
Pred. No. 1.3e-43;
 DB 2; Length 118;
 2; Indels
 3; Indels
 0
 0,
 Gaps
 Gaps
 61
 0
 0
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 Ś
 C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
 Matches
 Query Match
 Local Similarity
 101;
2 VLMTQTPLSLPVSLGDQASISCKSSQSIVHSSGNTYFEWYLQKPGQSPKLLIYKVSNRFS 61
 2 IVLTQSFLSLFVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIYKVSNRFS 61
 Conservative
 92.2%; Score 547; DB 2; Length 114; 90.2%; Pred. No. 1.6e-43;
 9;
 Mismatches
 Indels
```

밁 Q

Ig kappa chain precureor V region (12-40 and 5-14) - mouse CiSpactes: Mus musculus (Nouse mouse) CiPacte: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 21-Jul-2000 CiPacession: 194904; H34905

R.Bedayk, W.D., Herron, J.N., Zdmundson, A.B., Yoss Ur., E.W.
J. Biol. Chem. 255, 133-138, 1990
A.Title: Active site structure and antigen binding properties of idiotypically A.Tetesence number: A34901, WIDI:30094397, PMID:2104617
A.Recession: B45904 WIDI:40094897, PMID:2104617
A.Recession: B45904 WIDI:40094897, PMID:2104617
A.Statute: preclimitary, not compared with conceptual translation

A; Molecule type: mRNA A; Residues: 1-131 <BED>

C;Keywords: heterotetramer; immunoglobulin F;35-114/Domain: immunoglobulin homology <IVM> C; Superfamily: immunoglobulin V region; immunoglobulin homology A;Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:g639656; PIDN:AAA61589

Matches POCST 101, 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61 Similarity Conservative 92.1\*; Score 546; DB 2; Length 131; 91.0\*; Pred; No. 2.3e-43; 7; Mismatches 3; Indels 0 Gaps

Query Match

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#### B31485

Ig kappa chain V region (4.4.20) - mouse (fragment)
Clapacies: Mus musculus (house mouse)
Clapace 31.701.1999 #sequence\_revision 31-701.1989 #text\_change 21-701.2000
Clacesion: E31455
Reddyk, W.D.; Johnson, L.S.; Riodan, G.S.; Voss Jr., E.W.
Reddyk, W.D.; Johnson, L.S.; Riodan, G.S.; Voss Jr., E.W.
Ribdo: Cham, 46. 1565.1569, 1889; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 19

C;Keywords: heterotetramer; immunoglobulin F;16-95/Domain: immunoglobulin homology <IMM> A.jStatus: preliminary A.jStatus: preliminary A.jStatuse: 1-112 - ABED A.jReaiduse: 1-112 - ABED C.jSupertamily: immunoglobulin V region; immunoglobulin homology C.jSupertamily:

Best Los Matches Query Match Local Similarity Conservative 91.6%; Score 543; DB 2; 90.1%; Pred. No. 3.6e-43; 8, Mismatches DB 2; Length 112. Indels 0

밁 Š 2 VVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLRWYLQXPGQSPXVLIYKVSNRPS 61 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNIYLEWYLQKPGQSPKLLIYKVSNRFS

| Sea<br>Job                                | OY 2 TYLTOSPISLIVESLODASISCHSENSTYLENSTYLENTLOREGOGEFELLTYKTSTRES 61 1 TYMTOTPISLIVESLODASPSCHSSOSIVHISNOTYLENYLOGEGOGEFELLTYKTSNRES 80                                                                                                                                                                                                                                                         |  |
|-------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
| B 8                                       | Ouery Match 91.4%; Score 542; DB 2; Length 131; Best Local Shilarity 90.1%; read No. 5.3e-43; Length 131; Matches 100; Conservative 7; Mismatches 4; Indels 0; Gaps 0;                                                                                                                                                                                                                          |  |
| B &                                       | A;Kolocula type; profein<br>A;Kolocula type; profein<br>A;Residues: 20-23-2822.<br>C;Superfamily: immunoglobulin V region; immunoglobulin homology<br>C;Superfamily: immunoglobulin homology crews<br>F;35-114/Domain: immunoglobulin homology crews                                                                                                                                            |  |
| 7 C 2 X X X X X X X X X X X X X X X X X X | . Biol. Chem. 264, 1565-1569, 1989  Biol. Chem. 264, 1565-1569, 1989 A;Title: Comparison of variable region primary structures within an anti-fluorescein idi A;Reference number: A31485; WID:89109167; PMID:2492278 A;Accession: 131485 A;Accession: 131485                                                                                                                                    |  |
| 4400                                      | A/status: preliminary; not compared with conceptual translation A; Moderal type: mRM A; Moderal type: mRM A; Moderal type: mRM A; Moderal type: mRM                                                                                                                                                                                                                                             |  |
| A; E<br>A; Z<br>A; F                      | 7. Biol. 7 Chem. 18 1. 1911 1917. pandulusoul, A.B.; Voss 97., E.W.<br>A. 1914 19. Active 18 1. 33-1818. 990<br>A. 1914 19. Active 18 1. 38-1818. 990 and antigen binding properties of idiotypically cross-real<br>A. Reference number: JASSOS; WID: 50094387; PHID:2104617                                                                                                                    |  |
| A E N C C C S                             | hhain preoursor V region (3-24) - mouse Mus musculis (house mouse) 7-Jul-1990 feequance revision 27-Jul-1990 ftext. Mi CJ\$601, 131455                                                                                                                                                                                                                                                          |  |
| ARE S                                     | Oy 62 GYPDKESGSGSGTDETLKISKYEAEDLGYYYCFQGSHYPHTRGGGTKLEIK 112 Db 62 GYPDKESGSGSGTDETLKISKYEAEDLGYYYCFQSSGTEXTEGGGTKLEIK 112                                                                                                                                                                                                                                                                     |  |
| \$ \$ \$                                  | OY 2 ITUTOSPILLIVELLOOOASISCISSISCIVESNONTTLENKI/OKEROGEPILLIKVIOSMRES 61 1-                                                                                                                                                                                                                                                                                                                    |  |
| \$ & _                                    | Ouery Match 91.4; Score 54.5; DB 2; Length 112; Best Local Smilarity 91.94; Peed. No. 4.5-43; Length 112; Matches 102; Conservative 6; Mismatches 3; Indels 0; Gaps 0;                                                                                                                                                                                                                          |  |
| #00A                                      | A) Experimental source: strain Balb/c A) Note: this sequence was determined from the germline gene C) Comment: This chain was abolated from a hybridoma protein that binds influenza virus h C) Superfamily: immunoglobulin V region; immunoglobulin homology C) Newyords: heerocetramer; immunoglobulin C) Reynords: neerocetramer; immunoglobulin C) Reynords: immunoglobulin homology < 10M5 |  |
| 22222                                     | APTILE: Structural and functional implications of a restricted antibody response to a d<br>APREference number: A91043; MIID:86300658; PMID:2427335<br>A)Accession: E97887<br>A)Accession: E97887<br>A)MOLECULE type: DNA<br>A)MOLECULE type: DNA                                                                                                                                                |  |
| ERCCOE<br>BILLO                           | Farber Chain V region (HIC5-4D1) - mouse Lg Kappa chain V region (HIC5-4D1) - mouse C.Species: Was musculius (house mouse) C.Date: 15-Dec-1588 Hequanoe_revision 15-Dec-1588 #text_change 21-Jan-2000 C.Dates: 15-Dec-1588 Hequanoe_revision 15-Dec-1588 #text_change 21-Jan-2000 C.Accession: P27887 R.Caton, A.J., Brownlee, G.G., Staudt, J.M., Gerhard, M.                                  |  |
| RE<br>S1                                  | RESULT 12                                                                                                                                                                                                                                                                                                                                                                                       |  |
| 망                                         | Db 62 GVPDRFSSSGSCTDFTLKISRVEABDLGVYFCUSQSTHVFWTFDGGSTKLBIK 112                                                                                                                                                                                                                                                                                                                                 |  |
| Ş                                         | CY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLBIK 112                                                                                                                                                                                                                                                                                                                                   |  |

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RESHIT 14

SIGIL2

15 kappa chain V region (GZa) - mouse
C;Specias: Mus musculus (house mouse)
C;Date: 21-Nov.1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Date: 21-Stories #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: SIGIL2
R;Vassen, M.; Prosch, M.; Weisegerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suerm
R;Vassen, M.; Prosch, M.; Weisegerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suerm
R;Vassen, M.; Prosch, M.; Weisegerber, S.; 1991
R;Vassen, M.; Prosch, M.; Weisegerber, S.; 1992
R;Vassen, M.; Prosch, M.; Weisegerber, M.; Prosch, M.; Restaute, Protiminary
A;Mousemier, M.; 15112
A;Restaute; Protiminary
A;Mousemier, M.; SENT'>
A;Restaute; Protiminary
A;Mousemier, M.; SENT'>
A;Restaute; Protiminary
A;Mousemier, M.; SENT'>
A;Mous
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 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin C;Superfamily: immunoglobulin homology c;Petropologic immunoglobulin homology c;
 S
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 Query Match
Best Local Similarity
 Matches 100; Conservative
62 GVPDRF8GSGSGTDFTLKISRVEAEDLGVYFCFQGTHVPYTFGGGTRLETKR 113
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTPGGGTKLEIKR 113
 81
 62
 2 IVLTQSPLSLFVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 2 VVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLXWYLQKFGQSPKPLIYRVSNRFS
 GVPDKF8GSGSGTDFTLKISRVEAEDLGVYVCFQGSHVPWFFGGGTKLEIK 112
GVPDKF8GSGSGTDFTLKISRVEAEDLGVYVCFQGSHVPWFFGGGTKLEIK 131
 91.2%;
 10; Mismatches
 Score 541; DB 2;
Pred. No. 1.1e-42;
 Length 219;
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Affile: Structural and functional implications of a restricted antibody respon A; Reference number. A91043; MUID:8630058; MUID:2427335
A; Accession, A27887
A; Molecule type: DNA
A; Residues: 1-112 CCMT;
A; Residues: 1-112 CCMT;
A; Residues: 1-113 cource; strain Balb/c
A; Residues: 1-113 cource; strain Balb/c
C; Comment: This sequence was determined from the germline gene
C; Comment: This chain was solated from a hybridoma protein that binds influenza
C; Superfamily; immunoglobulin v region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <1M945
 Ig Mappa chair V region (H37-50) - mouse C;Spectes: Mus mouse thouse mouse) C;Spectes: Mus moustlus (house mouse) C;Date: 13-Dec-1988 Heavance_revision 15-Dec-1988 #text_change 21-Jan-2000 C;Accession: A27837 Excentee, G.G.; Staudt, L.M.; Gerhard, W. Brigol, S. 1577-1587, 1996
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Matches 62 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNONTYLEWYLQKPGQSPKLLIYKVSNRFS VVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFS Conservative 9; Mismatches 3, Indels

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Search completed: November Job time : 14.7342 secs

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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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|        | GTDFTI                                                   | 88.4%<br>tive<br>vsigpo                                                                                                                                                                                                                                                                                                                | Land,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 109<br>129<br>111<br>111<br>111<br>111<br>111<br>111<br>111<br>109<br>149<br>109                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|        |                                                          | DASI                                                                                                                                                                                                                                                                                                                                   | D; 1 Created) Last sequence of the light of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|        | RVEAEDI<br>       <br>RVEAEDI                            | SCRSSQS                                                                                                                                                                                                                                                                                                                                | ALIGNMEN  PRT; 111  ated)  at sequence upda  t annotation up  an 26-10. Conintan  tial Sciurognae  tial Sciu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | KV3D HUMAN KV3L HUMAN KV3K MOUSB KV3 K MOUSB KV3 E MOUSB KV3 E MOUSB KV3D MOUSB KV3D MOUSB KV3D HUMAN KV5A MOUSB KV3D HUMAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|        | GVPDXFSGSGSGTDFT1K1SRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR<br> | imilarity 88.4% Pred. No. 5.8-60, 113; COMBETVELTY 88.4% Pred. No. 5.8-60, 114; COMBETVELTY 88.4% Pred. No. 5.8-60, 114; INTOREDISLIPSICOSASISCESOSIVESNONTYLAWYLOXAGOSPALL INTOREDISLIPSICOSASISCESOSIVESNONTYLAWYLOXAGOSPALL VMRQCPELSLPVSLODQASISCESSOSIVESNONTYLAWYLOXAGOSPALL VMRQCPELSLPVSLODQASISCESSOSIVESNONTYLAWYLOXAGOSPALL | INMENTS  113 AA.  113 AA.  114 AA.  115 AA.  116 Long pdate)  117 Long pdate)  118 Long pda                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | HOWAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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|        | 113<br>113                                               | S 61<br>S 61                                                                                                                                                                                                                                                                                                                           | Mus.  Mus.  Dona                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | homo sapien homo sapien mus musculu homo sapien homo sapien homo sapien                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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GO; GO:GOGS55; Frankune response; NAS.
InterPro: IPRO0710; jg_-like.
InterPro: IPRO03506; jg_-MHC.
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Ffam; PRO0457; jg_-N.
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INTERPO: PRO0457;
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 EMBL; Z00020; CAA77315.1; -.
 Nucleic Acids Res. 13:6499-6513(1985).
 MEDLINE=86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini, Hominidae; Homo.
 Ig kappa chain V-II region RPMI 6410 precursor
Homo sapiens (Human)
 "Human immunoglobulin kappa light
 NCBI_TaxID=9606;
 01-JAN-1988
 SEQUENCE FROM N.A.
)1-JAN-1988 (Rel. 06, Last
5-JUL-1999 (Rel. 38, Last
 83
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 Similarity
 GVPDRFSGSGSGTDFTLKISKVEAEDVGVYYCMQGTHWSWTFGQGTKVEIKR
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FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-2.
 FRAMEWORK-4.
 COMPLEMENTARITY-DETERMINING-3
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15-JUL-1999 (Rel. 38, Last annote
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SMART; SM00406; IGV; 1.
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 MEDLINE-84191806; PahMed=6325927;
Kloheck H.G., Solomon A., Zachau H.G.,
"Contribution of human V kappa II germ-line genes to light-chain
 NCBI_TaxID=9606;
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 PROSITE
 PIR; A01889; K2HUGM.
 Nature 309:73-76(1984).
 Ig kappa chain V-II region GM607 precursor (Fragment).
Homo sapiens (Human)
 SEQUENCE FROM N.A.
 66
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
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 IVMTOSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRAS
 PSS0835; IG LIKE;
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 STANDARD;
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 12664 MW;
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 Score 457;
Pred. No. 1
 COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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 Catarrhini; Hominidae; Homo
 BY SIMILARITY
 FRAMEWORK-
 Craniata; Vertebrata; Euteleostomi;
 PRT;
 IG KAPPA CHAIN V-II REGION GM607
 92C57DC719E558B1
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Immunoglobulin V region; Benc
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
 patient with plasma cell dyscristis and amyloidosis,",

J. Clim. Invest. 52.1276-1288 (1972)

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 SEQUENCE (BENCE-JONES PROTEIN TEM).
MEDLINES-7414680) PubMed-4596149;
Putnam F.M., Whitley E.J. Jr., Paul C., Davidson J.M.;
Panino acid sequence of a kappa Bence Jones protein from a case
primary amylodeosis.";
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 PIR; A90370; K2HUTW.
 "Structural
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 MEDLINE=73166638; PubMed=4700495;
 Biochemistry 12:3763-3780(1973).
 SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW)
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 Similarity
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMZALQAPITFGQGYRLEIKR
 I VWTQSPLSLPVTPGEPASISCRSSQSLLHSDGFDYLNWYLQXPGQSPZLLIYALSNRAS
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 Bence-Jones protein; Amyloid.
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 Score 452;
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Immunoglobulin V region; Hybridoma.
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P03976;
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InterPro; IPR007110; Ig-like.
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 group A etreprococal polysaccharide.";
Hoppe-Sqylef: 8. Bhysiol. Otem. 365:1375-1383(1984).
--- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY
 NEDIJNE-$5128968; PubMed-6441768; Abbersold R., Herber H., Grutter T., Chang J.Y., Braum D.G., Putrine V kappa 23 and V kappa 27 amino-acid sequences of C5781/6 Oxigin; monoclonal antibodies 17829.1 and 22825.1 specific for the
 MOUSE
 PIR; A01912; KVMS17.
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Ig kappa chain V-II region
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 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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InterPro; IPR003596; Ig_v.
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 GO:0006955; P:immune response; NAS
 GO:0005576; C:extracellular; NAS
GO:0003823; F:antigen binding ac
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 IVLTOSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPXLLIYXVSNRFS
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FRAMEWORK-4.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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 "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-205(1969).
--- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV
 NCBI_TaxID=9606;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1996 (Rel. 01, Last sequence update)
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 MEDLINE=70063440; PubMed=4188189;
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 MEDLINE=68242259; PubMed=5586923;
 SEQUENCE
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 IVLTQSPLSLPVSLGDQASISCRSSQSIVHS-NGNTYLEWYLQXPGQSPKLLIYXVSNRF 60
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Pred. No. 4.6e-40;
IS; Mismatches 13;
 Pred. No. 3.4.
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Craniata; Vertebrata; Sciurognathi; Muridae;

Buteleostomi;
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RESULT 9

MOUSE STANDARD, PRT; 113 AA.
P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P01630; P016300; P01630; P01630; P016300; P016300; P016300; P016300; P016300; P016300; P016300; P016300; P016300;

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RESULT 8

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 Matches
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 "The genetic, molecular, and equation according to the confidence and unifying hypothesis," 153-367(1967). Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967). -- MISCELLAMBOOKS: THE CRESCON OF THIS CHAIN MAS THE INV
 KV2C HUMAN
P01616;
 Bukaryofa, Metazoa; Chordeta; Cranieta; Vertebreta; Buteleostomi;
Memmalla; Buteria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 21-TUL-1996 (Rel. 01, Created)
21-TUL-1996 (Rel. 01, Last sequence up
15-TUL-1999 (Rel. 38, Last amnotation
IG kappa chain V-II region MIL
Homo sapiens (Human)
 PIR; A01887; K2HUML.
HSSP; P80362; 1WTL.
 SEQUENCE
 InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
)reyer W.J.,
 63
 13
 N
 Similarity
TUTOSPLSLPVSLGDQASISCRSSQSTHSRGNYYLBYLQKPGQSPKLLYKYSRRFS
 SGVPDRFSGSGSGTDFTLKISRVQAEDVGVYYCMQRLEIPYTFGQGTKLEIRR 115
 SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVFWTFGGGTKLEIKR
 112 AA;
 Conservative
 Gray W.R., Hood L.E.; molecular, and cellular basis of antibody formation:
 STANDARD;
 72.4%;
 12055 MW;
 19;
 Score 429.5;
Pred. No. 1.:
 PRT;
 E5B22E2FA7ABE481 CRC64;
 ed. No. 1.2e-39,
Mismatches 13
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 DB 1;
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 Polt22:

Polt22: 1-7UI-1996 (Rel. 01, Created)

21-7UI-1996 (Rel. 01, Last sequence update)

15-7UI-1999 (Rel. 38, Last amotation update)

15-7UI-1999 (Rel. 38, Last amotation update)
 MEDILINE-84095.04.1; rumwww.m. BDILINE-84095.04.1; herbst H., Chang J.Y., Abertsold R., Braun D.G.; "Murine W25 isotype sequence: monoclonal antibody 281.3 specific for the group A streptcoorcel polysaccharide." Hoppe-684/er's Z. Physiol. Chem. 363:1069-1076(1982).

-i. MISCELLANDOUS: THIS CHAIN 1S FROM A HYBRIDMA-DERIVED MONOCLONAL ANTIFROMY MANINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
InterPro, IPRO07110, Ig-like.
InterPro, IPRO07100, Ig-MRC.
InterPro, IPRO03596, Ig-W.
Prem. PRO04596, Ig-V.
Prem. PRO04596, Ig-V.
SMART, SMO4464, Kg-T.
Immunoglobulin V region, Monoclonal antibody.
 MOUSE
 DOMAIN
 PIR; A01913; KVMS7S.
HSSP; P80362; AWTL.
InterPro; IPR007101; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
 HSSP; P01607; 1REI
 PIR; A01911
 MEDLINE=83055101; PubMed=7141411;
 NCBI_TaxID=10090;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; PS50835; IG LIKE; 1.
Immunoglobulin V region; Mono
 Chang J.Y., Herbet H., Abbersoid R., Braun D.G.,
"S new isotype sequence (V kappa 27) of the variable region of kappa-
light chains from a mouse hybridoma-deried anti-(streptococcal group
A polyseccharide) antibody containing an additional cysteline residue.
Applicantion of the dimethylaminoarchements isothicoyanter beninque
for the isolation of psptidose."

1211:173-180(1998)

1311:173-180(1998)

1411:173-180(1998)

1511:173-180(1998)

1511:173-180(1998)

1511:173-180(1998)
 KV2D_MOUSE
 SEQUENCE
 NON
 DISULFID
 DOMAIN
 DOMAIN
 DOMAIN
 SEQUENCE
 DOMAIN
 DOMAIN
 MEDLINE=83256427; PubMed=6409088
 82
 62
 N
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 79;
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 GVPDRFSGSGSGTAFTLRISRVBAEDVGVYYCMQQREYPYTFGGGTKLEIKR 113
 IVMTQTAPSALVTPGESVSISCRSSKSLLHSNGNTYLYWFLQRPGQCPQLLIYRMSNLAS
 ; KVMSS1
 Conservative
 STANDARD;
 AA;
 region; Monoclonal antibody; Hybridoma.
 12496 MW;
 70.5%
 70.7%;
 16;
 Pred
 Score 419;
 COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
 FRAMEWORK-3
 PRT;
 42C019D10ADA3C91 CRC64;
 Mismatches
 No.
 112
 1.7e-38;
 Š
 DB 1;
 17;
 Length 113;
 Indels
 0
 Gaps
 61
 61
 0;
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RESULT 11
KV4C_HUMAJ
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 Matches
 Query Match
Best Local
| Immunoglobuli V region, Signal. | Immunoglobuli V region, Signal. | SIGNAL | I GK |
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 8
 EMBL; X02990; CAA26733.1; -. HSSP; P80362; 1WTL.
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The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in oway modified and this statement is not removed. Usage by and for commercial.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 01-JNN-1988 (Rel. 06, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last amoration update)
15-JUL-1999 (Rel. 38, Last amoration update)
15-kBpga chain V.IV region B17 precursor.
 HUMAN
 DOMAIN
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 entities requires a
 Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
 Nucleic Acids Res.
 "Detection of a unique human V kappa IV germline gene CDNA probe.";
 MEDLINE=86041854; PubMed=2997713;
Marsh P., Mills F., Gould H.;
 NCBI_TaxID=9606;
 Homo sapiens (Human)
 KV4C HUMAN
P06314;
 DOMAIN
 REVISION TO 76
 SEQUENCE
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 SEQUENCE FROM N.A.
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 titles requires a license agreement (S send an email to license@isb-sib.ch).
 GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity; NAS.
GO:0006955; P:immune response; NAS.
 62
 62
 N
 N
 80;
 Similarity
 GVPDRFSGSGSGTDFTLRISRVEAEDVGVXYCANLQELPYTFGGGTKLEIK 112
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 ī vmī qaaf snevīlgīsas fscrsskslogsksi tylymylokes gabai i vonsnilas
 112 AA;
 Conservative
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23
 STANDARD;
 13:6531-6544(1985)
 23
39
54
61
93
102
112
 12221 MW;
 70.2%;
72.1%;
 13; Mismatches
 FRAMENORK-1.
COMPLEMENTALTY-DETERMINING-1.
FRAMENORK-2.
COMPLEMENTALTY-DETERMINING-2.
FRAMENORK-3.
COMPLEMENTALTY-DETERMINING-3.
FRAMENORK-4.
BY SIMILARITY.
BY SIMILARITY.
 IG KAPPA CHAIN V-IV REGION B17. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
 Pred. No.
 Score 416;
 PRT;
 BD5EF5E6D789FBEC CRC64;
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 (See http://www.isb-sib.ch/announce/
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 Length 112
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RESULT 12
KV48_HUMAN
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 Query Match
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Matches 78
 GO: 000:00055/6; C:extracellular; NAS.
GO: 000:00355 P:immune response; NAS.
InterPro; IPRO0710; Tg-like.
InterPro; IPRO07306; Tg-WHC.
InterPro; IPRO03566; Tg-WHC.
InterPro; IPRO03566; Tg-WHC.
IRSPRO; SPO04566; Tg-V:
EMART; SMO466; TGV-I.
IRSOSTITE; ES50457; TG-LIKE; 1.
IRSOSTITE; ES50457; TG-LIKE; 1.
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 single germline gene.";
Nucleic Acids Res. 13:6515-6529(1985).
 TWAB HUMAN SYNNDARD; PRT; 13 AA P06213, OLJAN-1988 (Rel. 06, Created) OLJAN-1988 (Rel. 06, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update 15 Auppa chain V-IV region JI precursor.
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 HSSP; P80362; 1WTL.
 BMBL; Z00022; CAA77317.1; -.
 "Subgroup IV of human immunoglobulin K light chains is encoded by
 MEDLINE=86041853; PubMed=2997712;
Klobeck H.G., Bornkamm G.W., Comb
 PIR; A01904; K4HUJI.
 Zachau H.G.;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 Mammalia; Eutheria;
 Eukaryota, Metazoa,
 Homo sapiens (Human)
 82
 61
 22
 Similarity
 SGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNLPWTFGQGTKVEIKR 134
 SGVPDKFSGSGSGTDFTLKISRVBAEDLGVYYCFQGSHVPWTFGGGTKLBIKR 113
 IVMTQSPDSLAVSLGERATINCKSSQSILYSSDNKNYLAWYQQKPGQPPKLLIYWASTRE
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGN-TYLEWYLQKPGQSPKLLIYKVSNRF
 Conservative
 76
83
115
122
122
134
 60
75
82
 Primates;
 Chordata;
 67.0%; Score 397.5; DB 1 69.0%; Pred. No. 4.4e-36;
 WW;
IG KAPPA, CIAN. V-IV REGION JI.
FRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMENORK-2.
FRAMENORK-3.
FRAMENORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMENORK-4.
FRAMENORK-4.
BY SHATLARITY-BY
BY S
 Combriato G., Mocikat R., Pohlenz H.D.,
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 BY SIMILARITY
 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
 COMPLEMENTARITY-DETERMINING-2.
 6413A22FD0738832 CRC64;
 Mismatches
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 DB 1;
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RESULT 14
KV4A_HUMAN
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 SST
 Query Match
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 Query Match
Best Local
 PIR, A01910, KVMSSI.

HSSP. P80362, MTL.

InterPro: JP8007110, Tg-Tike.

InterPro: JP8007100, Tg-WC.

InterPro: JP8001366, Tg-WC.

Pfam. P80047, 1397,
 KVZC MOUSE STAI
PO1628;
21-JUL-1986 (Rel. 1
21-JUL-1986 (Rel. 1
15-JUL-1999 (Rel. 1
 DISULFID
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SEQUENCE
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 Appella E.;
"Amino acid sequence of the light chain variable myeloma protein
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 Mus musculus (Mouse)
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence
15-JUL-1999 (Rel. 38, Last annotatio
Ig kappa chain V.II region MOPC 511.
 DOMAIN
 DOMAIN
 phosphorylcholine-binding murine myeloma protein
 SEQUENCE.
MEDLINE=81052016; PubMed=6776396;
 NCBI_TaxID=10090;
 . Immunol. 17:711-718 1980).
MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN
 BINDS PHOSPHORYLCHOLINE
 62
 62
 82
 61
 22
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 17; Conserv
 Similarity
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEJKR
 GVSDRFSGSGSGTDFTLEISRVKAEDVGVYYCQQLVEYPLTFGAGTKLELKR
 IVITODELSKRVTSGESVSISCRSSKSLLYKDGKTYLNWFLOGPOOSPRLLIYLMSTRAS
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 SGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYDTIP-TFGGGTKVEIKR 133
 SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 IVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRE
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGN-TYLEWYLQKPGQSPKLLIYKVSNRF
 133
133 AA;
 Conservative
 Conservative
 STANDARD;
 STANDARD;
 133
14632 MW;
 12496 MW;
 64.8%; Score 384;
66.1%; Pred. No. 1
 64.9%; Score 385; DB 1; 68.1%; Pred. No. 9.8e-35; tive 16; Mismatches 18
 Last sequence update)
 16;
 annotation
 COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4. BY SIMILARITY.
 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
 Craniata; Vertebrata;
Sciurognathi; Muridae;
 PRT;
 PRT;
 EFB0DC4DA2BD3450 CRC64;
 SFB3953066744AF4 CRC64;
 Mismatches
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 DB 1; Length 113;
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 Length 133,
 region of M511,
 Indels
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P01625;

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RESULT 15
KV31 MOUSE
ID KV31
AC PO165
DT 21-JU
DT 21-JU
DT 15-JU
DT 15 MUS n
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 Query Match
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KV31 MOUSE

P01661;

P01661;

21-JUL-1986

21-JUL-1999

15-JUL-1999
 DOMAIN
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 21.-UU.-1986 (Rel. Ol. Created)
21.-UU.-1986 (Rel. Ol. Last sequence update)
15.-UU.-1999 (Rel. 38, Last sequence update)
15 kuppa chain v.III region MOPC 63 precursor.
Mis musculius (Mouse)
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 pmb; SIUR; 28-NAR-O1.
60; GO:0005756 C.settreedlinlar; NAS.
60; GO:0005203; F.natigen binding activity; NAS.
60; GO:0006203; F.namune response; NAS.
60; GO:0006205; F.immune response; NAS.
60; GO:0006205; F.immune response; NAS.
60; GO:0006206; J. J. MC.
60; GO:0006206; J. J. M
 -!- MISCELLANGOUS: THE C REGION OF THIS CHAIN HAS
-!- MISCELLANGOUS: THE IS A BENCE-JONES PROTEIN.
DBB, LEEG, 01-FEB-01.
DBB, LEEG, 02-FEB-01.
DBB, LEEG, 03-FEB-01.
DBB, LIFQ, 03-FEB-01.
DBB, LIFQ, 03-FEB-01.
DBB, LIVE, 13-MAY-95.
DBB, SLVE, 13-MAY-95.
DBB, SLVE, 13-MAY-01.
 NEDLINE-76004342; PubMed-50995;
Schneider M. Hilschmann W. "The pricary structure C. a monoclonic immunoglobulin-I-chain
wThe pricary structure C. a monoclonic immunoglobulin-I-chain
subgroup IV of the kapps type (Bence-Jones protein Len).";
Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
 NON TER
 DOMAIN
 DOMAIN
 DOMAIN
 Immunoglobulin
DOMAIN
 Submitted (AUG-1996)
 Salomon A.
 SEQÜENCE
 DISULFID
 DOMAIN
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 21-JUL-1986
01-OCT-1996
 Homo sapiens
 Ig kappa chain V-IV region Len.
 REVISION TO 9.
 L5-SEP-2003
 62
 61
 N
 N
 76,
 Similarity
 IVLTQSPLSLPVSLGDQASISCRSSQSIVH-SNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60
 SGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPYSFGQGTKLBIKR
 SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR
 IVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTRE
 Conservative
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63
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23
 (Rel. 01,
(Rel. 34,
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 (Human)
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 region; Bence-Jones protein; 3D-structure.
23 FRAMEWORK-1.
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 64.7%;
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MECKann D.J., Bell M., Potter M.;

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Television of the MecKann D. M. (1983)

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 MEDIAINE-73.40255; PubMed-66915.7;
McKean D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Pattern of sequence variation among
kappa chains with limited sequence differences.";
Biochemistry 12.766-771 (1973).
 "Primary structures of N-terminal ertra peptide asoments linked to
the variable and constant regions of immunoglobulin light chain
precursors: implications on the organization and controlled
expression of immunoglobulin genes";
injochemistry 17:2392-440(1978).
 DOMAIN
 DOMAIN
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
 PIR; B90412; KVMSM6.
HSSP; P01679; 2FBJ.
 Burstein Y., Schechter I.;
 NCBI_TaxID=10090
 Mammalia; Butheria; Rodentia; Sciurognathi; Muridae;
 utingorfoundan
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 nterPro; IPR007110;
 SEQUENCE OF 21-131.
 MEDLINE=78235887; PubMed=98179;
81
 62
 22
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 76;
 Similarity
 GVPDKF8GSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
 PS50835; IG_LIKE; 1.
obulin V region; Signal.
1 20
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GVPARFSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPWTFGGGTKLEIK
 131 AA;
 Conservative
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 Score 379.5; DB 1
Pred. No. 3.8e-34;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
 BY SIMILARITY
 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
 FRAMEWORK-4
 D212EC9F08DC880A CRC64;
 Mismatches
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 Gaps
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Post-processing: Minimum Match 0%
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4: sp_human:*
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 QIVLTQSPLSLPVSLGDQAS..........FQGSHVPWTFGGGTKLEIKR 113
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 sp invertebrate:*
 sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| 16                 | 15     | 14     | . 13    | 12     | 11                 | 10     |        | œ                  | 7      | 1 01               | . UI   | 44     | نما .  | ٠.     | , <sub>1</sub>     |   | No.         | Result |
|--------------------|--------|--------|---------|--------|--------------------|--------|--------|--------------------|--------|--------------------|--------|--------|--------|--------|--------------------|---|-------------|--------|
| 335.5              | 337    | 337    | 338.5   | 339.5  | 368                | 368.5  | 383    | 431                | 456    | 465.5              | 467    | 505    | 505    | 536    | 564                |   | Score       |        |
| 56.6               | 56.8   | 56.8   | 57.1    | 57.3   | 62.1               | 62.1   | 64.6   | 72.7               | 76.9   | 78.5               | 78.8   | 85.2   | 85.2   | 90.4   | 95.1               |   | Match       | Query  |
| 108                | 109    | 107    | 103     | 108    | 109                | 111    | 148    | 239                | 239    | 114                | 239    | 239    | 104    | 238    | 238                |   | Length DB   |        |
| 11                 | 4      | 4      | 11      | 4      | 4                  | H      | 11     | 11                 | 4      | Α.                 | 4      | 11     | 11     | 1      | H                  | 1 | DB.         |        |
| OFIA80             | 987n60 | Q96SA9 | 0871.80 | Q9UL77 | Q9UL78             | Q920E9 | Q8K122 | Q8K0F8             | QBNEKO | Q9UL80             | QBTCDO | Q8VC55 | Q9JL82 | QSVCI6 | Q99M37             |   | ij          |        |
| Q8vij0 mus musculu |        |        |         |        | Q9ul78 homo sapien |        |        | Q8k0f8 mus musculu |        | Q9ul80 homo sapien |        |        | Bum S  | mus 1  | Q99m37 mus musculu |   | Description |        |

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| ű                  |                    | · C    | 2      | £      | 0      | 39     | 88     | 37     | 8      | S      | 34     | 3      | 32     | 2      | 30     | 29     | 28     | 27     | 26                 | 25     | 24     | 23                 | 22     | 21     | 20     | 19                 | 81     | 17                 |
|--------------------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------|--------|--------------------|--------|--------|--------|--------------------|--------|--------------------|
| 260.5              | 202                | 276.5  | 283    | 283.5  | 287.5  | 295    | 295.5  | 304.5  | 306.5  | 308.5  | 308.5  | 313    | 314.5  | 316.5  | 317    | 320    | 320    | 321    | 322.5              | 322.5  | 322.5  | 326                | 328.5  | 329.5  | 330    | 332.5              | 334.5  | 335.5              |
| 43.9               | 44.2               | 46.6   | 47.7   | 47.8   | 48.5   | 49.7   | 49.8   | 51.3   | 51.7   | 52.0   | 52.0   | 52.8   | 53.0   | 53.4   | 53.5   | 54.0   | 54.0   | 54.1   | 54.4               | 54.4   | 54.4   | 55.0               | 55.4   | 55.6   | 55.6   | 56.1               | 56.4   | 56.6               |
| 234                | 241                | 127    | 112    | 97     | 116    | 235    | 107    | 101    | 298    | 234    | 234    | 106    | 109    | 234    | 114    | 112    | 112    | 107    | 108                | 108    | 99     | 109                | 108    | 233    | 134    | 107                | 234    | 214                |
| 1                  | H                  | 1      | ä      | H      | 4      | 11     | 11     | 11     | ä      | 11     | 11     | σı     | 11     | 11     | H      | 1      | H      | 4      | 4                  | 4      |        |                    |        |        |        |                    |        | 11                 |
| Q8R028             | Q921A6             | Q925S9 | Q8K1F0 | Q9JL76 | Q96PF6 | Q91W12 | Q9JL84 | Q9JL78 | Q9QYF0 | QSVCPO | Q8R062 | 29U410 | Q920E6 | Q91WF8 | Q8K1F1 | Q8K1F3 | Q8K1F2 | Q9UL81 | Q9UL79             | Q9UL70 | Q9JL74 | Q9UL85             | Q9UL83 | Q91WS9 | Q8VDD0 | Q9ERZ9             | Q8NEK1 | Q9R1A5             |
| Q8r028 mus musculu | Q921a6 mus musculu | mus.   | mus    |        | ŏ      | 83     | Snu    |        | 8118   | Bull   | 825    | his    | Bum    | mus    | BUE    | Bum    |        | ĕ      | Q9ul79 homo sapien | ₫      | ana    | Q9ul85 homo sapien | Omo    | Bug    | mus    | Q9erz9 mus musculu | homo   | Q9rla5 mus musculu |

#### ALIGNMENTS

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InterPro; IPR003006; II_MHC.
InterPro; IPR003396; II_V.
InterPro; IPR003396; II_V.
Iffan; PF00047; iig; 2.
SMART, SM00406; IGV; 1.
PROSITE; PS00290; II_MHC; 1.
 Q9JL82;
 Q8VC16;
Q8VC16;
01-MAR-2002
01-MAR-2002
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NON_TER .
 InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
 Infect. Immun. 68:5803-5808(2000).
EMBL; AF206024; AAF69322.1; -.
HSSP; P01607; IREI.
 MEDLINE-20448942; PubMed=10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
M"-Cell-dependant antibody response to the dominant
streptococcal polysaccharide, N-acetyl-glucosamine,
 01-OCT-2000 (TREMELRE1. 15, Created)
01-OCT-2000 (TREMELRE1. 15, Last sequence update)
01-MAR-2003 (TREMELRE1. 12, Last sequence update)
Anti-myosin immunoglobulin light chain variable region
(Fragment)
Mus mucollus (Mouse)
Nus mucollus (Mouse)
 streptococcal polysaccharide, with cardiac myosin.";
 SEQUENCE FROM N.A.
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 01-MAR-2002 (TrEMBLrel 20, Cr
01-MAR-2002 (TrEMBLrel 20, La-
01-MAR-2003 (TrEMBLrel 23, La-
101-MAR-2003 (TrEMBLrel 23, La-
Hypothetical 26.2 kDa protein.
Mus musculus (Mouse)
 PROSITE; PS50835; IG_LIKE; 1.
 STRAIN=BALB/c;
 NCBI_TaxID=10090;
 Submitted
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Hypothetical protein.
 Strausberg R ;
 NCBI_TaxID=10090;
 rissum=Colon;
 SEQUENCE FROM N.A.
 101;
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 Similarity
 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPTFGGGTKLEIKR
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 VVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPXLLIYKVSNRFS
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 (DEC-2001) to the EMBL/GenBank/DDBJ databases
 238 AA;
 90.4%;
ilarity 90.2%;
Conservative
 PRELIMINARY;
 PRELIMINARY;
 26224 MW;
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 Created)
 Score 536; DB 11;
Pred. No. 4.9e-50;
 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
 PRT;
 35EC08E3DE5414AD CRC64;
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 Strauberg R.,
Submitted (JAM-2002) to the EW
BNEL, ECO21981, AN21791.1; -
InterPro; IRR003056; Ig WHC.
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SNART, SN0006; IOV 1.
 GBVC5;
01-MAR-2002 (TrEMBLrel. 20, Crea
01-MAR-2002 (TrEMBLrel. 20, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical 26, 3 kba protein.
Mus masculus (Mouse).
 QSTCD0;
Strausberg \tilde{R}_i , Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases. EMBL, ECC02352, AME2352.1i - InterPro; IPR007110; Ig-like.
 Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
 01-UUN-2002 (TYEMBLrel. 21, Created)
01-UUN-2002 (TYEMBLrel. 21, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
 NCBI_TaxID=9606;
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 Hypothetical protein. SEQUENCE 239 AA; 2
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 NCBI_TaxID=10090;
 82
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 69 GSGSGTDFTLXISRVEAEDLGVYYCFQGSHVPWTFGGGTXLEIK 112
 9 LSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIXKVSNRFSGVPDKFS
 95,
 Similarity
 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSNHLPYTFGGGTKLEIKR
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 GSGSGTDFTLKISRVEAEDLGVYFCSQTTHVPYTFGGGTKLEIK 104
 LSLPVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFS
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82.1%;
 85.2%;
91.3%;
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 Score 505; DB
Pred. No. 1.1e
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 Score 505; DB 11;
Pred. No. 3.9e-47;
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 PRT;
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HSBF P80325, 1MTL.
InterPro, IPR007010; Ig-11ke.
InterPro, IPR003006; Ig_MC.
InterPro, IPR003006; Ig_MC.
InterPro, IPR003065; Ig_W.
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Pfam, PF00017, 1g; 1.
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Interpro; IPR00356; Iq V.
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01-OCT-2002 (TrEMBLrel. 22,
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 SEQUENCE
 Clin. Immunol. Immunopathol. 87:184-192(1998)
 Wu X., Liu B., Van der Merwe P.L., Young D.C.;
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MEDLINE=98277139; PubMed=9614934;
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Bukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
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O1-MAY-2000 (TEMBLICE). 23, Last sequence update)
O1-MAY-2000 (TEMBLICE). 23, Last amnocation update)
MyOSIL-reactive immunojobolila light chain variable region
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 NCBI_TaxID=9606;
 (Fragment).
 62
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89; Conserv
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIYKVSNRFS
 87;
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSH-VPWTFGGGTKYLEIKR 113
 Similarity
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 VMTQSFLSLPVTLGQPASISCRSTQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRDS
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQCSHVPWTFGGGTKLEIKR 113
 114 AA;
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ilarity 78.8%;
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 78.8%; Score 467;
77.7%; Pred. No. 1
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2; Mismatches 11
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 FACEDC3A3B03871D CRC64;
 Mismatches
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Matches 86
 Query Match
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Matches 81; Conserv
 Strauberg R.,

Submitted (UM-2002) to the BMBL/GenBank/DDBJ da

BMBL, BC031998, AM31498.1;

InterPro, IRR002199, Apl short.

InterPro, IRR002599, 3g.—

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IREPTO, IRR003597, 1g.-

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InterPro IRROVILIO IG-like.
InterPro IRROVILIO IG-MC.
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01-CCT-2002 (TYEMBLrel. 22, Created)
01-CCT-2002 (TYEMBLrel. 22, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
 Hypothetical protein SEQUENCE 239 AA; 2
 PROSITE; PS00061; ADH SHORT; PROSITE; PS00290; IG_MHC; 1.
 Eukaryota; Metazoa; Chordata;
Mammalia; Euthería; Rodentía;
 Mus musculus (Mouse).
 Q8K0F8
 TISSUE=Breast tumor;
 NCBI_TaxID=10090;
 Hypothetical SEQUENCE 2:
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 Hypothetical protein.
Homo sapiens (Human).
 01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
 SEQUENCE FROM N.A.
 EMBL; BC030814; AAH30814.1;
 Strausberg R.;
 FISSUE=Prostate:
 Submitted
 EQUENCE FROM N.A.
 62
 22
 82
 N
 ; 98
 Similarity
 GVPDRFSGSGSGTDFTLKISKVEAEDVGIYYCMQGLQTPQTFGQGTKVEIKR
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 IVMTQSPLSLPVTPGSPASISCRSSQSLLHSDGYNYLDMYLQKPGQSPQLLIYLGSNRAS
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 (JUN-2002)
 239 AA; 26024 MW;
 Conservative
 PRELIMINARY;
 Conservative
 26366 MW;
72.7%; Score 431; DB 11; 72.3%; Pred. No. 1.2e-38; tive 14; Mismatches 17;
 76.9%; Score 456;
76.8%; Pred. No. 2
 to the EMBL/GenBank/DDBJ databases
 23,
 Last
Last
 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 PRT;
 D7BE84398AA341F0
 F5E20AD3B0552C0A CRC64;
 Mismatches
 sequence update)
annotation update)
 2.4e-41
 DB 4;
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 13;
 databases
 CRC64;
 Length 239
 Length
 Indels
 239
 0
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 Gaps
 81
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20 020E3

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Matches 71
 Strausberg R. Submitted (Mar-2002) to the EMBL/GenBank/DDBJ da Submitted (Mar-2002) to the EMBL/GenBank/DDBJ da EMBL, BC038925, AM728925.1, ... InterPro; IRR007110; Ig-tike. InterPro; IRR007110; Ig-tike. InterPro; IRR003006; Ig-MC. InterPro; IRR003065; Ig-MC. InterPro; IRR003956; Ig-V. Ffam; PR00471; Hg1 J. SMART; SMO4010; IG-J. SMART; SMO40109; IG-J. SMART; SMART; SMO40109; IG-J. SMART; SMART; SMO40109; IG-J. SMART; SMAR
 Q920E9
Q920E9;
01-DEC-2001
01-DEC-2001
 Q8K122,
ARKİM JÜ, Tape A., Jemingd I.G., Horakis O., Cotton "Definition of the Idiscope of Persin-Mindcking Antibod in Mammalian Cells", and Mammalian Cells "Submitted (ISEP-2000) to the EMBL/GenBank/DDBJ databass BMBL, AE207935, RAL09419.1; ". Incepto, IPROVIDIO, Jejlike.
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 Eukaryota; Metazoa; Chordata; Craniata; Verebrata; Euteleostoni;
Mammalla; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
HBI_TaxID=10090;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
 Mus musculus (Mouse).
 UI-MAK-2003 (TREMBLrel. 23, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable
 Mus musculus (Mouse).
 01-OCT-2002
01-OCT-2002
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Hypothetical protein.
SEQUENCE 148 AA; J
 PROSITE; PS50835; IG_LIKE; 1.
 SEQUENCE FROM N.A.
 TISSUE -Salivary gland;
 81
 62
 21
 82
 62
 22
 N
 71;
 Similarity
 GVPDKFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHVP 100
 VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 GVPDKEGGGGGTDFTLKISKVEABDLGVYYCFGGSHVFFFYTGGGTKLEIKR
 VMTQTELTLSVTIGQPASISCKSSQSLFYTNGKMYLSWLLQRPGQSPKRLISLVSKLDS
 IVLTQSPLSLFVSLGUQASISCRSSQSIVHSNGNTYLEWYLQXFGQSFKLLIYKVSNRFS
 Conservative
 (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
 PRELIMINARY;
 PRELIMINARY;
 16345 MW;
 64.6%;
71.7%;
 15;
 Score 383; DB 11;
Pred. No. 1.1e-33;
 PRT;
 183920BBD9F3BS21 CRC64;
 Mismatches
 111
 148
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 13;
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 Antibodies Expr
 Length 148;
 Indels
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 133
 113
 Gaps
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 81
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 Query Match
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Matches 71
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Best Local Similarity
 InterPro; IPR003006; Ig_MRC.
InterPro; IPR003598; Ig_v.
InterPro; IPR003598; Ig_v.
InterPro; IPR003598; Ig_v.
InterPro; IPR003598; Ig_v.
InterPro; IRR InterPro; IRR InterPro; IRR InterPro; InterPro; IRR InterPro;
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Q1-MAY-2000
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 BMBL; AF035036; AAD56272.1; -.
HSSP; P80362; IWTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00306; Ig_WHC.
 SEQUENCE
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
 Clin. Immunol. Immunopathol. 87:184-192(1998)
 Young D.C.,
 SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 Homo sapiens (Human)
 SEQUENCE
 "Myosin-reactive autoantibodies in
 NCBI_TaxID=9606;
 (Fragment).
 12
 57
 61
 61
 62
 Liu B.,
 74;
 Similarity
 QIVLTQSPLSLFVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF
 TGIPDRFSGSGSTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKV5IKR
 SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 GVPARESGSGSGTDFTLNIHPVEEEDAATYYCQHSRELPYTFGGGTKLEIK
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
 IVLTQSPLSLEVSGGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIYKVSNRES
 EIVLTQSPGTLSLSPGERATLSCRASQSV----SSSYLAWYQQKPGQAPRLLIYGASSRA
 IVETQSPASLAVSEGORATISCRASKS-VSTSGYSYMHWYQQKPGQPPKLLIYLASNLES
 109
109 AA;
 111 AA,
 (TrEMBLrel. 13,
 Conservative
 Conservative
 PRELIMINARY;
 Van
 109
11646 MW; 5F675C52EC7EE197 CRC64;
 der Merwe
 62.1%;
 12046 MW;
 62.1%;
 μ
 19;
 11; Mismatches
 Created
 Score 368.5; DB :
Pred. No. 2.8e-32
 Score 368; DB 4;
Pred. No. 3.1e-32;
 P.L.,
 Craniata; Vertebrata; I
Catarrhini; Hominidae;
 PRT;
 1E46988AA6858526 CRC64;
 Mismatches
 rheumatic carditis and normal
 Kalis N.N.,
 108
 DB 4; Length
 ζ
 DB 11;
 19;
 25;
 Berney
 Indels
 Indels
 Length
 Euteleostomi; Homo.
 region
 S.M.
 111,
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 Gaps
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 THE PRODUCT IS 11ke.

RE INTERPO; IRROUSSOS; IQ-MSC.

RE PÉRM; PRODUCT; IQ-V.

RE PÉRM; PRODUCT; IQ; 1.

SMART; SMOUGOS; IG-V.

PROSTIE; PSEOSS; IG-LKE; 1.

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 fetus.",
Clin. Immunola. Immunopa:
Clin. Immunola., AAD5627
EMBL; AR036037, IRBI., IRB
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003506; Ig_v.
InterPro; IPR003506; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0577PR: DEFCASE:
 087L80
EMBL; AF206026; AAF69324.1; -.
 with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
 Malkiel S., Liao L., Cunningham M.W., Diamond B., "T-Cell-dependent antibody response to the dominant streptococcal polysaccharide, N-acetyl-glucosamine,
 01-OCT-2000 (TrENBLrel. 15, Created)
01-OCT-2000 (TrENBLrel. 15, Last sequence update)
01-MAR-2003 (TrENBLrel. 23, Last annotation updat
Anti-myosin immunoglobulin light chain variable r
 HSSP; P80362; 1WTL.
 MEDLINE=20448942; PubMed=10992488; Malkiel S., Liao L., Cunningham M.
 Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090
 Mus musculus (Mouse).
 (Fragment)
 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L.,
 SEQUENCE
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 Young D.C.;
 NCBI_TaxID=9606;
 Eukaryota; Metazoa;
 01-MAY-2000
 Mammalia; Eutheria; Primates;
 Homo sapiens (Human)
 (Fragment).
 Myosin-reactive
 01-MAR-2003
 57
 62
 66;
 mmunol. Immunopathol.
 Similarity
 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIKR
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 INTIOSETSTEAMORISCESSOSINHSNGNTÄTEMÄTÖKEGOSEKTTIÄKKÄNKES
 TOMTOSPSSLSASVODRVTTTCRASOSI----SSYLNWYQOKPCKAPNLLTYAASSLOS
 108 AA;
 PRELIMINARY;
 Conservative
 (TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
tive immunoglobulin light chain variable region
 AAD56273.1; -
 11738 MW;
 57.3%;
 Chordata;
 15;
 Score 339.5; DB 4
Pred. No. 3.7e-29;
 87:184-192 (1998)
 Craniata, Vertebrata, Euteleostomi, Sciurognathi, Muridae, Murinae, Mus.
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 C06681716C4D16F3 CRC64;
 Mismatches
 annotation update)
chain variable region
 Kalis N.N., Berney
 103
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 Indels
 Length 108;
 epitope of is cross-reactive
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 Gaps
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AC Q9UL6
AC Q9UL6
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DT 01-M9
DT 01-M9
DT MYOSI
DE (Frag
OS Homo
OC Bukar
OX NCBI_
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 antibody V region genes."

J. Immunol. 161:12020-2031(1998).

BMBL; U96396, AAB68785.1;.

RMETPTO; IPRO07110; Ig-like.

InterPro; IPRO03006; Ig-MHC.

InterPro; IPRO03906; Ig-MHC.

InterPro; IPRO03906; Ig-V.
 01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
 OSULB6;
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SEQUENCE
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=966;
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01-MAR-2003 (TrEMBirel. 23, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable
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01-DEC-2001 (TERBELZel.) 19. Last sequence update)
01-MR-2003 (TERBELZel.) 21. Last sequence update)
Anti-streptococcal/anti-syocini immunoglobulin kappa 1
variable region (Fragment).
Simo sapitas (Human)
Chordata; Craniata, Vertebrata; F
Mananaia, Experia) Framces; Catarriini; Hominidae;
 Q96SA9;
 (Fragment).
Homo sapiens (Human)
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
 Adderson B.B., Shikhman A.R., Mard K.E., Cunningham M.M.
"Molecular analysis of polyreactive monocolonal antibodies from
Theumatic carditis; human anti-N-acetylglucosamine/anti-myosin
 MEDLINE=98375893; PubMed=9712075;
 NCBI_TaxID=9606;
 SEQUENCE
 SEQUENCE FROM N.A.
 57
 62
 61
 N
 68;
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 5
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 65;
 Similarity
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 GVÞSRÉSGSGSGTDETLTÍSSLQPEDFATÝÝC-QQSYSTLTFGGGTKVEÍKR
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
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 103
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 -SSYLNWYQQKPGKAPKLLIYAASSLQS
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RP SEQUENCE FROM N.A.

RP MEDLINE-BROTTISH PubMed=9614934;

RR MEDLINE-BROTTISH PubMed=9614934;

RA MU X., ILI B., Van der Nerwe P.L., Kalis N.M., Berney S.M.,

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DR HSSF, P800362, JATL.

DR HSSF, P
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MAD 1A7 light

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GenCore version 5.1.6
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Compugen Ltd.
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| 113  | TFGGGTKLEIKR                  | SHVPW   | FQ      | 1 QIVLTQSPLSLPVSLGDQASFQGSHVPWTFGGGTKLEIKR 113 | 1 QIVLTQS        | sequence:                         |
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Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62

Total number of hits satisfying chosen parameters: 1107863

1107863 seqs, 158726573 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum Match 100%

Database

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| WOW-1 Fab light ch | AAY95258  | 21 |                          | 94.8  | 562   | ø   |
|--------------------|-----------|----|--------------------------|-------|-------|-----|
| Monoclonal antibod | AAY21545  | 20 |                          | 94.9  | 563   | 8   |
| Anti-idiotype mono | AAW03199  | 17 |                          | 94.9  | 563   | 7   |
| Mouse monoclonal a | AAE15704  | 23 |                          | 95.3  | 565   | o   |
| pscFvNQ11 encoding | AAR21262  | 13 | 249                      | 95.6  | 567   | v   |
| Chimeric Fv (BABS) | AAB62301  | 22 |                          | 95.6  | 567   | 4   |
| Light chain variab | AAP81364  | 9  |                          | 95.6  | 567   | ω   |
| Biosynthetic antib | AAP80154  | 9  |                          | 96.1  | 570   | N   |
| Anti-FIX/FIXa anti | AAB20434  | 22 |                          | 100.0 | 593   |     |
| Description        | ID        |    | Query<br>Match Length DB | Query | Score | No. |
| ES                 | SUMMARIES |    |                          | ·*    |       |     |

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#### ALIGNMENTS

Wariable light cha Murine IgG monoclo Fv region SC100 an Paraquat binding a Mouse monoclonal a Amino acid sequenc 4-4-20 VL / 217/

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BR55-2 light chain
WO9932650 Seq ID 3

VL region of anti-Humanised antibody Monoclonal antibod

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AAB20434 standard; Protein; 249 AA.

AAB20434;

21-JUN-2001 (first entry)

Anti-FIX/FIXa antibody 193/K2 scFv.

Factor IX, FIX, Factor IXa, FIXa, serv, antibody, procosquiant, Factor VIII cofactor, blood cosquiation discorder, haemophilia h, haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

Chimeric - Mus musculus Chimeric - Synthetic.

| đđ           | × | PN              | × | Ŧ            | H      | FT         | Ą       | 4              | Z,      | TT           | 3      | F          | 3       | FH                  | ğ |
|--------------|---|-----------------|---|--------------|--------|------------|---------|----------------|---------|--------------|--------|------------|---------|---------------------|---|
| 22-MAR-2001. |   | WO200119992-A2. |   |              | Region |            | Protein |                | Peptide |              | Region |            | Protein | Key                 |   |
|              |   |                 |   | /label= CDR3 | 230238 | /label= VL | 136249  | /label= Linker | 122135  | /labe1= CDR3 | 98110  | /label= VH | 1121    | Location/Qualifiers |   |

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 Or The present sequence is that of a single chain by (scFV) derivative of antibody 191/Kz, comprising the heavy (VII) and 161mt (VI) chain variable regions of 193/Kz 79 inted by an artificial, flexible linker peptide. The scFV was obtained by PCR smplification of cDNAs for 193/Kz 194 and VI regions and cloning in vector phaps. 193/KZ is antibodies of that imment sector in FITY/INSERIVATE ARCOLF IN (FITA) of the scenario of the school of the schoo
 Matches
 Query Match
 Biosynthetic antibody binding site; framework region; assay; imaging; multifunctional protein.
 31-OCT-2002
01-JAN-1980
 New factor IX/factor IXa antibodies and their derivatives useful for
increasing amidolytic activity of factor IXa, and for treating blood
congulation disorders such as hemophilia A and haemorrhagic disthesis
 19-MAY-1988;
 01-DEC-1988
 W08809344-A
 Synthetic
 Biosynthetic
 AAP80154;
 AAP80154 standard; protein;
 Sequence
 diathesis.
 Claim 10; Fig 15; 138pp; English.
 Homo sapiens
 WPI; 2001-290358/30.
 Scheiflinger F,
 13-SEP-2000; 2000WO-EP08936
 Local
 197
 137
 al Similarity
 61 SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFFGGGTKLEIKR 113
 AAF30724.
 QIVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIYKVSNRF
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 249 AA;
 Conservative
 antibody binding site.
 (updated)
(first entry)
 88WO-US01737
 99AT-0001576
 Kerschbaumer R,
 100.0%; Score 593; DB 22;
100.0%; Pred. No. 1.5e-44;
tive 0; Mismatches 0;
 249 AA
 Falkner F,
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 Indels
 Length 249;
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AAP81364
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 19-MAY-1988;
 31-OCT-2002
17-OCT-1990
21-MAY-1987;
 01-DEC-1988
 WO8809344-A
 Synthetic
 Light chain variable domain; biosynthetic antibody binding domain
 Light chain variable domain of biosynthetic antibody binding domain.
 Homo sapiens
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(updated) (first entry)

195 0

87US-0052800 88WO-US01737

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co multifunctional protein which also comprises an effector protein, an ACC and sequence capable of CC acidd sequence capable of binding to a solid support. The BABS comprises the framework region from the murine anti-digoxin monoclonal antibody 36-10 heavy chain variable region and an algoryme specificity. The effector protein is an ariable region and an algoryme specificity, the effector protein is an cor antimetrabolice or The sequence specificity and the conditional corresponding to the sequence capable of binding to solid support is streptavidin or suprotein A fragment. The protein may be used to correspond to the corresponding assays affinity purifican, blocatalysts drug tragetting, inaging and immunological treatment of cocognic etc.

CC diseases. The protein offers fewer cleavage sites to circulating corresponding to the correspo
 Best Local Sin
Matches 106;
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AAP81364;
 AAP81364 standard; protein; 115
 Sequence
 The biosynthetic antibody binding site forms part of a recombinant
 Disclosure; Page ?; 15pp; English
 solid support.
 Recombinant multifunctional protein - having antibody binding site sequence for biological activity, ion sequestering or binding to a
 N-PSDB; AAN80180
 Huston JS, Oppermann H;
 21-MAY-1987;
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 (Updated on 31-OCT-2002 to add missing OS field.)
 mmunogenicity
 196
 136 VVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKAGQSPKLLIYKVSNRFS
 62
 N
 Similarity
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
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94.6%;
 Score 570; DB 9;
Pred. No. 1.6e-42;
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21-MAY-1987;
12-MAR-1992;
19-OCT-1993;
 Blosymthetic, antibody binding site, binding smay, drug targeting; blocatalysis, imaging; affinity purification; immunologial; blocatalysis, imaging; affinity purification; immunologial; proceeding infectious disease; murine; monorlonal 26-11; anti-digodin; ovcostatio;
 Mus sp
 18-DEC-1995;
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 29-JUN-2001
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 Sequence
 Disclosure; Page ?; 15pp; English.
 support.
 Recombinant multifunctional protein - having antibody binding sequence for biological activity, ion sequestering or binding
 (Updated on 31-OCT-2002 to add missing OS field.)
 WPI; 1988-353928/49
 Huston JS,
 (CREA-) CREATIVE BIOMOLECULES
 Local
 105;
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 62
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
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 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
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 Oppermann
 (BABS) light chain variable domain
 Conservative
 (first entry)
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 95US-0575724.
 93US-0139901
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23-JAN-1992 WO9201047-A Protein Protein ĕ Synthetic

Peptide

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pscFvNQ11 encoding anti-oxazalone antibody

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 Query Match
Best Local :
 Matches 105;
 The invention relates to a blosynthetic antibody binding site that comprises disulfide bonded heavy, light variable region (FWR, LVR) defining single, complete antigen (AgI) binding site. HWR, LVR have polyperise domain having sets of complementarity determining regions (CRR) and framework (FR) amino acid sequences homologous to first and second immunoplobulin, respectively. The blosynthetic antibody binding sites are useful in specific binding assays, affinity purification, bloomthytis, drug targeting, imaging hammological treatment of various recommended infectious diseases. The present sequence represents the companies of th
 Sequence
 21-MAY-1992
 AAR21262;
 AAR21262 standard; Protein; 249 AA.
 Disclosure; Fig 4D; 26pp; English.
 Novel biosynthetic antibody binding site having chimeric polypeptide which defines eelective antigen binding region and has CDR and framework amino acid sequences homologous to different immunoglobulin
 WPI; 2001-280767/29.
N-PSDB; AAF57658.
 morecures
 (CURI-) CURIS INC
 30-JUN-1998;
 64
 62
 4
 N
 JS,
 Similarity
 GVPDRFSGSGSGTDFTLKISRVEAEDLGIYYCFQGSHVPWTFGGGTKLEIKR
 GVPDKFSGSGSGTDFTLKISRVBAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 VMTQTELSLEVSLGDQASISCRSSQSIVHSNGNTYLDWYLQKAĞQSEKLLIYKVSNRES
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 115 AA,
 Conservative
 Oppermann
 (first entry)
 98US-0213671.
 95.6%;
 ×
 6
 Score 567; DB 22;
Pred. No. 1.3e-42;
 Mismatches
 22;
 Length 115;
 Indels
 ٥,
 Gaps
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RESULTA

A PAREZIA

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 Query Match
Best Local S
 Matches 108;
 Region
 Wouse; humanised form; monoclonal antibody alpha 340; gene therapy;
epidexnal growth factor receptor; BGF; cancer; colorectal; lung; breast;
gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
 Mouse monoclonal antibody alpha 340 light chain variable (VK) region.
 Cowasalons is a hapten used for studying the immune response and the anti-oxasalone antihody. Will, has been described by E. Gheradi, R. Fannell, and C. Milstein, U. Immunol. Method 126 61-69). A plasmid contg, the VH and VL genes of WOll was converted to the sery form by inserting the BstEII/SacI fragment of serVoll.3 myc (mucleotides 432-439 of AdQ1095) between the VH and VL genes to generate into Griphy MI ges AdQ1095) to generate pub Woll. The specific binding see tho Milstein AdQ1095 to generate pub Woll.

The specific binding see also MARC1095 to 93112 AMR22450, 565-581.
 15-MAY-1991;
10-JUL-1990;
19-OCT-1990;
12-NOV-1990;
06-MAR-1991;
 Region
 de snw
 inhibitor
 12-MAR-2002
 AAE15704;
 AAE15704 standard; Protein;
 Sequence
 Producing members of specific binding pairs - by expression recombinant host cells with a secreting replicable genetic
 McCafferty J,
Jackson RH, J
 Example 9; Fig 13; 209pp; English
 WPI; 1992-056862/07.
 (CAMB-)
 10-JUL-1991;
 138 IELTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 62
 GP, Bonnert TP;
 Similarity
 CAMBRIDGE ANTIBODY.
MED RES COUNCIL.
 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGGTKLEIKR 249
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 249 AA;
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 Holliger KP,
 91GB-0010549.
90GB-0015198.
90GB-0022845.
90GB-0024503.
 /note= "Complementarity determining region 1" 55..68
 91GB-0004744
 91WO-GB01134.
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 Location/Qualifiers
 entry
 95.6%;
 Johnson
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 112
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 Score 567; DB 13;
Pred. No. 2.9e-42;
3; Mismatches 1;
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 98
 Hoogenboom HRJ, Griffiths
Clackson TP, Chiswell DJ;
 Length 249;
 Indels
 Griffiths AD
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 177
 Gaps
 197
 61
 0
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Ellis JRM,
 19-MAY-2000; 2000GB-0011981
24-AUG-2000; 2000GB-0020794
 21-MAY-2001; 2001WO-GB02226
 Region
 ($CAN-) SCANCELL LTD.
 22-NOV-2001
 W0200188138-A1
 2002-062384/08.
 Durrant
 /note= "Complementarity determining region
95..102
/label= CDR3
 /note= "Complementarity determining region
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New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and overlan

Claim 6; Fig 2; 53pp; English

or The present invention relates to a humanised form of the antibody 340 (a course monotonal antibody which binds to egidermal growth factor (EGP) or receptor and inhibits binding of EXP), obtainable from the coll line of deposited with the EXACC under accession number 97021438. The humanised come form of the antibody 340 is useful in gene therapy, medicine and in the communicative of a medicament for treating to propely asks of cancer. The invention is useful for treating colorectal, lung, breast, pastric or convertion oncers or also for preventing the recurrence of cancer after intial treatment or surgery. The invention is also useful for enhancing procestive immuse response against cancer by optimised immunication and procestive humanised form of the antibody and has reduced communicative but subset shall mention that the colls expressing EXP remaining the colls of the control of the surface of the colls of the control of the surface of the colls of the control of the surface of the colls of the control of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the colls of the col Sequence 112 AA;

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Query Match
Best Local S
Matches 104
 104;
 Similarity
 Conservative
 95.3%;
 6;
 Score 565; DB 23;
Pred. No. 1.9e-42;
 Mismatches
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 Length 112;
Indels
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Gaps
0
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62
 62
 N
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEI 111
 UMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLBWYLQKPGQSPKLLIYKVSNRFS
GVPDRFSGSGSGTDFTLKISRVEAEDLGIYYCFQGSHVPWTFGGGTKLEI 111
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
 2
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AAW03199 standard; Protein; 149
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AAW03199;
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25-MAR-2003 (updated) (first er entry)

Anti-idiotype monoclonal antibody 1A7 variable light chain.

AAW03199
ID AAW0
XX AAW0
AC AAW0
XX 25-A
DT 26-E
XX Anti
XX Muri
KW Muri Murine; mouse; anti-idiotype; monoclonal antibody; MAb; 1A7; variable light chain; ganglioside 2; GD2; 14G2a; neuroblasto 14G2a; neuroblastoma;

```
Claim 8; Fig 1; 141pp; English.
 Monoclonal antibody 1A7
polypeptide(s) - useful
 Chatterjee M,
 17-JAN-1995;
16-JAN-1996;
 Region
 Region
 glycosphingolipid; human; neuroectodermal; tumour; glioma; lung; malignalt melanoma; soft tissue sarcoma; small cell carcinoma; vaccine; trachment; palliake; detection; diagnosis; recombinant production; purification; probe; primer; assay;
 (KENT) UNIV
 16-JAN-1996
 17-JAN-1995;
 17-JAN-1996;
 WO9622373-A2
 Region
 Region
 Region
 Region
 Region
 Peptide
 Mus musculus.
 amplification; gene therapy.
 al antibody 1A7 and related polynucleotide(s) and ide(s) - useful to treat or palliate a GD2-associated e.g. melanoma and glioma
 KENTUCKY.
 95US-0372676.
96US-0591196.
95US-0372676.
96US-0591196.
 Chatterjee
 96WO-US00882
 /note=
81..11;
 /note=
59.,73
 /note= "framework region
74..80
 /note=
 /note= "framework region
 note= "complementarity determining region
 /label= sig_peptide
 Location/Qualifiers
 "framework region
 "framework region
 "complementarity determining region
 "complementarity determining region
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The present segmence is that of the mutine anti-idiotype monoclonal that body (Mbb) 1A7 variable 1ght chain, Mb 1A7 variable against the anti-ganglioside 2 (DD2) Mb 1402a, which binds a raised against the pitope of DD2. As the glycosphingolipid GD2 is expressed WP 100 chainsty by human neuroscrodernal tumpours, e.g. malignatum almona, of the lung, Mb 1A7, or its cDNA can be used in a vaccine to treat of the lung, Mb 1A7, or its cDNA can be used in a vaccine to treat risk of recurrence of a clinically detectable tumour, and detect an x4b 1A7 overcomes immune tolerance and induces an immune response against GD2, which comprises anti-GD2 bh (Mmoral response) and GD2-specific cells (cellular response). It can be used to rest of the comprise anti-DA7 LAM1), anti-GD2 bh (Ma), detectable tumour, and detect anti-LA7 or anti-GD2 in a sample or measure the level of cellular anti-1A7 or response in a sample or measure the level of cellular anti-1A7 or response or the comprise of the comprise anti-DA7 (DA1), anti-GD2 bh (Ma). anti-GD2 activity.
The CDNA can be used in expression systems for 1A7 prodm., and in the progm. of probes and primers to respectively sassy for 1A7 CDNA, and amplify desired polynucleotides for use in gene therapy invaried on 25-MAR-2003 to correct PR field.)

Sequence

149

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81

Conservative

94.9%;

Score 563; DB 20; Pred. No. 3.8e-42;

Length 149; Indels

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Gaps

0

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Mismatches

GVPDRFSGSGSTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 132

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 Matches
 Query Match
Best Local
 Matches
 Sequence
 Treatment
 AAY21545;
 AAY21545
 105;
 82
 Similarity
GVPDKFSGSGGGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNRNTYLEWYLQKPGQSPKLLIYKVSNRFS
 149 AA;
```

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Query Match
Best Local :
The invention provides a method of treating of peoriasis by administering an antigen which has similar immunogenic properties to an antigen expressed on cells of peoriatic tissue so that an immunological response is elicited in the individual. The antigen stimulates the generation of causing the peoriasis are method is used to treat peoriasis, especially experience of the peoriasis. The method is used to treat peoriasis, especially expert plaque type pooriasis or peoriatic actions of people allow the subministry pooriatic expenses allow the individual's com immune system to cat solids. The composition allow the present sequence represents the light can writing the sequence regression of monocoronal antibody law.
 Disclosure; Fig 2; 48pp; English
 WPI; 1999-347407/29
 Chatterjee M,
 16-NOV-1998;
17-NOV-1997;
 Unidentified.
 Psoriasis; immunological response; anti-idiotype antibody; chronic plaque; pustular; plaque-type psoriasis; psoriatic monoclonal antibody; 1A7.
 03-AUG-1999
 (KENT) UNIV KENTUCKY RES FOUND
 17-NOV-1998;
 27-MAY-1999
 WO9925380-A2
 Monoclonal antibody 1A7 light chain variable region
 62 GVPDKFSGSGSGTDFTLKISRVEABDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 21 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS
 105;
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 Similarity 93.8
05; Conservative
 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLBIKR
 of psoriasis
 standard; Protein; 149
 (first
 Foon
 98US-0192838
97US-0065774
 98WO-U$24607
 ζ
 entry)
 94.9%;
 s
 Score 563; DB 17;
Pred. No. 3.8e-42;
 Mismatches
 Length 149;
 Indels
 0
 Gaps
 80
 61
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 RESULT 9
AAY95258
ID AAY9
 c novel monovalent ligand-minerio ther selectively bunder to serie and traced traced by tronfectin receptor alpha ve bera-3. ROW: I plan was exceed by replacing the 19 amino acid heavy chain complementarity determining cregion 3 (CRR) of FACI Fab with the 50 amino acid alpha version 3 (CRR) of FACI Fab with the 50 amino acid alpha version 3 (CRR) of FACI Fab with the 50 amino acid alpha version acceptance of the selection of th
 Matches
 Query Match
Best Local :
 osteoclasts and tumour cells. The agent in the therapeitic composition is preferably a biologically active compound, especially a gene, antisense nucleic acid or catalytic nucleic acid (claimed).
 (Novs)
 Sequence
 The present sequence is that of the light chain of WOW-1 Fab,
 Claim 18; Page 15; 42pp; English.
 Novel monoclonal antibody that selectively binds activated vitronactin receptor useful for detecting the presence of activated vitronactin receptor in tissue and for delivering therapeutic composition to the
 WOW-1; Fab; single chain antibody; PAC-1; monoclonal antibody; mouse; integrin; vitronectin receptor alpha-v beta-3; drug delivery; gene therapy; ligand mimetic.
 N-PSDB;
 WPI; 2000-442184/38
 Shattil SJ, Nemerow GR,
 (NOVS
 04-DEC-1998;
 23-JUL-1999;
 03-DEC-1999;
 15-JUN-2000
 WO200034780-A2
 Mus musculus.
 AAY95258 standard; Protein; 219 AA
 WOW-1 Fab light chain
 12-SEP-2000
 N
 N
 Similarity
 NOVARTIS AG.
NOVARTIS-ERFINDUNGEN VERW GES MBH.
SCRIPPS RES INST.
GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 VLMTQTPLSLPVSLGDQASIPCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 IVETQSPLSLEVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKDGQSDKLLIYKVSNRFS 61
 AAA27849
 219 AA;
 Conservative
 (first entry)
 98US-0110950.
99US-0145458.
 99WO-EP09460
 94.8%;
 Hato T,
 Score 562; DB 2
Pred. No. 7e-42;
6; Mismatches
 Stupack DG,
 DB 21;
 Length 219;
 Pampori NA
 Indels
 0;
 Gaps
 13
 0,
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밁
62
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RESULT 10
ANY49209.
ID ANY49209
XX ANY49209
XX DAY49
XX D
 17-JAN-1995;
 02-NOV-1999
 US5977316-A
 Monoclomal antibody; MAb; 1A7; GD2; immune response; melanoma; neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma; tumor-associated antigen.
 07-PEB-2000
 16-JAN-1996;
 Synthetic.
 MAD 1A7 light
 AAY49209
 AAY49209 standard; Protein;
 (first entry)
 chain variable
 95US-0372676
 96US-0591196
 149 AA
 region
```

WPI; 1999-619711/53. Foon KA, (KENT ) UNIV KENTUCKY Chatterjee SK, Chatterjee 3

Monoclonal antibody 1A7 which elicits an anti-GD2 immunological response, useful for the development of products for the detection treatment of cancers

N-PSDB;

AAZ31365

Claim 1; Fig 1; 74pp; English

The invention provides a monoclonal antihody (MAD) designated 17, which elicits an anti-fo22 (tunor-associated antigen) immunicational response in sequences. The MAD 1A7 has defined light and heavy chain variable regions anti-GD2 immune response. The polypeptides can be used for eliciting an anti-GD2 immune response. The polypeptides can be used for eliciting or purifying anti-GD2 antibody. The products can be used for treating GD2 associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for politating the disease or for reducing the risk of recurrence. The present sequence represents the light chain variable a region of MAD 1A7.

Sequence 149 AA;

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RESULT 11
AAY28468
ID AAY28
XX
AC AAY28
 밁
 8
 밁
 S
 Matches
 Query Match
 AAY28468 standard; Protein; 149 AA
 Local
 81
 62
 105;
 21
 Similarity
 GVPDKF8GSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLBIKR 113
 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQ3SHVPWTFGGGTKLEIKR 132
 VFMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPNLLIYFVSNRFS
 Conservative
 94.6%;
 4;
 Score 561; DB 20;
Pred. No. 5.8e-42;
 Mismatches
 ω,
 Length 149
 Indels
 0,
 Gaps
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80 0

AAY28468;

S

62

21 VFWTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS

80 63

IVEFQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS

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N

Query Match 94.6 Best Local Similarity 93.8 Matches 105; Conservative

94.6%;

Score 561; DB 20; Pred. No. 5.8e-42;

Length 149;

4;

Mismatches

Indels

0,

Gaps

0

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mis polyrepride is the variable light chain region of monoclonal anti-diotype antibody 1A7. The polyrepride has three CDBs (complementarity determining regions) and four frame work regions. Men administered to an individual the 1A7 antibody induces an immune response against ganglioside GD2. The heavy chain variable regions of the 1A7 antibody share antibody and 11ght chain variable regions of the 1A7 antibody produce anti-GD2 T cell and antibody responses. The peptides and antibodises may be useful for the modulation of ganglioside GD2, and particularly for the treatment of GD2-associated ummours e.g. melamona, including small cell lung concer).
 Claim 1; Fig 1; 84pp; English.
 Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas
 N-PSDB; AAX89552
 WPI; 1999-457600/38
 Chatterjee M,
 21-NOV-1996;
 21-NOV-1996;
 US5935821-A.
 (KENT) UNIV
 16-JAN-1996;
 10-AUG-1999
 Region
 Region
 Domain
 Region
 Domain
 Region
 Region
 17-JAN-1995;
 Domain
 Protein
 Key
 Mus musculus.
 ganglioside
 Light chain
 Light chain variable region of MAb 1A7
 06-OCT-1999
 Peptide
 variable region; antibody 1A7; T cell response; melanoma, GD2; CDR; complementarity determining region; carcinoma.
 KENTUCKY
 (first entry)
 96US-0752844.
95US-0372676.
96US-0591196.
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 96US-0752844
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 Location/Qualifiers
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 note= "Complementarity Determining Region
 label= "CDR 3"
 label= "Framework
 note=
 'label= "CDR 2"
 labe1
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 'label= "CDR 1"
 'label= "signal peptide
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Sequence

149 AA

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RESULT 12
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17-JAN-1995;
16-JAN-1996;
 Sequence
 This polymppide is the product of pox amplification and the joining of PCR products. Creating Wr. (Mk.) "In 6 antibody 117. Both the hary and light chain variable regions of the 1x antibody produce anti-CO2 T cell and antibody resources the populses and antibody produce to the treatment of the control of gasglioside CO2 and particularly for the treatment of GD2 antibody the control of gasglioside CO2 and particularly for the treatment of GD2 and particularly for the treatment of GD2 and particularly for the treatment of GD2 and particularly for the creatment of GD2 and GD2 an
 Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas
 Example 7; Fig 15; 84pp; English.
 WPI; 1999-457600/38
 Chatterjee M,
 21-NOV-1996;
 US5935821-A
 Synthetic
 antibody 1A7;
 Vh-(Lk)-Vl; Heavy chain variable region; light chain variable region,
 Vh-(Lk)-Vl of antibody 1A7
 AAY28470
 (KENT) UNIV
 10-AUG-1999
 06-OCT-1999
 AAY28470 standard; Protein;
 Local
 153 VIMTQTPISLPVSIGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPNLLIYFVSNRFS
 62
 104;
 81
 Similarity
 AAX89572
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 263
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR
 263
 Conservative
 KENTUCKY
 (first entry
 ganglioside GD2; carcinoma; melanoma.
 AA,
 Chatterjee
 96US-0752844.
95US-0372676.
96US-0591196.
 96US-0752844
 94.1%;
 SK
 263 AA
 Score 558; DB 20;
Pred. No. 1.9e-41;
 Mismatches
 Foon KA
 20;
 Length
 Indels
 263;
 0
 132
 Gaps
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HESULT 13
ABP52310
XX AP523
XX AP523
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XX AP523
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 The present invention describes the use of a polypopride (1) in the communication of a medicament for stimulating a cytoroxic Total response, where (1) comprises a first portion comprising the part of human Fe that the binds to Chef and a second portion comprising the part of human Fe that the polypoprise in a platient quot as a mamma, preferably human, by the comprise in a platient quot as a mamma, preferably human, by the part of human is polypoprise in a patient quot as a mamma, preferably human, by the part of the patient (1) has cytoriatic activity and can be unsafelying to polypoprise in a patient (1) has cytoriatic activity and can be unsafely in the manifecture of a medicament for extending (1) are certain active that the manifecture of a medicament for preventing addor treating contains a concert, or coall response. The polypoptides and nucleic acide are useful in the coal coal response. The polypoptides and nucleic acide are useful in coal coal coal patient of coal patients and polypoptides and nucleic acide are useful in a coal coal coal patient of the coal patients and patients and patients and patients and patients and patients and patients are useful in a vaccinus for enhancing a protective immune of coal patients and patients are useful and a patient of the coal patients and patients are patients and patients and patients are patients and patients and patients are patients and patients and patients and patients are patients and patients and patients and patients and patients and patients are patients and patients and patients and patients and patients and patients are patients and patient
 Query Match
Best Local
 Matches 102;
 Use of polypeptides and nucleic acids encoding the polypeptides, in manufacturing endicament for stimulating a cytocoxic T cell response and for preventing or treating cancer, e.g. colorectal, lung, breast ovarian cancer.
 Sequence
 Durrant LG,
 28-JAN-2002; 2002WO-GB00354
 Synthetic
 tumour; immune
 Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;
 an example
 Example 11; Page 38; 87pp; English
 WPI; 2002-608418/65
 26-JAN-2001; 2001GB-0002145
 W0200258728-A2
 Mus musculus.
 Fv region SC100 antibody light chain related amino acid sequence #1
 ABP52310;
 ABP52310 standard; peptide; 109 AA
 (CANC-)
 17-OCT-2002
 62
 62
 2 IVLTQSPLSLFVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 Similarity
 SCANCELL LTD.
CANCER RES CAMPAIGN TECHNOLOGY.
 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKL
 GVPDRPSGSGSGTDFTLXISRVEAEDLGIYYCFQGSHVPWTFGGGTKL
 VLMTQTFLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
 from the present invention.
 109 AA;
 Conservative
 Parsons
 (first entry
 response; cancer; vaccine; antibody
 93.8%;
 Robins A;
 Score 556; DB 23;
Pred. No. 1.1e-41;
 Mismatches
 ٥,
 Length 109;
 Indels
 100
 109
 0,
 Gaps
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 61
 61

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 S
 AAY17416
 Matches
 Query Match
Best Local
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The invention provides a monoclopal antibody (Mab) designated 1N, which elicits an anti-GD2 (twoer-associated antiden) immunological response in sequences. The Mab 1N7 has defined light and heavy chain variable region sequences. The Mab 1N7 and polypeptides can be used for eliciting an anti-GD2 immune response. The polypeptides can be used for liciting an anti-GD2 immune response. The polypeptides can be used for provider and the season of the se
 Disclosure; Fig 3C; 74pp; English.
 Monoclonal antibody 1A7 which elicits an anti-GD2 immunological response, useful for the development of products for the detection
 WPI; 1999-619711/53
 Foon
 Konoclomal antibody; MAb: 1A7; GDZ; immune response; melanoma; neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma; tumor-associated antigen.
 07-FEB-2000
 AAY49217;
 AAY49217 standard; Protein; 112 AA.
 17-JAN-1995;
 16-JAN-1996;
 02-NOV-1999
 US5977316-A
 Synthetic.
 Light chain variable region consensus sequence
 (KENT) UNIV KENTUCKY
 of cancers
 Chatterjee SK,
 (first entry)
 9508-0372676
 96US-0591196
 Chatterjee M;
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AAY17416 standard; Protein,
 104;
 62
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
 N
 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKGQSPKLLIYFVSNRFS
 IVLTQSFLSLFVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXFGQSFXLLIYXVSNRFS 61
 Conservative
 Score 555; DB 20;
Pred. No. 1.4e-41;
5; Mismatches 2;
 Indels
 0;
 Gaps
 61
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Sequence

112 AA;

Similarity

93.6%;

tength 112;

0

Mouse; immunoglobulin E; IgE; allergy; transgenic animal

Mouse immunoglobulin E light chain.

26-JUL-1999 AAY17416;

(first entry)

Mus sp.

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 8
 Ouery Match 93.6%; Score 555, DB 20; Length 23
Best Local Similarity 92.9%; Fred. No. 3.2e-41;
Matches 104; Conservative 6; Mismatches 2; Indels
 The present invention describes a transgenic, non-human animal with its genome altered to committatively express a molecula having a consent region which can bind an IgE receptor on mast cells in the animals, the wolecula having an immunopicabilin structure and being further capable of specifically binding a predetermined antigen. The transgenic animal is useful as a nodel for evaluating the activity and the ability of substances i.e. with antiallargic activity, to affect any allergic reaction caused in the animal by the administration of the antigen to the animal, and applying the substance to be evaluated. The present expanses is the mouse immunopicabilin is (193) 1191 this in, yiven in
 Sequence
 the present invention.
 Claim 28; Page 30-32; 42pp; English.
 Transgenic non-human animal allergy models
 N-PSDB; AAX61085.
 13-NOV-1998;
 09-JUN-1999
 Protein
 Key
Peptide
 WPI; 1999-315404/27.
 Karasuyama H, Matsuoka K, Taya C,
 (SANY) SANKYO CO LTD.
(TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.
 14-NOV-1997;
 EP921189-A1
62 GVEDKESGGSGEDETLKISVBAEDLGVYYGEDGSHVENTGGGTKLEIKR 113
81 GVEDREFGGSGGTDFTLKISKPEAEDLGVYYGETGGSKVELTFGAGTKLEIKR 132
 238 AA;
 97JP-0313989.
 98EP-0309340.
 1..19
/label= signal
20..238
/label= immunoglobulin_B_light_chain
 Location/Qualifiers
 Yonemawa H;
 Length 238;
 0;
 Gaps
 0
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Search completed: November 7, 2003, 07:27:01 Job time: 49.7303 secs

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| 525               | 525               | 526               | 531             | 534                  | 535              | 535                | 541               | 541               | 551               | 555              | 558               | 561               | 563               | 571               |  |
| 88.5              | 88.5              | 88.7              | 89.5            | 90.1                 | 90.2             | 90.2               | 91.2              | 91.2              | 92.9              | 93.6             | 94.1              | 94.6              | 94.9              | 96.3              |  |
| 252               | 131               | 112               | 111             | 131                  | 132              | 132                | 140               | 114               | 132               | 112              | 263               | 149               | 149               | 112               |  |
| 10                | 12                | ä                 | 10              | 12                   | 12               | 9                  | 10                | ø                 | 14                | 15               | 15                | 15                | 10                | 11                |  |
| US-09-887-853-4   | US-09-947-839-95  | US-09-518-737-4   | US-09-948-049-2 | .2 US-10-010-942B-14 | US-10-231-452-64 | US-09-796-744-16   | US-09-341-894-4   | US-09-217-268B-27 | US-10-006-773-15  | US-10-153-401-15 | US-10-153-401-66  | US-10-153-401-2   | US-09-990-205-2   | US-09-995-529-10  |  |
| Sequence 4, Appli | Sequence 95, Appl | Sequence 4, Appli | Ņ               | Sequence 14. Appl    | 2                | Sequence 16. April | Sequence 4. Appli | 27,               | Sequence 15, Appl | Sequence 15 Appl | Sequence 66, Appl | Sequence 2, Appli | Sequence 2, Appli | Sequence 10, Appl |  |

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| RESULT 2<br>US-09-990;<br>Sequence;<br>Patent 1  |                                | • •                                       | Query Ma<br>Best Loo<br>Matches | 1 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            |                                  |                      |           |          |                    |                      |        |                     |                      |                                                          |          |          |                |  |
| SULT 2<br>-09-990-20<br>Sequence 2<br>Patent No. |                                |                                           | C st                            | SULT 1 -03-955-529 -03-955-529 Sequence 10 publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication publication                                                                                                                                                                                                                                                                                                                                                                                                                             |            | 444                              | 444                  | 40        | 38       | 365                | ω ω ω<br>Δ ω Ν       | 3130   | 200                 | 202                  | 222                                                      | 3 10 1   | 2 12     | 176            |  |
| 1 200                                            |                                |                                           | 6 F.                            | 9-95-5<br>9-95-5<br>9-95-5<br>9-10-2<br>PPLICAN<br>PPLICAN<br>PPLICAN<br>PPLICAN<br>PPLICAN<br>PPLICAN<br>PPLICAN<br>PPLICAN<br>PPLICAN<br>PPLICAN<br>PRESSY<br>UNBER O<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWAREN<br>OFTWARE |            |                                  |                      |           |          |                    |                      |        |                     |                      |                                                          |          |          |                |  |
| 0 0                                              |                                |                                           | 22.22                           | 5-52 ce 1 Included in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of                                                                                                                                                                                                                                                                                                                                                                                                                             |            |                                  |                      |           |          |                    |                      |        | 51                  |                      |                                                          |          |          |                |  |
|                                                  | 62                             | N N                                       | 10 10                           | -529<br>100<br>1NF<br>1NF<br>1NF<br>1NF<br>1NF<br>1NF<br>1NF<br>1NF<br>1NF<br>1NF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |            | 444                              | L In tr              | 500       | 5 5      | 55                 | 5 5 5                |        |                     | ១១១                  | ម្ចាស់                                                   | n yn s   | 200      | 523            |  |
| ž Ar                                             | 9=9                            | <b>≨</b> ∷                                | ich<br>al simi<br>106;          | i des Predicte o se                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            | ں زت شہ                          | nõõ                  | ឆិស៊ី     | ŭμ       | 5 7                | ສັສັນ                | กกา    | ກ່ານຕໍ່             | 9 9                  | 666                                                      | ř        | 3 83     | 523            |  |
| 200                                              | GVPDKF:<br>    : <br>GVPDRF:   | TATA                                      | o E                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |                                  |                      |           |          |                    |                      |        |                     |                      |                                                          |          |          |                |  |
| 200                                              | 8-8                            | 3S                                        | lari                            | DPlicat US20G ATION: ATION: L'AIR WITON HITON TO ATION TO                                                                                                                                                                                                                                                                                                                                                                                                                             |            | 82                               | 44.                  | 44        | 4.5      | 35                 | 5 6 6                | 888    | 200                 | 87.                  | 87.                                                      | 383      | 888      | 888            |  |
| 150                                              | 8 <u>—</u> 8                   | E=E                                       | ity                             | icati<br>\$2003<br>ON:<br>ON:<br>Will<br>ON:<br>HION:<br>FOIX<br>ION:<br>NOS:<br>NOS:<br>NOS:<br>Ofor                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |            | φ h *                            | <b>ω</b> ω           | 77        | 80       | N UI               | 1 1 0                | ww.    | 2 4 4               | 000                  | ທທ່                                                      | nφ       | 0        | ว่มม           |  |
| 57                                               | 89—88<br>89—88                 | £=£                                       | larity<br>Conservat             | E gwnla lent en                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |                                  |                      |           |          |                    |                      |        |                     |                      |                                                          |          |          |                |  |
| 2<br>Application US/09990205<br>US20020150572A1  | SGSGSGTDFTLKISRVEAEDL          | TVLTQSPLSLPVSLGDQA<br>:::  :              | 1.99                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | 138                              | ::::                 | :::       | 11       | 255                | 2 1 2                | 551    |                     | <b>H</b> N           | NNF                                                      | 1 22 1   | ŅŅ,      | 121            |  |
| 18/0                                             | 3-3                            | គ្គភ្ន                                    | 96.3<br>95.5                    | US/<br>1965<br>TY<br>1965<br>Sate<br>1961<br>1961<br>1961<br>1965                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |            | 80.                              | , i- ö               | 999       | õ'n      | 000                | 200                  | F 50   | 3 7 2               | 14                   | 757                                                      | ÷ 00 1   | 277      | 2 % C          |  |
| 99                                               | 5-5                            | ğ=ğ                                       | **                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | 9 2 2                            | 15                   | 11.0      | 21       | BE?                | 440                  | ويوبو  | ٠.                  |                      | 15 15                                                    | 401      |          | 444            |  |
| 90                                               |                                | S=13                                      | UT .                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | -                                |                      | · ~ ~     | 0 10     | ~ ~ ,              | - 21                 | -01    | ຸ່                  | 100                  | U1 U1 U                                                  | `        | יוטיה    | nNN            |  |
| ĝ,                                               | <u>%</u> _%                    | 8 = S                                     | Scor<br>Pred                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | SSS                              | -80                  | US-09-753 | SDS      | ន្លន               | 808                  | 888    | 3 5 5               | 88                   | US-10-138-505-10<br>US-10-138-505-40<br>US-10-138-505-34 | 3 10 5   | 38       | 888            |  |
|                                                  | æ=æ                            | 82-83                                     |                                 | 29<br>lag<br>ods                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ALIGNMENTS |                                  | 20-09                | 16        | 승분       | 226                | 379                  | 00     | 1 8 1               | 94                   | غ ښ ښ                                                    | . 60     | 44.      |                |  |
|                                                  | 얼그얼                            | 8 <u>—8</u>                               | 9 - 0                           | n 5 Ten                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ତ୍ରି       | 9-8                              | 10-194-              | 9-753-436 | 95       |                    | 200                  | 996    | 72                  | 90                   | 222                                                      | . 6      | 10-1     | 99             |  |
|                                                  | <u>8</u> =8                    | <u>==</u>                                 | 371;<br>lo.                     | 4.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | N.         | 8 4 6                            | 194-                 | 8 4       | 40       | 31                 | 126                  | 726    | 33-                 | 138                  | 385                                                      | üς       | 386      | 277            |  |
|                                                  | 8=8                            |                                           | ğ "                             | O 9 PE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Ĭ,         | 960                              | 4 01                 | 3-94      | 44       | 44                 | 7.4.2                | 26     | 4 2 6               | 65                   | այն այն                                                  | 137      |          | 447            |  |
|                                                  | S-S                            | <u> </u>                                  |                                 | <del>b</del>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 0,         | . 9 4                            | , ու թ               | 42-       | 552      | 555                | 55.6                 | 58.    | 5 6 6               | 39.                  | 305                                                      | 90       | 3 65 6   |                |  |
|                                                  | 38<br>- 88                     | は二世                                       | -49                             | Antibodies<br>29                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |            | 23.4                             | 1126                 | 6 6       | 28       | Ĺż.                | 40                   | υ i i  | 500                 | 123                  | 4.00                                                     |          | 30       | 55             |  |
|                                                  | 3=3                            |                                           | 0.4.1.                          | C C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            |                                  | 9                    |           |          |                    |                      |        |                     |                      |                                                          |          |          |                |  |
|                                                  | \$ <b>=</b> \$                 | <u> </u>                                  |                                 | a nd                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            |                                  |                      |           |          |                    |                      |        |                     |                      |                                                          |          |          |                |  |
|                                                  | ₽—₽                            | 유그유                                       | 5 5                             | ā.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |            |                                  |                      |           |          |                    |                      |        |                     |                      |                                                          |          |          |                |  |
|                                                  | DLGVYYCFQGSHVPWTFGGGTKLEIK<br> | 8=8                                       | Length<br>Indel                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |                                  |                      |           |          |                    |                      |        |                     |                      |                                                          |          |          |                |  |
|                                                  | 골드물                            | 28<br>                                    | CO .                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | 8                                |                      | . o       |          |                    | o                    |        | σ.                  |                      |                                                          | s.       |          |                |  |
|                                                  | H—H                            | 有二百                                       | 112                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | Sequence<br>Sequence<br>Sequence | ĕĕ                   | eg.       | Sec.     | Seguenc<br>Seguenc | Sec                  | Sec    | Sequence            | Sec                  | 360                                                      | Sequence | Sequenc  | Sequenc        |  |
|                                                  |                                | 5=5                                       | ° .                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | en Pue                           | 등                    | ien,      | ă.S.     | 92                 | 5 5                  | 2 2 2  | Jer Ju              | and<br>and           | 122                                                      | en       | 32,0     | 3 4            |  |
|                                                  | 112<br>112                     | 2=2                                       |                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | Sequence<br>Sequence<br>equence  | Sequence<br>Sequence | 90        | Sequence | 000                | Sequence<br>Sequence | n n c  | Sequence<br>equence | Sequence<br>Sequence | Sequence<br>Sequence<br>Sequence                         | equence  | Sequence | 8 8            |  |
|                                                  |                                | \$ — \$                                   | Gap                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | 8 2 4                            |                      | _ o       | 00       |                    | ,                    |        | . 4. 0              | 000                  |                                                          | *        |          |                |  |
|                                                  |                                | ISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS | sq                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | 3,00                             | 19                   | e 66, A   | 4,6      | 5.5                | 8 4 2                | 3.4.5  |                     | 32,                  |                                                          |          | ζ,       | ຸ້າຄຸ້         |  |
|                                                  |                                |                                           |                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | Appl<br>Appli<br>Appli           | ` <b>&gt;</b>        | AB        | > >      | y y to             | Đ»                   | A O F  | Ap.                 | > > :                | > > >                                                    | ģ,       | » è      | Appli<br>Appli |  |
|                                                  |                                | 13                                        | •                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | 1,50,50                          | A P                  | 경호:       | 당당:      | g g f              | gg.                  | g d g  | D.D.                | g g                  | 985                                                      | 1.5      | dd       | ZZ.            |  |
|                                                  |                                |                                           | Č.                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |                                  | <u>,</u>             | _         |          |                    | <b>P. P</b>          | P P. F | . ب                 | 77                   |                                                          | , -      | , – ,    | . р. р.        |  |

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 US-10-153-401-2
 ; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-990-205-2
 Sequence 2, Application US/10153401 Publication No. US20030114398A1 GENERAL INFORMATION:
 Matches 105;
 Query Match
Best Local Similarity
 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
 GENERAL INFORMATION:
 CUURENT APPLICATION NUMBER: US/09/990,205
CURRENT FILING BATE: 2001-11-20
CURRENT FILING BATE: 100.19/192,838
PRIOR APPLICATION NUMBER: U.S. 09/192,838
PRIOR APPLICATION NUMBER: U.S. 60/065,774
PRIOR FILING BATE: 1997-11-17
 APPLICANT: COON, KENNET A.
APPLICANT: CHATTERJEE, MALAYA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 304142010501
 NUMBER OF SEQ ID NOS: 5
NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
CLASSIFICATION: CURROWN
PRIOR APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 POON, KENNELLA.
Chatterjee, Sumil K.
TITLE OF INVENTION: MONCOLOMAL ANTIBODY 1A7 AND USE FOR THE
TERATMENT OF MELANOMA AND SMALL CELL CARCINOMA
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
 APPLICANT: Chatterjee, Malaya
 81
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFOGSHVPWTFGGGTKLEIKR 113
 21 VLMTQTPLSEPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS 80
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIXX 132
 APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 ZIP: 94304-1018
 COUNTRY: USA
 STATE: CA
 CITY: PALO ALTO
 Conservative
 94.9%;
 5
 Score 563; DB 10; Length 149; Pred. No. 1.7e-48;
 Mismatches
 Indels
 0
 Gaps
 0
```

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```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-153-401-66
 RESULT 4
US-10-153-401-66
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 US-10-153-401-2
 Sequence 66, Applicati
Publication No. US2003
GENERAL INFORMATION:
 Matches 105;
 Query Match
 Best Local Similarity
 TELEX: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
 INFORMATION FOR SEQ ID NO: 2:
 PRIOR APPLICATION INTERER: US 09/293,533
PILING DATE: 1999-04-15
PILING DATE: 1999-04-15
PILING DATE: 1999-04-15
PILING DATE: 1999-04-15
PILING DATE: 1999-04-15
PILING DATE: 1999-01-1
PILING DATE: 1995-01-1
PILING DATE: 1995-01-16
PILING DATE: 1995-01-16
PILING DATE: 1995-01-16
PILING DATE: 1995-01-16
 SPARE: CA.

COUNTRY: USA.

COUNTRY: USA.

COMPUTER READABLE FORM:

COMPUTER: LIM FC COMPACIBLE

OPERATING SYSTEM: CC-DOS/MS-DOS

SPERATING SYSTEM: CC-DOS/MS-DOS

CURRENT AFELICATION DAYA:

CURRENT AFELICATION DAYA:
 NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
 POOD, Kenneth A.
FOOD, Kenneth A.
Chatterjee, Sunil K.
Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCHAIL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: MONOCHAIL ANTIBODY 1A7 AND SMALL CELL CARCINOMA
 APPLICANT: Chatterjee, Malaya
 MOLECULE TYPE: protein SEQ ID NO:
 SEQUENCE
 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 132
 62 GVPDXFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 21 VFMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS
 2 IVLTQSPLSLFVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
 TYPE: amino acid
 TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
 APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
 LENGTH: 263 amino acids
 CITY: PALO ALTO
 TOPOLOGY: linear
 TYPE: amino acid
 TELEX: 706141
 LENGTH: 149 amino acids
 Application US/10153401
lo. US20030114398A1
 Conservative
 CHARACTERISTICS:
 94.6%;
 4; Mismatches
 Score 561; DB 15;
Pred. No. 2.6e-48;
 2
 Length 149;
 Indels
 0
 Gaps
 80
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 US-10-153-401-15
 US-10-153-401-15
 Sequence 15, Application US/10153401 Publication No. US20030114398A1
 Matches 104; Conservative
 Query Match
 Matches
 Query Match
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO. 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: anino acids
 Local Similarity
 Local Similarity
 ATTORNEY/AGENT INFORMATION:
ANTO: CECHECINE M. POLIZZÍ
REGISTRATION NUMBER: 40,130
REFERENCE/COUTT NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
 SOFTWARE: RetentIn Release #1.0, Version #1.30
CURRUM REPLICATION INTER
REPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Mag-2002
FILING DATE: 27-Mag-2002
FILING DATE: 37-Mag-2002
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
COMPUTER: DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
 STRANDEDNESS; single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 PRIOR APPLICATION DATA
 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
 Chatierjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
THE THE OF INVENTION: MONOCLONAL ANTIBODY AND SWALL CELL CARCINOMA
 APPLICANT: Chatterjee, Malaya
 NUMBER OF SEQUENCES:
 213 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 263
 153 VIMTQTPLSLPVSLGDQASISCRSSQSTVHSNGWTYLEMYLQXPGQSFWLLIYFVSNRPS 212
 104;
 62 GVPDKFSGSGSGTDFTLK15RVEAEDLGVYYCFQGSHVFWTFGGGTKLEIK 112
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPXLLIYXVSNRFS 61
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
 APELICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
VIMTQTPLSIPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKGQSPKLLIYFVSNRFS 61
 TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
 STATE: CA
 CITY: PALO ALTO
 COUNTRY: USA
 Conservative
 Foon,
 93.6%;
 94.1%;
 Kenneth A.
 5;
 5; Mismatches
 Score 555; DB 15; Length 112; Pred. No. 7.5e-48;
 Score 558; DB 15; Length 263; Pred. No. 9.98-48;
 Mismatches
 2, Indels
 Indels
 0,
 0
 Gaps
 Gaps
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 US-09-217-268B-27
 RESULT 7
US-09-217-268B-27
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 US-10-006-773-15
 US-10-006-773-15
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 Sequence 27, Application US/09217268B
FRIEDRIN NO. US/0020065398A1
GREERLI IMPORMATION:
APPLICANT: HER HER OF A ROSEA del Rio, Christina M
APPLICANT: Rediquez, Rolando P
APPLICANT: ROSEA DEL SECULIA SECULIA DEL SECULIA SEC
 GENERAL IMPORATION:
APPLICANT: JUNGDans, Richard P
RITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against TV
 SEQ ID NO 15
 Sequence 15, Application US/10006773 Publication No. US20020132983A1
 Matches
 SEQ ID NO 27
 Matches
 Query Match
 Query Match
 CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
PRIOR FILING DATE: 2000-11-30
 NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
 FILE REFERENCE: 003
 PERATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: Deduced amino acid sequence of VK of murine R3 antibody
 TYPE: PRT
ORGANISM: Murine R3 antibody
 ORGANISM: Mus sp.
 TYPE: PRT
 LENGTH: 114
 ENGTH:
 Local
 Local
62 GVPDKFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 101, Conservative
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 2 TULTGSFLSLEVISLGDQASISCRSSQSIVHSKONTYLEWILQKFGQSFKLLIYKYSKRRS 60
2 TULTGSFLSLEVISLGDQASISCRSSQSIVHSKONTYLEWILQKFGQSFKLLIYKYSDRSS 80
 103;
 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFQGSHVPYAFGGGTKLEIKR 132
 2 TUTOSPILSI-PVSLGODASI SCRSSON THISNONTYLEWILDKIEGOSPILLI TKYSNRES 61 THISNONTYLEWILDKIEGOSPILLI TKYSNRES 61 THISNONTYLEWILDKIEGOSPILLI TKYSNRES 61 THISNONTYLEWILDKIEGOSPILLI TKYSNRES 61
 132
 Similarity
 Similarity
 Conservative
 92.9%;
 91.2%; Score 541; DB 9; Length 114; 90.2%; Pred. No. 1.9e-46;
 8;
 6; Mismatches
 Score 551; DB 14; Length 132; Pred. No. 2.3e-47;
 Mismatches
 1; Indels
 Indels
 0;
 0,
 Gaps
 Gaps
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62

GVPDRFRGSGSGTDFTLKISRVEAEDLGVYYCFQYSHVPWTFGGGTKLEIKR 113

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US-09-796-744-16
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 US-09-796-744-16
 US-09-341-894-4
 US-09-341-894-4
 APELICANT: SHITANA, KENYA
APPLICANT: HANAI, MOBUO
APPLICANT: SHOJI, ENI
APPLICANT: SAKURADA, MIKKIKO
APPLICANT: FUBUYA, KAKIKO
APPLICANT: MAKAMURA, KAZUYASU
 GENERAL INFORMATION:
APPLICANT: Piechaczyk, Marc
APPLICANT: No. US20020168339A11, Daniele
 SEQ ID NO 16
 GENERAL INFORMATION:
 Seguence 16,
 Matches 101;
 SEQ ID NO 4
 REPLICANT: SIMPA, REVERI
APPLICANT: SIMBATA, KENIA
APPLICANT: SIMBATA, KENIA
APPLICANT: SIMBATA, KENIA
TITLE OF INVENTION: GERE RECOMBINANT ANTIBODY AND ANTIBODY FRAGMENT THERBOF
FILL REFERENCE: 249-170
CURRENT PELLIKOTATON UNBERE: US/09/796,744
CURRENT PELLIKO DATE: 2002-01-04
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
 Sequence 16, Application US/09796744
Patent No. US20020098527A1
 Query Match
Best Local Similarity
 PEATURE:
NAME/KEY: misc feature
LOCATION: (1). (420)
OTHER INFORMATION: Seque
OTHER INFORMATION: ain
 Sequence 4, Application US/09341894
Patent No. US20020168339A1
 FILE REFERENCE: 19904-002
CURRENT APPLICATION NUMBER: US/09/341,894
CURRENT FILING DATE: 1999-12-15
PRICOR APPLICATION NUMBER: FR97/00540
PRICOR FILING DATE: 1997-01-20
UNDSER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.1
 LENCTH: 132
TYPE: PRT
ORGANISM: Mus musculus
 SOFTWARE: PatentIn version 3.1
 TITLE OF INVENTION: Biological material for treating a mammal by antibody gene transferred OF INVENTION: pharmaceutical composition containing same
 ORGANISM: Mus musculus
 LENGTH: 140
TYPE: PRT
 18
 62 GVPDKFSGSGSGTDFT1KISKVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 2 IVLTQSPLSLEVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIYKVSNRFS
 GVPDRFSGSGSGTDFTLKISRVEAEDLGLYYCFQGSHIPFTFGSGTKFEIKR 132
 VVMTQTPLSLSVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRLS
 Conservative
 Sequence coding for the variable region of the antibody
 91.2%;
 Score 541; DB 10;
Pred. No. 2.4e-46;
 Mismatches
 Length 140;
 Indels
 0;
 80
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 US-10-010-942B-14
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 S
 US-10-231-452-64
 US-10-231-452-64
 CURRENT APPLICATION INDERS: US/10/10/010,9428
CURRENT FILLING DATS: 200-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR PILLING DATS: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
 Sequence 14, Application US/100.0042B
publication No. US20030165496A1
GENERAL IMPORMATION: BASIS, OUTIG
APPLICANT: BASIS, OUTIG
APPLICANT: SAIdanha, JUSE
APPLICANT: SAIdanha, JUSE
APPLICANT: SAIdanha, JUSE
APPLICANT: GAIDONK, TUSE
APPLICANT: TOTANICANI HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: BEATA ANTICID PETIDE
TILS REFERENCE: ELM-002
 CURRENT APPLICATION NUMBER: US/10/231,452
CURRENT FILING DATE: 2003-04-18
REIOR APPLICATION NUMBER: UP 2001-265144
REIOR FILING DATE: 2001-08-31
NUMBER OF ERQ ID NOS: 78
SOFTWARE: Parentin Ver. 2.1
SEQ ID NO 64
 GENERAL INFORMATION:
 Matches
 Best Local Similarity
 Query Match
 Publication No.
 Matches
 Query Match
Best Local Similarity
 APPLICANT: NAKAMIRA, KAZIYASU
APPLICANT: POANAKA, RAI
APPLICANT: KORAKA, AKIKO
APPLICANT: KORAKA, AKIKO
APPLICANT: KORAKA PARAKA DIR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF
TILE SEPERBUGE: 249-273
 APPLICANT: SHITARA, KENYA
 LENGTH: 131
TYPE: PRT
ORGANISM: Mus musculus
 LENGTH: 132
TYPE: PRT
ORGANISM: Mus musculus
PEATURE:
NAME/KEY: SIGNAL
 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCPQGSLLPWTFGGGTRLEIRR 132
 21 VLMTQTPLSLPVSLGDQASISCRSSRNIVHINGDTYLEWYLQRPGQSPKLLIYKVSNRFS
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSLLPWTFGGGTRLEIRR 132
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 21 VLMTQTPLSLPVSLGDQASISCRSSRNIVHINGDTYLEWYLQRPGQSPKLLIYKVSNRFS
 2 IVLTQSPLSLEVSIGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIYKVSNRFS 61
 2 IVLTQSPLSLPVSLGUQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIYKVSNRFS 61
 Application US/10231452
to. US20030175273A1
 Conservative
 Conservative
 90.2%; Score 535; DB 12;
87.5%; Pred. No. 8.8e-46;
tive 12; Mismatches 2
 90.2%; Score 535; DB 9;
87.5%; Pred. No. 8.8e-46;
 12; Mismatches
 DB 12;
 2; Indels
 Length 132
 Length 132;
 Indels
 0,
 0
 Gaps
 Gaps
 80
 80
 0
```

LOCATION: (1) ... (19)

61 61

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US-09-518-737-4
 뮺
 US-09-948-049-2
 S
 밁
 US-09-948-049-2
 GENERAL INFORMATION:
APPLICANT: MACHA, SATORIH
APPLICANT: MACHA, SATORIH
APPLICANT: MACHA, SATORIH
APPLICANT: MACHA, SATORIH
APPLICANT: SATO, MACH
ITTLE OF INVENTION: MACHAL
ITTLE OF INVENTION: MACHAL
ITTLE OF INVENTION: PROSPHATEVLINOSITOL-3,4-DIPHOSPHATE
FILE REFERENCE: 1,956/4951
 US-10-010-942B-14
 SEQ ID NO 4
 Sequence 4, Application US/09518737 Publication No. US20030008321A1
 CURRENT APPLICATION NUMBER: US/09/518,737
CURRENT FILING DATE: 0000-03-03
PRIOR APPLICATION NUMBER: JP 1999-250209
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 10
 Sequence 2, Application US/09948049 Patent No. US20020156036A1 GENERAL INFORMATION:
 Matches
 Query Match
 SEQ ID NO 2
 SOFTWARE: Patentin Ver.
 Best Local Similarity
 Query Match
Best Local Similarity
Matches 97; Conserv
 TYPE: PRT
 SOFTWARE: PatentIn version 3.1
 NUMBER OF SEQ ID NOS:
 PRIOR FILING DATE: 2000-09-06
 APPLICANT: Nicolau, Yves Claude
ORGANISM: Mus musculus
 TYPE: PRT
ORGANISM: Murinae gen. sp
 LENGTH:
 63
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLE 110
 111
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
 21 VIMTQTPLSLPVSLGDQASISCRSSQNIIHSNGNTYLEWYLQXPGQSPKLLIYKVSNRFS 80
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRPS 61
 GVPDRFSGSSSGTDFTLKIKKVSAEDLGIXYCFQGSHVPLTFGAGTKLE 111
 VLMTQTPLSLPVSLGDQASISCRSSQNIIHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 62
 GVPDRFSGSGSGTDFTLKIKKVEAEDLGIYYCFQGSHVPLTFGAGTKLELE 131
 Conservative
 Conservative
 89.5%;
 90.1%;
 2.1
 11; Mismatches
 Score 531; DB 10;
Pred. No. 1.8e-45;
9; Mismatches 3;
 Score 534; DB 12;
Pred. No. 1.1e-45;
 DB 12; Length 131;
 3; Indels
 Length 111;
 Indels
 0;
 0,
 Gaps
 Gaps
```

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US-09-947-839-95
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 US-09-947-839-95
 RESULT 14
 US-09-518-737-4
 Query Match
Best Local Similarity
 Sequence 95, Application US/09947839 Publication No. US20030138428A1 GENERAL INFORMATION:
 Matches
 Query Match
 TELEX: n.a.
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
 COMPUTES: IDM 1000 COMPUTES: 100 COMPUTES: 100 COMPUTES: 100 COMPUTES: 100 COMPUTES: 200 5.0

PRINCES PROFINES REPORT RE-1005/RS-100 5.0

CHRESET APPLICATION NUMBER: US/09/947,839

FILIND APPLICATION NUMBER: US/09/947,839

FILIND APPLICATION NUMBER: 09/96,280

PPLICATION NUMBER: 09/976,280

 Local
 MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
 NAMS: Viviana Ameel Ph.D.
REGISTRATION NUMBER: 30,950
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2,13) 622-7700
 Peterson Dr., Jerry A.

Peterson Dr., Jerry A.

Peterson Dr., Jerry A.

Peterson Dr., Jerry A.

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Peterson Dr., Jerry A.

Peterson Dr., Jerry A.

Peterson Dr., Jerry A.

Peterson Dr., Jerry A.

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Peterson Dr., Jerry A.

Peterson Dr., Jerry A.

Peters
 COMPUTER READABLE FORM:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 APPLICANT: do Couto Dr., Fernando J.R.
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 COUNTRY: USA
ZIP: 90071
 STREET: 444 South
CITY: Los Angeles
STATE: California
 TELEFAX: (213) 489-4210
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88.5%; Score 525; DB 12;
87.4%; Pred. No. 8.7e-45;
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Best Local Similarity 88.4%; Prod. NO. 180-44;
Matches 99; Conservative 8; Mismatches 5; Indels
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Patent No. US20020168375A1
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 CITY: Boston....

STATES Messachusetts
COUNTRY: USA
ZIP. 02109

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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: NOTA: 1.0, Version #1.25
CHEASYN APPLICATION MYMESR: US/09/887,853
FILING DATE: 21-JOU-2001
CLASSIFFCATION: UMBER: UMAROWND
 CORRESCONDENCE ADDRESS:

CORRESCONDENCE ADDRESS:

CORRESCONDENCE ADDRESS:

CORREST: Exchange Place, 53 State Street
 Oppermann, Hermann
Houston, L. L.
Ring, David B.
 NUMBER OF SEQUENCES: 11
 APPLICANT: Huston, James S.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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sequence: Perfect score: US-09-661-992B-84\_COPY\_137\_249 593 1 QIVLTQSPLSLPVSLGDQAS......FQGSHVPWTRGGGTKLBIKR 113

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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## SUMMARIES

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| 00-00-000-019-19  | 10 00 00 00 00 00 00 00 00 00 00 00 00 0 | -08-759-8043- | US-08-331-397B-34 | US-08-331-398A-34 | US-09-227-693-34  | PCT-US94-06687-3  | US-09-657-274-3   | US-09-227-693-48  | US-09-002-753A-3 | US-08-759-804A-48 | US-08-331-397B-48 | US-08-077-252B-3  | US-08-331-398A-48 | US-09-192-545-4 | US-09-293-533-15  | US-08-591-196-15 | US-08-752-844-15 | US-09-293-533-66 | US-08-752-844-66 | US-09-293-533-2 | US-08-591-196-2   | US-08-752-844-2 | US-08-759-804A-66 | US-08-331-397B-67 | US-08-331-398A-67 | US-09-324-191-2   | US-09-192-838B-2  | , | ID          |        |
| sequence 19, Appl | ,                                        | ۲,            |                   | Sequence 34, Appl | Sequence 34, Appl | Sequence 3, Appli | Sequence 3, Appli | Sequence 48, Appl | ω                |                   | 48                | Sequence 3, Appli | 48                | 4               | Sequence 15, Appl | 15               | 15               | 66               | 66               | 2               | Sequence 2, Appli | Ņ               | Sequence 66, Appl | 67                | Sequence 67, Appl | Sequence 2, Appli | Sequence 2, Appli |   | Description |        |

UNS-05-234-191-2

Sequence 2. Application US/09324191

Patent No. 6562798

GREERAL IMPORMATION

APPLICANT: CHATTEROIS, MALAYS

APPLICANT: CHATTEROIS, MALAYS

APPLICANT: CHATTEROIS, MALAYS

APPLICANT: POON, Kenneth A.

TITLE OF INVENTIONS HATTHOODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS

FILE REFERENCE: 304142006540

CURRENT PILLING DATE: 1999-66-02

EARLIER PILLING DATE: 1999-66-02

EARLIER PILLING DATE: 1999-16-02

EARLIER FILLING DATE: 1999-16-02

SOFTWARE: PatentIn Ver. 2.0

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| at Toppendo | US-09-443-213-21 | US-09-166-094-21 | US-09-172-019-21 | -09      | US-09-166-750-21 | US-08-926-789-12 | US-08-392-338A-21 | US-08-224-591-12 | US-08-053-171-9 | US-08-053-171-5 | US-08-560-558E-27 | US-08-497-312-18 | US-08-888-366-16 | US-08-859-648-29 | US-08-859-648-19 | US-08-207-861-29 | US-08-207-861-19 | US-08-859-649-29 |  |
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|             | Appl             | Appl             | Appl             | Appl     | App1             | Appl             | App1              | Appl             | Appli           | Appli           | Appl              | Appl             | App1             | App1             | Appl             | Appl             | Appl             | App1             |  |
|             |                  |                  |                  |          |                  |                  |                   |                  |                 |                 |                   |                  |                  |                  |                  |                  |                  |                  |  |

## ALLGMENT'S

US-09-192-838B-2

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 믕
 US-09-192-838B-2
 Sequence 2. Application US/091928388

Sequence 2. Application US/091928388

ERRERL HROWSSEAU.

APPLICANT: COMMITTENIES, MALAYA

APPLICANT: COMMITTENIES, MALAYA

TITLE OF INVESTION: METHOUS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS

FILE REFERENCE: 904442000500

CURRENT PELLING DATE: 1998-11-16

PRIOR APPLICATION NUMBER: 05/05/192,838B

REGURE APPLICATION NUMBER: 05/05/744

REGURE TITLE DATE: 1997-11-15

PRIOR FILING DATE: 1997-11-15

PRIOR FILING DATE: 1997-11-15

PRIOR FILING DATE: 1997-11-15

APPLICATION DATE: 1997-11-15

APPLICATION DATE: 1997-11-15

APPLICATION DATE: 1997-11-15

APPLICATION DATE: 1997-11-15

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APPLICATION DATE: 1997-11-15

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REGISTRATION WINEER: 38,498
REFERENCE/DOCKET NUMBER: 0.152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9600
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TELEPHONE: (415) 543-567
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 ORGANISM: Mus Musculus
 TYPE: PRT
 APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David
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 APELICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-191
PRICH REPLICATION DATA:
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FILING DATE: 12-CCT-1990
ATTORNEY/AGENT INFORMATION:
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 REPLICANT: Pai, Lee
TITHE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITHE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION:
OTHER INFORMATION:
 SEQUENCE CHARACTERISTICS:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
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 TOPOLOGY:
 APPLICATION NUMBER:
FILING DATE: 28-OCT
 COUNTRY:
 CITY: San Francisco
STATE: California
 ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Plaza
 STRANDEDNESS:
 LENGTH: 125 amino acids
TYPE: amino acid
 67, Application US/08331398A
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APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
 TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 67:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS: Townsend and Townsend and Crew
ADDRESSIE: Townsend and Townsend and Erret
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
 TITLE OF INVENTION:
TITLE OF INVENTION:
 TELEPHONE: (415) 543-9600
 FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
 MOLECULE TYPE:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 01
 MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TOPOLOGY:
 TYPE: amino acid
 APPLICATION NUMBER: US 07/596,289 FILING DATE: 12-OCT-1990
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 FILING DATE: 28-OCT-1994
 APPLICATION NUMBER:
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 NAME/KEY: Region
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 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 66
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATCHITA BACHESE #1.0, Version #1.30
CURRENT PSPILCHTION BAFM:
 APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David
APPLICANT: Brinkmann, Ulrich
 FEATURE:
 SEQUENCE CHARACTERISTICS
 ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 12-OCT-1990
 CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/331,398
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
 TITLE OF INVENTION: Tumor-Specific Antibody Fragments, TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
 TOPOLOGY: 111
 REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES:
 APPLICANT:
 LOCATION: 1..125
OTHER INFORMATION:
OTHER INFORMATION:
 STREET:
 Local Similarity
 NAME/KEY: Region
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 APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
 FILING DATE:
 APPLICATION NUMBER: US/0
FILING DATE: 03-DEC-1996
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 STATE:
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 San Francisco

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amino acid

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: Sequence 2. Application US/08591196
| Patent No. 5971216
| GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT POOR, Menneth A
APPLICANT: Poor, Menneth A
APPLICANT: Poor, Menneth A
APPLICANT: Poor, Menneth A
I TITUS OF INVESTITION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
 US-08-591-196-2
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 ; MOLECULE TYPE: protein US-08-752-844-2
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 US-08-752-844-2
 Sequence 2, Mys-
 Matches
 Query Match
 TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
 CLASSIFICATION: 424
ATTOMNEY/AGENT IMPORMATION:
NAME: SCHIEF, J. Michael
REGISTRATION NUMBER: 40,253
REGERRACE/DOCKET NUMBER: 3041
TELECOMMUNICATION IMPORMATION:
TELECHNONE: (4,11) 813-5600
 GENERAL INFORMATION:
 MEDIUM TYPE: Floppy disk
COMPUTER: IRW PC compactible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 APPLICANT: Coch. Kenneth A.
APPLICANT: Chatesjee, sunil K.
TITLE OF INVENTION: MONOCIONAL ANTIBODY LA7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANCHA AND SMALL CELL CARCINOMA
KUMBER OF SEQUENCES: 65
 SEQUENCE CHARACTERISTICS
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
 APPLICANT:
 TOPOLOGY:
 TYPE:
 LENGTH:
 APPLICATION NUMBER: US/08/752,844 FILING DATE:
 STATE: CA
 CITY: PALO ALTO
 Local
 COUNTRY:
 105; Conservative
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 21 VFWTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS 80
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 132
 62 GVPDRESGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGSGTKLEIKR 113
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
 94304-1018
 Similarity
 : 149 amino acide
amino acid
 Application US/08752844
 USA
 Chatterjee, Malaya
 linear
 94.6%;
 4; Mismatches
 30414-20002.21
 Score 561; DB 2; Length 149;
Pred. No. 1.8e-47;
 3; Indels
 0;
 Gaps
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US-09-293-533-2
 Patent No.
 Sequence 2, Application US/09293533
Patent No. 6509016
 Matches 105;
 Best Local Similarity
 Query Match
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
ZIF: 94304-1018
COMPUTER REALDREE POOM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
 TITLE OF INVENTION:
 APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
 MOLECULE TYPE: protein
 ATTORNEY/AGENT INFORMATION:
NAME: SCLIEF, J. MICHAEL
REGISTRATION MUNBER: 40,253
RESERVEY/DOCKET NUMBER: 30414-20002.20
TELECOMMUNICATION INFORMATION:
TELECPHONE: (415) 813-5600
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC comp
 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
 NUMBER OF SEQUENCES:
 STREET: PALO ALTO
 NUMBER OF SEQUENCES:
 TITLE OF INVENTION:
 STREET: 755 PAGE
CITY: PALO ALTO
STATE: CA
 COUNTRY:
 ADDRESSEE: MOKKADON COAD
 TOPOLOGY:
 TYPE:
 TELEPHONE: (415) 494-0792
 FILING DATE: 16-JAN-1996
CLASSIFICATION: 424
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 LENGTH: 149 amino acids
TYPE: amino acid
 APPLICATION NUMBER:
 COUNTRY:
 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 132
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 21 VFMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
 94304-1018
 70614
 USA
 Conservative
 USA
 Floppy disk
 TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
 94.6%; Score 561; DB 2; Length 149; 93.8%; Pred. No. 1.8e-47;
 TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
 66
 57
 US/08/591,196
 4
 Mismatches
 Indels
 <u>.</u>
 Gaps
 80
 0
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 US-08-752-844-66
 US-09-293-533-2
 Patent No. 5935821
GENERAL INFORMATION:
 Sequence 66, Application US/08752844 Patent No. 5935821
 Matches 105; Conservative
 Query Match
 TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS;
 TELEFAX: (415) 494-0792
TELEFAX: (66141
INFORMATION FOR ESQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: BETT 2515
 ATTORNEY/AGENT INFORMATION:
NAME: SCHIEF, J. MICHAEL
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 3041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
 ATTORNEY/AGENT INFORMATION:
NAME: SCHIEF, J. MICHAEL
RECISTRATION NUMBER: 40,253
RESERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 813-5600
 SOPTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA, APPLICATION UNBER: US/08/752,844 FILING DATE: 424 CLASSIFICATION: 424
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
OPERATING SYSTEM: FC-DOS/MS-DOS
 APPLICANT: Chaiterjee, Malaya
APPLICANT: COM. Kenneth A.
APPLICANT: Chaiterjee, Sunil K.
TITLE OF INVENTION: MANCECOMAL ANTHEODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOWA AND SMALL CELL CARCINOMA
 CORRESPONDENCE ADDRESS:
 LENGTH: 149 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
 NUMBER OF SEQUENCES:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 TELEPHONE: (415) 494-0792
 COUNTRY: USA
ZIP: 94304-1018
 CITY: PALO ALTO
 STATE:
 ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
LENGTH: 263 amino acids
 Local Similarity
 TELEPHONE: (415) 494-0792
 CLASSIFICATION:
 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 132
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 21 VENTQTELSLEVSLGDQASISCRSSQSIVHSNGNTYLBWYLQKFGQSENLLIYFVSNRFS
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
 ß
 94.6%;
93.8%;
 66
 US/08/752,844
 4; Mismatches
 Score 561; DB 4;
Pred. No. 1.8e-47;
 30414-20002.21
 Version #1.30
 3; Indels
 Length 149;
 0
 Gaps
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ropology:

MOLECULE TYPE: protein

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 ; MOLECULE TYPE; protein
US-09-293-533-66
 US-09-293-533-66
 Query Match
 Patent No. 65090
 Sequence 66,
 Matches
 Query Match
 TELEX: 706141
INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
 GENERAL INFORMATION:
 APPLICANY: Chatterjee, Malaya
APPLICANY: foon, Konneth A.
APPLICANY: Chatterjee, Sunil K.
TITLE OF INVENTION: WOOCLOANL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TRANYEST OF MELANOMA AND SMALL CELL CERCINOMA
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
 ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER:
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 STREET: 755
 LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
 COUNTRY:
ZIP: 943
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Watch Watch 94.1%; Score 558, DB 4; Length 263; Match Similarity 93.7%; Pred. NO. 6.66-47; es 104; Conservative 5; Mismatches 2; Indels
 TELEFAX:
 TELEPHONE:
 CLASSIFICATION:
 FILING DATE:
 APPLICATION NUMBER: US/09/293,533
 ADDRESSEE:
 Local
213 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 263
 213 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 263
 153 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS 212
 104;
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYXCFQGSHVPWTFGGGTKLEIK 112
 62 GVPDKFSGSGSGTDFTLKISRVBAEDLGVYYCFQGSHVPWTFGGGTKLBIK 112
 2 IVLTQSPLSLEVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPXLLIYKVSNRFS 61
 h 94.1%; Score 558; DB 2; Length 263; Similarity 93.7%; Pred. No. 6.6e-47;
 94304-1018
 Application US/09293533
 E: MORRISON & FOERSTER
755 PAGE MILL ROAD
 (415) 494-0792
 USA
 Conservative
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 US/08/752,844
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 30414-20002.21
 Mismatches
 2; Indels
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 Gaps
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 RESULT 11
US-08-752-844-15
 # Sequence 15, Application US/08591196
| Patent No. 5977316
| GENERAL INFORMATION:
 US-08-591-196-15
 US-08-752-844-15
 Sequence 15, Application US/08752844
Patent No. 5935821
 Matches 104; Conservative
 Query Match
 GENERAL HEORAWITON:
APPLICANT: Chartezjee, Malaya
APPLICANT: FROM. Kemmeth A.
APPLICANT: FROM. Kemmeth A.
APPLICANT: OF INVESTION: MONOCLOWAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVESTION: MONOCLOWAL ANTIBODY 1A7 AND SWALL CELL CARCINONA
TITLE OF INVESTION: TEMPORATION OF SELANOWA AND SWALL CELL CARCINONA
 TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICANT: CDARLEYJGE, MALAYA
APPLICANT: CDARLEYJGE, SUNLI K.
APPLICANT: CDARLEYJGE, SUNLI K.
APPLICANT: CDARLEYJGE, SUNLI K.
TITLE OF INVENTION: MONOCIONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SQUINCES: 57
CORRESPONDENCE ADDRESS: 57
CORRESPONDENCE ADDRESS: 57
CORRESPONDENCE MOREIGON & FORRITER
ADDRESSE: MOREIGON & FORRITER
STREET: 755 PAGE MILL KOLD
 TOPOLOGY: 1:
MOLECULE TYPE:
 ATTORNEY /ACSET INFORMATION:
NAME: SCHIEF, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION: INFORMATION:
 OPERANTWA SYSTEM; PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Vergion #1.30
CIRRENT APPLICATION DATA:
PILING DATE:
PILING DATE:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: WORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
 NUMBER OF SEQUENCES:
 COUNTRY:
 TYPE: amino acid
 Local Similarity
 STRANDEDNESS:
 TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
 CLASSIFICATION:
 ZIP: 94304-1018
 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIX 112
 62 GVPDKFSGSGSGTDFTLKISRVEREDLGVYYCFQGSHVPWTFGGGTKLEIK 112
 2 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKGQSPKLLIYFVSNRFS 61
 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIYKVSNRFS 61
 PALO ALTO
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 USA
 linear
 peptide
 single
 424
 93.6%; Score 555; DB 2;
93.7%; Pred, No. 5e-47;
 66
 5; Mismatches
 DB 2; Length 112;
 2; Indels
 0;
 Gaps
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 US-09-293-533-15
 US-08-591-196-15
 Sequence 15, Application US/09293533
Patent No. 6509016
GENERAL INFORMATION:
 Matches 104; Conservative
 Query Match
Best Local Similarity
 ZIP: 94304-1018
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: LIBM PC compatible
OPERATING SISTEM: PC-DOS/MS-DOS
SOTTMARE: Facturin Release #1.0, v
CURRENT APPLICATION DATA:
 NAME: SChiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 304.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (115) 494-0792
 TELEX: 706141
INFORMATION FOR SEQ ID NO:
 APPLICANT; Charterjee, Malaya
APPLICANT; Conterjee, Malaya
APPLICANT; Charterjee, Sunil K.
TITLE OF INVENTION; MONCHONAL ANTIBODY LAT AND USE FOR THE
TITLE OF INVENTION; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
 COMPUTER READABLE FORM:
MEDIUM TYPE: #loppy disk
COMPUTER: IBM PC Compatible
COMPATER: IBM PC Compatible
OPERATING SYSTEM: 9C-DOS/M9-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 1
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES: 6
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 SEQUENCE CHARACTERISTICS
 ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER:
 ZIP: 94304-1018
 COUNTRY:
 STATE:
 STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
 ADDRESSEE: MORRISON & FOERSTER
 STRANDEDNESS:
 FILING DATE: 16-JAN
CLASSIFICATION: 424
 LENGTH:
 APPLICATION NUMBER: US/08/591,196
 COUNTRY:
 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVXYCFQGSHVPWTFGGGTKLEIK 112
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 2 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKGQSPKLLIYFVSNRFS
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US/08/752,844
 US/09/293,533
 5; Mismatches
 Score 555; DB 2.
Pred. No. 5e-47;
 30414-20002.20
 Version #1.30
 DB 2;
 2; Indels
 Length 112;
 0
 Gaps
 61
 0,
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; Sequence 48, Application US/08331398A; Patent No. 5608039; GENERAL INFORMATION:
 RESULT 15
US-08-331-398A-48
 . LENGTH: 238
; TVPS: PRT
; TVPS: PRT
; OGGANISM: Artificial Sequence
; PERTURE: Description of Artificial Sequence: Designed heavy
US-09-197-815-1
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 US-09-192-545-4
 US-09-293-533-15
 EARLIER APPLICANTON NUMBER: JP HEI 9-313989
EARLIER FILMA DAME: 1997-11-14
NUMBER OF SEQ ID NOS: 12
SOFTHARE: Patentin Ver: 2.0
SEQ ID NO 4.
 IMEDEX: 70415) 494-0792
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHERACTERISTICS:
LENGTH: 112 mino ecid
STRANDEDESS; sindla
TYPE; maino ecid
STRANDEDESS; sindla
 Matches 104; Conservative
 GENERAL INFORMATION:
 Sequence 4, Application US/09192545
Patent No. 6118044
 Query Match
Best Local Similarity
 Query Match
 APPLICANT: Taya, Choi
APPLICANT: Mespota, Kunie
APPLICANT: Mespota, Kunie
TITE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their U
FILE REFERENCE: T99P95970
CURRENT APPLICATION NUMBER: US/09/192,545
CURRENT FAILUR DAIRS: 1196-11-3
 Matches
 APPLICANT: Karasuyama, Hajime
APPLICANT: Yonekawa, Hiromichi
APPLICANT:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
 MOLECULE TYPE: peptide
 ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
 Local Similarity
nes 104; Conserv
 REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30
 81
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
 21 VIMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPXLLIYKVSNRFS
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 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
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 93.6%; Score 555; DB 4; Length 112;
93.7%; Pred. No. 5e-47;
ative 5; Mismatches 2; Indels
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 30414-20002.21
 Score 555; DB 3;
Pred. No. 1.2e-46;
 Mismatches
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 Gaps
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 80
 61
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APPLICANT: Willingham, Mark
APPLICANT: Eticofadl, David
APPLICANT: Eticofadl, David
APPLICANT: Eticofadl, David
APPLICANT: Eticofadl, David
APPLICANT: Eticofadl, David
APPLICANT: Eticofadl, David
APPLICANT: Eticofadl, David
APPLICANT: Eticofadl, David
APPLICANT: Eticofadl, David
Title OF INVENTION: Single Chain B3 Antibody Fusion Protesins
TITLE OF SEQUENCES: 68
INVENTION: Experiment of Crew
STREET: One Market Plaza, Stewart Street Plaza
CTY: San Francisca
CTY: San
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 Post-processing: Minimum Match 0%
Maximum Match 100%
 Maximum
 Minimum
 Total number of hits satisfying chosen parameters:
 Searched:
 Scoring table:
 Sequence:
 Perfect score:
 Run on:
 OM protein
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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492.5
489
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486.5
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500.5
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 510.5
 514.5
514.5
514.5
514.5
 539.5
518
517.5
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length: 2000000000
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2: pir2:*
3: pir3:*
4: pir4:*
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 79.9
79.8
79.8
79.3
79.0
79.0
79.0
 Listing first 45 summaries
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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 119
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B31790
A27888
$26790
$38808
 S63597
B26471
 S55536
S55537
 809258
 SUMMARIES
 FTVNWYFDVWGAGTLVTVSA 122
 283308
 Description
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A:Experimental source: strain Balb/c
A:Hore: this sequence was determined from the germline gene
C:Comment: This chain was alsolated from a hybridoma protein that binds influenz
C:Comperfanily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <1MM>

A; Molecule type: DNA A; Residues: 1-122 < CAT>

CjAccession: R27888

R;Geton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

BWBO J. 5, 1577-1587, 1986

BWBO J. 5, 1577-1587, 1986

A;Title: Structural and functional implications of a restricted antibody respon

A;Beference number: A91043; WIID:86300658; PMID:2427335

A;Accession: E27888

Ig heavy chain V region (H35-CG) - mouse C:Species: Mhs mascilus (house mouse) C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996

| 483.54<br>483.54<br>483.54<br>482.54<br>480.55<br>497.55<br>477.55<br>477.55<br>477.55<br>477.55<br>477.55<br>477.55<br>477.55                                                                                                                                                                                                        |  |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
| 77777777777777777777777777777777777777                                                                                                                                                                                                                                                                                                |  |
| 121<br>121<br>121<br>128<br>129<br>129<br>129<br>129<br>142<br>142<br>142<br>142<br>143<br>143<br>143<br>144<br>145<br>147<br>147<br>147<br>147                                                                                                                                                                                       |  |
| 000000000000000                                                                                                                                                                                                                                                                                                                       |  |
| B27888 PH1007 PH1007 P27888 S20641 P47888 I27888 G27888 G27888 G27888 G37888 I27888 G37889 I377889 I377889 PH1008 C36005                                                                                                                                                                                                              |  |
| Ig beavy chain V Ig heavy chain IV Ig heavy chain IV Ig heavy chain IV Ig heavy chain V |  |

#### ALIGNMENTS

| RESULT 2<br>S26327<br>Ig heavy<br>C; Species<br>C; Date: 1<br>C; Accessi<br>R; Stark,<br>J. Exp. h                                                                                                                                                                                                                                                                                                          | В          | Ş          | Вb                                                                  | Ş                                                                   | 망                                                                 | Ø                                                                 | Matcher                                                    | Query Match<br>Best Local                                                                         |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|------------|---------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------------------------------------------|-------------------------------------------------------------------|------------------------------------------------------------|---------------------------------------------------------------------------------------------------|
| RESULT 2 S163237 Shain V region - mouse (fragment) GD heavy : Nha muselia (house misson 19-Mar-1998 #text_change 21-Jan-2000 C)Abtes: 19-Mar-1998 Heequenous_revision 19-Mar-1998 #text_change 21-Jan-2000 C)Abcession: 863627 Heequenous_revision 19-Mar-1998 #text_change 21-Jan-2000 C)Abcession: 8617 Gloon, A.J. N.Stark, B.B.: Guton, A.J. N.Stark, B.B.: Guton, A.J. U. Szp. Med. 174, 613-624, 1991 | 121 VS 122 | 120 VS 121 | 61 PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCTRQGEGYRYDDYAMDYWGQGTSVT 120 | 61 PDSVKGRFTISRDNAKNTLYLQNSSLRSEDTAMYYCTREGGGFTVNWY-FDVWGAGTLVT 119 | 1 DVKLVESGGGLVKPGGSLKLSCAASGETPSSYTMSWVRQTPEKRLEWVATISSGGSYTYY 60 | 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60 | Matches 105; Conservative 6; Mismatches 10; Indels 1; Gaps | Query Match 83.8%; Score 539.5; DB 2; Length 122; Best Local Similarity 86.1%; Prod. No. 6 5e-41; |
|                                                                                                                                                                                                                                                                                                                                                                                                             |            |            | 20                                                                  | 19                                                                  | ٥                                                                 | ٥                                                                 | Ľ,                                                         |                                                                                                   |

A. Title: Antibodies that are specific for a single amino acid interchange A. Facterance number: 826309; MUID:91341421; PMID:1908510
A. Faccastion: 826327
A. Faccatic type: mBNA
A. Faccation: 1-112 eSTBA. Faccatic type: mBNA
A. Faccation: 1-112 eSTBA. Cross-reference: BMBL-X59192
C; Superfamily: immunoglobulin V region; immunoglobulin homology

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A, Molecule type: DNA
A, Beacidues: 1.19 <CAT>
A, Experimental source: scrain Balb/c
A, Experimental source: scrain Balb/c
A, Experimental source: scrain Balb/c
A, Experimental source: scrain Balb/c
C, Comment: This chain was isolated from a hybridoma procesin that binds influenza virus
C, Comment: This chain was isolated from a hybridoma process
C, Supportantly: immunoglobulin vegology. Immunoglobulin
F, 15-98/Domain: immunoglobulin to-mology. Info:
F, 15-98/Domain: immunoglobulin to-mology. Info:
F, 15-98/Domain: immunoglobulin to-mology. Info:
 R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. Jung, Ned. 171, 265-297, 1990
A;Title: Anri-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PLO231, NUID:90111618; PMID:2104919
A;Accession: PLO231,
 C;Species: Mus musculus (house mouse)
C;Species: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: FL0249
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 A;Catton, A.J., Brownlee, G.G.; Staudt, L.M.; Gerhard, W. BMEO J. 5177-1587, 1986 G.; Staudt, L.M.; Gerhard, W. A;Thile: Structural and functional implications of a restricted antibody response A;Reference number: A91043, MUID:8630658; PMID:2427355 A;Recession: F721888
 C;Accession: F27888
 Ig beary chain V region (H158-89H4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1998 #sequence_revision 15-Dec-1998 #text_change 16-Aug-1996
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 F;109-117/Region: framework 4
 F:50-66/Region: complementarity-determining F:67-98/Region: framework 3
 F;36-49/Region: framework 2
 F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMN
F;31-35/Region: complementarity-determining 1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
 A; Residues: 1-117 <SHL>
 A; Molecule type: mRNA
 Ig heavy chain V region (anti-DNA, 3E12VH) - mouse Crapecies: Mus musculus (house mouse)
 C; Keywords: heterotetramer; immunoglobulin F;9-91/Domain: immunoglobulin homology < IM
 99-108/Region: complementarity-determining
 Query Match
 Matches 101;
 Query Match
 Matches
 Local Similarity
 Local Similarity
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 60
 67
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 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTFEKRLEWVATISSGGSSTYY
 SGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASISSGG-STYYPDSVKG
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVMGAGTLVTV 120
 EVKLVESGGGLVKPGGSLKLSCAASGPTFSSYTMSWVRQTPAKKLEWVANISRRGGSTYY 60
 RETISRDNARNILYLOMSSLRSEDTAMYYCARLYGNY---WYEDVWGAGTTVTVSS 112
 RFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTVSA 122
 SGGGLVKPGGSLKLSCAASGETFSSYTMSWVRQTPEKRLEWVATISSGGSSTYYPDSVKG 66
 PDSVKGRFTISRDNARNTLYLOMSSLRSEDTAVYYCARRDYS---HWFFDVWGAGTTVTV
 immunoglobulin homology < IMM>
 Conservative
 Conservative
 80.4%;
 83.3%;
 4;
 5;
 Score 517.5; Pred. No. 5.5e
5; Mismatches
 Score 518; DB 2; Length 112;
Pred. No. 4.7e-39;
 Mismatches
 .5e-39;
 DB 2;
 12;
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 Indels
 Length 117;
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 4.
 Gaps
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 117
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 SSSSI7 Wregion pe21 - mouse (fragment)

Capacies Mus musculus (bouse mouse)

Capacies Mus musculus (bouse mouse)

Capacies Mus musculus (bouse mouse)

Capacies Musculus (bouse mouse)

Capacies Musculus S
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Ajkolecula type: mRMA
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 A; Status: preliminary
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Ig heavy chain V region pe20 - mouse (fragment)
Clapacias: Num unaculius (house mouse)
Clate: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
Clacession 55556
K; Boetcest, V; Boetcey, A.; Lane, E.S.; Spruce, B.A.
J. Nol. Biol. 247, 932-966, 1995
M; Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibod utations in the variable region genes.
 C superfamily: immunoglobulin V region; immunoglobulin homology C; superfamily: immunoglobulin D; revyocrds: heteroretramer; immunoglobulin R_114-97/\text{Domain}: immunoglobulin homology <104/>>
 A;Residues: 1-120 <BOB>
A;Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
 A; Molecule type: mRNA
 A;Status: preliminary
 A; Reference number: 855528; MUID: 95239763; PMID: 7536850 A; Accession: 855536
 Query Match
Best Local Similarity
 Matches
 Matches
 Query Match
Best Local :
 119 $ 119
 121 8 121
120 S 120
 122 A 122
 102;
 102;
 61
 61
 62
 62 DSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTVS 121
 1 DVKLVESGGGLVKPGGSLKLSCÅÅSGFTFSSYTMSWVRQTPEKRLEWVATISSGGSYTYY
 1 EVQLQESGGGLVKPGGSLKLSCAASGETFSSYTMSWVRQTPEKKLEWVATISSGGSSTYY
 Similarity
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVMGAGTLVTV
 DSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCARLYYDYD-PYVMDYWGQGTTVTVS
 VQLQESGGGLVKPGGSLKLSCAASGFTFSTYAMSWVRQTPEKRLEWVATISSGGSYTYYP
 VQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYYF
 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCPR--GETYYDYAMDYWGQGTSVTV
 Conservative
 Conservative
 84.3%;
 79.9%;
 ū
 4
 Score 516; DB 2;
Pred. No. 7.6e-39;
 Score 514.5;
Pred. No. le
 Mismatches
 Mismatches
 1e-38;
 B
 14; Indels
 2;
 Length 119
 Length
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 2;
 Gaps
 Gaps
 120
 60
 61
 119
 60
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| ESULT 8  Z78877  Z78877  Z78874  Z7887 | guesda Mai muccium (house mouse)  place 29-Jan-1933 Heeglence_revision 29-Jan-1933 Hext_change 23-Jul-1999  place 29-Jan-1933 Heeglence_revision 29-Jan-1933 Hext_change 23-Jul-1999  place 29-Jan-1933 Heeglence_revision 29-Jan-1933 Hext_change 23-Jul-1999  placesson; 509258  plac | COMPTY MARCH  ORDER TABLE  ST. 14, PERG. NO. 16-38;  BREET LOCAL SEMILARITY ST. 14, PERG. NO. 16-38;  MATCHES 103; CONSETVATIVE 3; MISMATCHES 14; Indels 1; Gaps 1;  MATCHES 103; CONSETVATIVE 3; MISMATCHES 14; Indels 1; Gaps 1;  VOLOBSOGGLYKPOGSLIKSCANGETYSSYTMSNYROPERKLEMYNTISGASTYVP 61  1 |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| RESULT 10 27 889 y chain 27 889 y chain 28 penses was 25 penses was 25 penses was 25 penses was 25 penses was 25 penses was 25 penses was 25 penses was 26 penses was 27 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 penses was 28 p | Jg beavy chain  CjSpecies Mus  CjDate: 14-Sep  CjAccession: PI  R. Shlomchik, Mt.  R. Shlomchik, Mt.  J. Exp. Med. 11  A. Reference num  A | Query Match Beef Local Si Matches 101;  Oy 1 H Db 1 E Db 61 P Db 61 P Db 121 S Db 121 S Db 121 S                                                                                                                                                                                                   |

FCCACAAAAAARCCCCGGSB

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F;15-98/Domain: immunoglobulin homology <IMM>
 ry Match 79.8%;
t Local Similarity 83.5%;
ches 101; Conservative
 61
 61
 PDSVKGRFTISRDNAKWTLYLQMSRLRSEDTAMYYCAREEGLRLEDYAMDYWGQGTSVTV 120
 PDSVKGRFTISRDNAKWILYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGILVTV
 Mismatches
 Score 514; DB 2;
Pred. No. 1.2e-38;
 Length 121;
 Indels
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0 Gaps

0

120 60

# wavy chain V region (anti-DNA, clones 2E3VH, 688VH, and 309VH) - mouse (fragrecter, Num musculus (house mouse) re: [4-Sep-1939 Heaquence\_revision 16-Sep-1992 #text\_change 16-Aug-1996 resion: E0252; PLOZ3H \_ revision 18-Sep-1992 #text\_change 16-Aug-1996 resion: E0252; PLOZ3H \_ revision H.; Radio, M.Z.; Pisetsky, D.; Marshak-Roth (omnth, M.; Maccelli, M.; Shan, H.; Radio, M.Z.; Pisetsky, D.; Marshak-Roth (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171, 265-297, 1990 (op. Med. 171,

121 S 121 S 121

121

98/Region: framework 3 108/Region: complementarity-determining 0/Region: framework 1
98/Domain: immunoglobulin homology <IMM>
35/Region: complementarity-determining 1
49/Region: framework 2 oeule type: mRNA idues: 1-117 <8HL> verfamily: immunoglobulin V region; immunoglobulin homology words: heteroterramer; immunoglobulin -117/Region: framework 4 56/Region: complementarity-determining 2

## 61 PDSVKGRFTISRDNARNTLYLQMSSLRSEDTAVYYCARRDYS---HWFFDVMGAGTTVTV 61 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120 99; EVILVESGGGIVKEGGSIKISCAASGFTESSYTMSWVGQTPAKRIEWVAISSRGGSTYY EVILVESGGGIVKEGGSIKISCAASGFTESSYTMSWVGQTPAKRIEWVANISRRGGSTYY EVILVESGGGIVKEGGSIKISCAASGFTESSYTMSWVGQTPAKRIEWVANISRRGGSTYY Conservative 5

117

h 79.3%; Similarity 82.5%;

Score 510.5; DB 2 Pred. No. 2.3e-38; Mismatches

DB 2;

Indels Length 117, ω ••

Gaps

60

60

B 8 B 8 P 9

COOPEREERGOODER

#### 8 F3 10

eavy chain V region (H36-2) - moube scies: Mus musculius (house mouse) re: i.5-Dec-1988 #eequence\_revision 15-Dec-1988 #rext\_change 16-Aug-1996 ression: D27889

Com. A.J.: Eromhee, G.G.: Staudt, L.M.: Gerhard, W. U. S. 1577-1587, 1986
U. S. 1577-1587, 1986
ference number: A20043; MUID:86300658; PMID:2427335
feesaion: D2788)
Agoult 1278: D38.

idues: 1-119 <CAT>

perimental source: strain Balb/c
re: this sequence was determined from the germline gene
re: this sequence was determined from a hybridoma protein that binds
perfamily: immunoglobulin V region; immunoglobulin homology

influenza

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RESULT 11
S55539
 ig heavy chain V region (H37-40) - mouse cyspecies: Nus musculis (house mouse) cyspecies: Nus musculis (house mouse) cyspecies: Nus musculis (house mouse) cyspecies: Nus musculis (house mouse) cyspecies: Nus musculis (house mouse) cyspecies: Nus
 Ig heavy chain V region p624 mouse (fregment)
ClSpecies Mas musculus (house mouse)
C.Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
C.Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
C.Date: 37-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
C.Date: 37-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
C.Mol. Biol. 247, 92-945, 1995
 C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
 A;Cross-references: EMBL.X82593; NID:g854312; PIDN:CAA57929.1; PID:g854313; C:SuperEmily: immunoglobulin V region; immunoglobulin homology
C:SuperEmily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heerotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <INM>
 A,Fitle: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
utations in the variable region genes, 63, protection and the variable region genes, 63, protection animber: 85528, WUID:95239763; PMID:7536850
A,Accession: 8552939
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 RESULT 12
H27888
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 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
A.Experimental source: strain Balb/c
A.Experimental source: strain Balb/c
A.Mote: this sequence was determined from the germline gene
C.Comment: This chain was isolated from a hybridoma protein that binds influenza virus
 Matches
 Query Match
Best Local
 Matches
 Local Similarity
 Local Similarity
 119
 121 ș 121
 120 S 120
 122 A 122
 101;
 61
 61 PDSVKGRFTISRDNAKWTLYLOMSSLRSEDTAMYYCTREGGGETVNWYFDVWGAGTLVTV 120
 52
 62
 1 EVQLQESGGGLVKPGGSLKLSCAASGETPSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 ,..
 , 99
 SDTVKGRFTISRDNAKNNLYLQMSSLKSBDTAVYYCARD--RYDLDGYFDVWGAGTTVTV 118
 DSVKGRETMSRDNAKNTLYLQMSSLRSEDTAMYYCVRLYXDYD-PYVMDYWGQGTTVTVS
 DSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTVS 121
 $ 119
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSDYYNYMVRQTPEKRLEMVATISDGGSFTYY 60
 VQLQESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISSSGSYTYYP
 VOLOESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYYP 61
 Conservative
 Conservative
 79.0%;
 79.0%;
81.8%;
 7; Mismatches
 4
 Score 508.5;
Pred. No. 3.5
 Score 509; DB 2;
Pred. No. 3.1e-38;
 Mismatches
 .5e-38;
 DB 2;
 15;
 Length 119;
 Indels
 Indels
 Length 120;
 23-Jul-1999
 antibody response to a
 16-Aug-1996
 1;
 2
 Gaps
 Gaps
 6
 119
 60
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 BH0098
 Query Match
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RESULT
S55538
 C superfamily, immunoglobulin V region, immunoglobulin homology Cykoyords: heterotetramer; immunoglobulin (jkeywords: heterotetramer; immunoglobulin komology «IM»)
 Matches
 Query Match
Best Local Similarity
 13
 121 8 121
 121 S 121
 61 PDTVTGRFTISRDNAKNTLYLEMGSLKSEDTAMYYCAREEGYYGSSDAMDYMGQGTLVTV 120
 61 PDSVKGRFTISRDNAKGTLYLØMSSLRSBDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 1 EVQIQESGGGLVKPGGSIKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 99;
 EVQLVESGGGLVQPGGSLNLSCAASGFTFSSYAMSWVRQSPEKRLEWVABISSGGSYTYY
 Conservative
 78.9%;
 6
 Score 508; DB 2;
Pred. No. 3.9e-38;
 Mismatches
 Length 121
 Indels
 0
 Gaps
 60
 120
 60
```

0

A. Pitle. Comprehensive apitope analysis of monoclonal anti-proenkephalin antibod unations in the variable region genes A. Jedference number: 855528, MUID:95239763, PMID:7536850 Ig heavy chain V region pe22 - mouse (fragment)
C:Species: Mus muscultus (house mouse)
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999
C:Accession: \$55538 R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B. J. Mol. Biol. 247, 932-946, 1995

A;Cross-references: EMBL:X82591; NID:g854308; PIDN:CAA57927.1; PID:g854309 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotertamer; immunoglobulin F;14-97/Domain: immunoglobulin homology <1769> A; Molecule type: mRNA A; Residues: 1-120 < BOE> A<sub>i</sub>Status: preliminary A; Accession: S55538

```
Matches
120 S 120
 122 A 122
 61 DSVKGRFTMSRDNAKNTLYLQMSSLRSEDTAMYYCVRLYYDYD-PYVMDFWGQGTTVTVS
 62
 N
 99,
 VKLQESGGGLVKPGGSLKLSCAASGFTPSSYAMSWVRQTPEKRLEWVATISSSGNYTYYP
 VQLQESGGGLVKPGGSLKLSCAASGFTFSSYIMSWVRQTPEKRLEWVATISSGGSSTYYP
 DSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTVS
 Conservative
 6;
 Mismatches
 123
 60
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Local

Similarity

77.9%; 81.8%;

Score 501.5; DB 2 Pred. No. 1.5e-37;

15, 22

Indels Length 120;

Gaps

۳.

#### RESULT 14

MG1. Immunol. 27, 1025-1038, 1990
A;Title: Analysis of the structural diversity of monocional antibodies
A;Reference number: PH0087; MUID:91042649; PMID:2122240
A;Accession: PH0098
A;Mocession: PH0098
A;Mocession: PH0098 G.F.; Kocher, H.P.; Quesniaux, 6 cyclos

A.Residues: 1-119 <5CHs
A.Residues: 1-19 <5CHs
A.Note: the authbors translated the codon GTG for residue 104 as
A.Note: the authbors translated the codon; immunoglobulin homology Gly

```
C:Reywords: heterotetramer; immunoglobulin F:15-98/Domain: immunoglobulin homology :17M5 F:31-38/Region: complementarity-determining 1 F:50-68/Region: complementarity-determining 2 F:59-105/Region: complementarity-determining 3
 A. Accession: C27888
A. Polecule type DNA
A. Polecule type DNA
A. Polecule type DNA
A. Polecule type DNA
A. Polecule type DNA
A. Polecule type DNA
A. Polecule type DNA
A. Polecule type DNA
A. Polecule type DNA
A. Polecule type DNA
A. Polecule type DNA
A. Polecule type DNA
A. Polecule type DNA
C. Composite the type DNA
C. Keywords: heterocetramer; immunoj.obulin
C. Keywords: heterocetramer; immunoj.obulin
F. 15-9 DNOmain: immunoj.obulin
 Ig heavy chain V region (H37-62) - mouse (189celse: Mus musculus (house mouse) (19peclse: Mus musculus (house mouse) (19pece: 15-Pec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996 (1)Accession: C27888
Search completed: November 7, 2003, 07:36:20 Job time: 16.8997 secs
 R;Caton, A.J., Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 196
A;Title: Structural and functional implications of a restricted antibody response to a
A;Teference number: A91043; MUID:86300658; PMID:2427335
 RESULT 15
C27888
 Query Match 77.7%;
Best Local Similarity 79.0%;
Matches 98; Conservative
 Query Match
Best Local Similarity
 Matches
 121
 118 YTVS 121
 116 SS 117
 121 SA 122
 61 PDSVKGRFTISRDNARDTLSLQMSSLRSEDTAFYYCSRQAGNYAGGPYYYAMDSWGQGTS 120
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGETVNWYF----DVWGAGTL 117
 61 POSVKGRFTISRDMAKNTLYLQWSSLGSBDTANYYCTREGGGFTVMWFDTWGGGTLVTV 120
61 PDSVKGRFTISRDMAKNTLYLQWSSLGSBDTAVYYCT----IPSNMGVDYMGGGTTLTV 115
 1 EVOLOSEGGGLYKEGGSLKLSCHAGGFTESSYTMSWYRGTESKILEWYATISGGGSYTY 60
 97;
 VTVS 124
 Conservative
 77.7%;
 Score 500.5; DB 2
Pred. No. 1.8e-37;
7; Mismatches 13
 Score 500.5; DB 2;
Pred. No. 1.9e-37;
8; Mismatches 15;
 DB 2;
 15; Indels
 13;
 Indels
 Length 124;
 Length 119;
 3,
 5
 Gaps
 Gaps
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# GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 7, 2003, 07:21:18 / Search time 8:79573 Seconds (without alignments) 652:278 Willion cell updates/sec

Title:
PetFect Score: 644
Sequence: 1 EVQL/GESGGGL/WFGGSLKL......FTVNW/FDVWGAGTL/VTVSA 122

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMAR

|               |        |                |        |      | SUMMARIES   |                    |
|---------------|--------|----------------|--------|------|-------------|--------------------|
|               |        | *              |        |      |             |                    |
| Result<br>No. | Score  | Query<br>Match | Length | DB   | ID          | Description        |
| - !           | 469    | 72.8           | 117    | ۳ ا  | HV55 MOUSE  | P18526 mus musculu |
| 2             | 464    |                | 117    | щ.   | HV54 MOUSE  | mus                |
| ω             | 462    |                | 98     | ۲    | HV57_MOUSE  | mus                |
| 4.            | 460.5  | 71.5           | 97     | _    | HV56_MOUSE  | mus                |
| s             | 453    |                | 117    | щ    | HV58 MOUSE  | Bum                |
| 6             | 441    | 68.5           | 136    | _    | HV16_MOUSE  | 3 mus              |
| 7             | 433    | 67.2           | 117    | μ.   | HV53_MOUSE  | mus                |
| œ             | 426    | 66.1           | 117    | _    | HV59_MOUSE  | P18530 mus musculu |
| 9             | 419    | 65.1           | 117    | μ    | HV3C_HUMAN  | P01764 homo sapien |
| 10            | 417    | 64.8           | 122    | н    | HV3G HUMAN  | homo               |
| ::            | 416    |                | 119    |      | HV38 MOUSE  | mus n              |
| 12            | 113    | 9 4            | 111    | . ,  | MANUAL SEAN | Tonic              |
| 1 5           | 11 400 |                | 101    | ٦,   | NAME TENE   | PO1777 homo ganien |
| 15 :          | 404.5  | 62.8           | 115    | _    | HV32 MOUSE  | mus n              |
| 16            | 404    | 62.7           | 116    | _    | HV3T HUMAN  | home               |
| 17            | 402.5  | 62.5           | 123    | _    | HV18 MOUSE  | mus                |
| 18            | 402    | 62.4           | 122    | ,    | HV21_MOUSE  | Bum                |
| 19            | 402    | 62.4           | 126    | _    | HV3K_HUMAN  |                    |
| 20            | 401.5  | 62.3           | 123    | . ب  | HV19_MOUSE  |                    |
| 21            | 401.5  | 62.3           | 142    |      | HV01_RAT    |                    |
| 22            | 400.5  | 62.2           | 117    | ٠,   | HV02 CANEA  | _                  |
| 23            | 400.5  | 62.2           | 123    | ٠,   | HV22 MOUSE  | Bum                |
| 24            | 399.5  | 62.0           | 115    | . ,  | HV3D_HUMAN  | nomo               |
| ) N           | 398.5  |                | 170    | . ,  | HV35 HUDAN  | POINT BOND BADIEN  |
| 27            | 397.5  | 61.7           | 123    | ا سا | HV23 MOUSE  | P01792 mus musculu |
| 28            | 397.5  | 61.7           | 123    | ,    | HV24_MOUSE  | Britt              |
| 29            | 397.5  | 61.7           | 144    | _    | HV26_MOUSE  | P01795 mus musculu |
| 30            | 397    | 61.6           | 122    | ь    | HV3A_HUMAN  | P01762 homo sapien |
| 31            | 396.5  | 61.6           | 115    | ,    | HV33_MOUSE  | P01802 mus musculu |
| 32            | 396.5  | 61.6           | 116    | ,    | HV05_CARAU  | P19181 carassius a |
| 33            | 394.5  | 61.3           | 113    | ,,   | HV27_MOUSE  | P01796 mus musculu |
|               |        |                |        |      |             |                    |

Db RESULT 2 HV54\_MOUSE

> 0; 60

| 394.5 61.3 113 1 1770 MONSE<br>393.5 31.13 1 1770 MONSE<br>393.5 61.6 113 1 1772 MONSE<br>390.5 61.6 113 1 1772 MONSE<br>390.6 61.13 1 1772 MONSE<br>390.6 61.13 1 1772 MONSE<br>390.6 61.11 1 1772 MONSE<br>390.6 61.11 1 1772 MONSE<br>390.6 61.11 1 1772 MONSE<br>390.6 61.12 1 1772 MONSE<br>390.7 61.2 1 1772 MONSE<br>390.7 61.2 1 1772 MONSE<br>390.7 61.2 12.3 1 1772 MONSE<br>390.7 61.2 12.3 1 1772 MONSE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 61.3 113 1<br>60.8 115 1<br>60.6 113 1<br>60.6 113 1<br>60.6 113 1<br>60.5 113 1<br>60.5 113 1<br>60.4 1122 1<br>60.2 120 1<br>59.9 123 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
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| 113<br>119<br>115<br>1115<br>1111<br>1111<br>1119<br>1119<br>1122<br>1122                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 113 1 HY10 MOUSES 114 1 HY17 MOUSES 115 1 HY17 HYMAN 115 1 HY17 HYMAN 115 1 HY17 HYMAN 115 1 HY17 HYMAN 115 1 HY17 HYMAN 115 1 HY17 HYMAN 115 1 HY18 HYMAN 115 1 HY18 HYMAN 115 1 HY18 HYMAN 115 1 HY18 HYMAN 115 1 HY18 HYMAN 117 1 HY18 HYMAN 118 1 HY18 HYMAN 119 1 HY18 HYMAN 111 1 HY18 HYMAN 111 1 HY18 HYMAN 111 1 HY18 HYMAN 111 1 HY18 HYMAN 111 1 HY18 HYMAN 111 1 HY18 HYMAN 111 1 HY18 HYMAN 111 1 HYMAN 111 HYMAN 1 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 1 HYTO MODES 1 HYTO MODES 1 HYTO MODES 1 HYTO MODES 1 HYTO MODES 1 HYTO MODES 1 HYTO HYTOM 1 HYTO HYTOM 1 HYTO HYTOM 1 HYTO HYTOM 1 HYTO HYTOM 1 HYTO HYTOM 1 HYTO HYTOM 1 HYTO HYTOM 1 HYTO HYTOM 1 HYTO HYTOM 1 HYTO HYTOM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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| HY30 MOUSE HY37 MOUSE HY3E HY3N MOUSE HY3E HY3N HY31 MOUSE HY3E MOUSE HY3E HY3N HYNN HY3E HYNN HY3E HYNN HY3E HYNN HY3E HYNN HY3E HYNN HY3E HYNN HY3E HYNN HY3E HYNN HY3E HYNN HY3E HYNN HY3E HYNN HY3E HYNN HY3E HYNN HYSE HYNN HYNN HYNN HYNN HYNN HYNN HYNN HYNN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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#### ALIGNMENTS

| 8 8                                                                                                          | B 8                                                                                                                                                                                     | % # Q                                                  | \$2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | RESULT |
|--------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------|
| 61 PI                                                                                                        | 1 BV                                                                                                                                                                                    | Query Match<br>Best Local Sir<br>Matches 90;           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | LT 1   |
| PDSVKGRPTISRDNAKNTLYLØMSSLRSEDTAMYYCTR<br>  :                    <br> PDTVKGRPTISRDNAKNTLYLØMSSLKSEDTAMYYCAR | RVOLDESGGGLYKPGGSLKLSCAASGPRESYTMSWYRQTPBERLEWYNTSGGGSTYV<br>RVOLDESGGGLYKPGGSLKLSCAASGPAPSSYDMSWYRQTPBERLEWYNLTSGGGSTYV<br>RVOLDESGGGLYKPGGSLKLSCAASGPAPSSYDMSWYRQTPBERLEWYNLTSGGGSTYV | 1 72.8%;<br>Similarity 91.8%;<br>90; Conservative      | AMDARD,  16, Cr.  16, La.  16, Cr.  16, La.  2 region  a. Rode  a. |        |
| TISRDNAKNTLYLOMSSLRSEDTAMYYCTR<br>              <br>TISRDNAKNTLYLOMSSLKSEDTAMYYCAR                           | GSLKLSCAASGFT<br>         <br> SLKLSCAASGFA                                                                                                                                             | 8%; Score 469; D<br>8%; Pred. No. 1.1<br>2; Mismatches | MDAND; PRT; 117 AA.  16, Created)  16, Last sequence update)  16, Last sequence update)  18, Last sequence;  18 Chordata; Craniata; Verte;  18 Chordata; Craniata; Verte;  19 Chordata; Craniata; Verte;  10 Uv / Lebecque S.G., Gee  matic mutation in immunogal  10 Tellike;  10 JG-11ke;  16 JG-WC.  16 JG-WC.  16 JG-WC.  16 JG-WC.  16 JG-WC.  17 JG-LIKE;  18 JG-WC.  19 JG-HEAVY CHAIN V.  11 PRAMEMORY.  11 PRAMEMORY.  11 FRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  12 PRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  12 PRAMEMORY.  12 PRAMEMORY.  13 PRAMEMORY.  14 PRAMEMORY.  15 PRAMEMORY.  17 PRAMEMORY.  18 CONTROL OF THE PRAMEMORY.  19 PRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  12 PRAMEMORY.  11 PRAMEMORY.  12 PRAMEMORY.  12 PRAMEMORY.  13 PRAMEMORY.  14 PRAMEMORY.  15 PRAMEMORY.  17 PRAMEMORY.  18 PRAMEMORY.  19 PRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  12 PRAMEMORY.  12 PRAMEMORY.  13 PRAMEMORY.  14 PRAMEMORY.  15 PRAMEMORY.  16 PRAMEMORY.  17 PRAMEMORY.  17 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  19 PRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  12 PRAMEMORY.  12 PRAMEMORY.  11 PRAMEMORY.  12 PRAMEMORY.  12 PRAMEMORY.  13 PRAMEMORY.  14 PRAMEMORY.  15 PRAMEMORY.  16 PRAMEMORY.  17 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  19 PRAMEMORY.  19 PRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  12 PRAMEMORY.  12 PRAMEMORY.  12 PRAMEMORY.  13 PRAMEMORY.  14 PRAMEMORY.  16 PRAMEMORY.  17 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  19 PRAMEMORY.  19 PRAMEMORY.  10 PRAMEMORY.  11 PRAMEMORY.  11 PRAMEMORY.  12 PRAMEMORY.  12 PRAMEMORY.  11 PRAMEMORY.  12 PRAMEMORY.  12 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMORY.  18 PRAMEMO |        |
|                                                                                                              | FSSYTMSWVRQTI<br>           <br>FSSYDMSWVRQTI                                                                                                                                           | B 1;<br>e-40;<br>6;                                    | turi<br>turi<br>turi<br>turi<br>turi<br>bul<br>the<br>bul<br>the                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |        |
| 98<br>117                                                                                                    | PEKRLEWVATIS:<br>                                                                                                                                                                       | Length 117;<br>Indels 0                                | BF7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |        |
| •                                                                                                            | SGGSSTYY                                                                                                                                                                                | ; Gaps                                                 | stomi;<br>;; Mus.<br>during                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |        |

```
THE STATE OF
 Query Match
Best Local S
Matches 88
 HV54 MOUSE
P18525;
01-NOV-1990
 DOMAIN
 pids29.

01-MOV-1990 (Rel. 16, Created)

01-MOV-1990 (Rel. 16, Last sequence update)

15-SEP-2003 (Rel. 42, Last anotation update)

15-SEP-2003 (Rel. 42, Last anotation update)

1g heavy chain V region 6.96.

Mus muscultu (Mouse)

Mus muscult
 CHAIN
 SIGNAL
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; BS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
 the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
-1- MISCELLANEOUS: THIS SEQUENCE
 Ol-NOV-1990 (Rel. 16, Created)
Ol-NOV-1990 (Rel. 15, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region 5-84 precursor.
 HV57
 MOUSE
 InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 PIR; JT0505; HVMS84.
HSSP; P01810; 2FBJ.
 NCBI_TaxID=10090;
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
 MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque
"Early onset of somatic mutation in
 STRAIN=BALB/CJ;
 NCBI_TaxID=10090;
 SEQUENCE
 NON TER
 DISULFID
 DOMAIN
 DOMAIN
 "Early onset of somatic mutation in
 MEDLINE=89279149; PubMed=2499654;
 STRAIN-BALB/CJ;
 SEQUENCE FROM N.A.
 Mus musculus (Mouse)
 SEQUENCE FROM N.A.
 MISCELLANEOUS: THIS SEQUENCE BELONGS
 MOUSE
 08
 51
 20
 Similarity
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTR
 EVKLVESGGGJVQPGGSLKLSCAASGFTFSSYTWSWVRQTPEKRLEMVAYISNGGGSTYY
 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTWSWVRQTPEKRLEWVATISSGGSSTYY
 PDTVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAR
 117 AA;
 Conservative
 41
50
50
50
41
 STANDARD;
 STANDARD;
 12872
 72.0%;
 MW;
 IG HEAVY CHAIN V REGION 5-84.

REAMENORY. 1.
COMPLEMENTARITY-DETERMINING-1.

REAMENORK-2:
COMPLEMENTARITY-DETERMINING-2.

REAMENORK-3:
BY SHILARITY.
 5
 Pred. No. 3.7e
5; Mismatches
 Score 464;
 PRT;
 PRT;
 234055CB6A469861
 BELONGS
 S.G., Gearhart immunoglobulin
 S.G., Gearhart
immunoglobulin
 117
 98
 3.7e-40;
 8
 ö
 TO THE VH7183 SUBFAMILY
 ζ
 SHI
 117
 98
 Length 117;
 CRC64;
 VH7183 SUBFAMILY
 Indels
 P.J.;
VH genes
 ≨."
 genes
 0
 during
 Gaps
 79
 60
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STTWEE
 ALC CARTER RECOCCES OF THE SECOND SEC
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 RESULT 4
HV56_MOUSE
밁
 S
 맑
 5
 Query Match
Best Local S
Matches 89
 Query Match
Best Local S
Matches 90
 Pfam; PF00047; ig; 1.
SMARY; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1
Immunoglobulin V region.
DOMAIN

>98
 NON TER
 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation updat g heavy chain v region 914.
Mus musculus (Mouse)
 HV56_MOI
 -!- SIMILARITY: Contains 1 immunoglobulin-like domain
PIR, JT0901, HVMS96.
HSSP; P01772; 2FB4
 InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 SEQUENCE
 J. Exp. Med. 169:2007-2019(1989).
-I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH718:
-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 Levy N.S., Malipiero U.V., Lebecque "Early onset of somatic mutation in the primary immune response.";
 MEDLINE=89279149; PubMed=2499654;
 SEQUENCE FROM N.A.
STRAIN=BALB/CJ;
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 NON TER
 PIR; JT0504; HVMS91.
HSSP; P01810; 2FBJ.
 NCBI_TaxID=10090
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 MOUSE
60
 61
 2
 61
 14
 μ
 , 68
 μ
 90;
 Similarity 90.1
89; Conservative
 Similarity
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTR
 EVQLQESGGGLYKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTR
 EVQLQESGGGLYKPGGSLKLSCAASGFTFSSYIMSWVRQTPEKRLEWVATISSGGSSTYY
 PDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAR
 EVQLVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTPEKRLEWVATISDGGSYTYY
PDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCAR
 EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASISSGG-STYY
 98 AA;
 97
 98
 Conservative
 97
 Ą,
 STANDARD;
 10661 MW;
 11007 MW;
 71.7%;
 71.5%;
 Score 460.5;
Pred. No. 6.7e
3; Mismatches
 1,
 Score 462; DB 1;
Pred. No. 4.8e-40
 IG-LIKE
 B8644F7F92FBF95B CRC64;
 IG-LIKE
 C23CB33FF55DA893 CRC64;
 PRT;
 Mismatches
 S.G., Gearhart P.J.;
immunoglobulin VH ge
 update)
 97
 6.7e-40;
 8
 DB 1; Length
 THE VH7183
 8
 98
97
 86
 Length
 Indels
 Indels
 genes
 SUBFAMILY
 98
 97;
 during
 0
 Gaps
 Gaps
 59
 60
 60
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RAX PROCESS DE DE LA COMPANIO DE LA
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 RESULT 5
HV58_MOUSE
ID HV58_MOUSE
 Query Match
Best Local S
Matches 87
 HV16 MOUSE
P01783;
21-JUL-1986
 DOMAIN
 Bukaryota; Metazoa;
Mammalia; Eutheria;
 Mus musculus (Mouse)
 MOUSE
 NON_TER
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; P850835; IG LIKE; 1.
 MEDLINE=81234548, PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
 NCBI_TaxID=10090;
 21-JUL-1986
15-SEP-2003
 PIR; JT0506; HVMS57.
HSSP; P01810; 2FBJ.
 STRAIN=BALB/CJ;
MEDLINE=89279149; PubMed=2499654;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Ig heavy chain V region 5-76 precursor Mus musculus (Mouse)
 01-NOV-1990
 01-NOV-1990
 P18529;
 SEQUENCE FROM N.A.
 SEQÜENCE
 DOMAIN
 DOMAIN
 CHAIN
 SIGNAL
 InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 J. EXP. Med. 169:2007-2019(1989).
 "Early onset of somatic mutation in
 Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 SEQUENCE FROM N.A.
 15-JUL-1999
 [mmunoglobulin
 -JUL-1986 (Rel. 01, Created)
-JUL-1986 (Rel. 01, Last sequence update)
-SEP-2003 (Rel. 42, Last amnotation update)
heavy chain V region MOPC 21 precursor (Fragment).
 primary immune response."
 61
 9
 20
 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 87;
 Similarity
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTR 98
 EVHLVESGGGLVKPGGSLKLSCVVSGPTFNKYAMSWVRQTPEKRLEWVATISSGGLYTYY 79
 (Rel. 16, Last sequence update)
(Rel. 38, Last annotation update
 Conservative
 41
41
41
41
41
 V region;
 STANDARD;
 117
 Rodentia;
 Chordata;
 70.3%;
 12991 MW;
 Created)
 Signal.
 IG HBAVY CHAIN V REGION 5-76.
PRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEMORK-2.
COMPLEMENTARITY-DETERMINING-2.
PRAMEMORK-3.
 Score 453; DB 1;
Pred. No. 4.8e-39;
 Reth M.,
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
 BY SIMILARITY.
 PRT;
 93A04782B78B8FA0
 Mismatches
 BELONGS TO THE VH7183 SUBFAMILY
 immunoglobulin VH genes during
 136
 117 AA.
 Imanishi-Kari
 update;
 £
 10;
 Length 117;
 CRC64;
 Indels
 .7
 Rajewsky K.,
 ç,
 Gaps
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RESULT
HV53_MC
 밁
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 8
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 Query Match
Best Local S
Matches 89
 P18524.

01-WOV-1990 (Rel. 16, Created)

01-WOV-1990 (Rel. 16, Last sequence up

15-WUL-1999 (Rel. 38, Last annotation

Ig heavy chain V region RF precursor.

Mus musculus (Mouse)
 MOUSE
 CONFLICT
 CONFLICT
 DOMAIN
 NON TER
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 ESQUENCE OF 17-136.
WEDLINE-77100361, PubMed=401050;
MEDLINE-7100361, PubMed=401050;
Medrugbo K., Milstein C., Secher D.S.;
MALECULAR analysis of spontaneous somatic mutante.";
Neture 25:29-30(1377).
 "Heavy chain variable region contribution to the NPb family of antibodies: sometic mutation evident in a gamma 2a variable region.", Ceil 24:625-637(1981).
SEQUENCE FROM N.A.
STRAIN=BALB/CJ;
 SEQUENCE
 NON
 CHAIN
 InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MFC. InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
 PIR; E90809; G1MS21.
PDB; 1IGC; 03-JUN-95.
 NCBI_TaxID=10090;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 EMBL; J00522; AAD15290.1; -.
 ROSITE;
 MOUSE
 134
 120
 77
 61
 7
 89;
 Similarity
 PS50835; IG_LIKE; 1.
obulin V region; Signal;
 ADTYKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARWG---NXFYYAMDYWGQGTSVT
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWY-FDVWGAGTLVT
 DVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTLHY
 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 VSS 136
 VSA 122
 136 AA;
 Conservative
 STANDARD;
 112
78
90
115
120
 15071
 68.5%;
72.4%;
 Œ,
 10;
 HYAD -> DYAH (IN REF. 2).
DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
 Pred. No.
 Score 441;
 JH4 SEGMENT.
 IG HEAVY CHAIN V REGION MOPC
 2276A98DBDBF7016 CRC64;
 SEGMENT
 Mismatches
 3D-structure
 update)
on update)
 117
 9.3e-38
 DB 1;
 Š
 Length 136
 Indels
 21.
 4,
 Gaps
 133
 76
 60
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InterPro; IPRO0357,
InterPro; IPRO0357,
InterPro; IPRO0357,
IR SWART; SW00406; IGV; 1.

R PROSITE; SESS0835; IGLIES; 1.

R PROSITE; SESS0835; IGLIES; 1.

R PROSITE; SESS0835; IGLIES; 1.

TO STIGNAL

 Query Match
Best Local :
 Matches
 HV59 MOUSE
P18530;
 pir, JT0507; HVMS39.

HSSP, P01810, 2FBJ.

InterPro, IPR007210; Ig-like.

InterPro, IPR003006; Ig_MHC.

InterPro, IPR003596; Ig_v.
 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence upd
15-7UL-1999 (Rel. 38, Last annotation u
1g heavy chain V region 7-39 precursor.
 NON TER
SEQUENCE
 Immunoglobulin V regTon; Hybridoma; Signal SIGNAL 1 19
 InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
-!- MISCELLANEOUS: THIS SEQUENCE BELONGS
 J. Exp. Med. 169:2007-2019(1989)
 MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque
"Early onset of somatic mutation in
 SEQUENCE FROM N.A.
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 Mus musculus (Mouse)
 MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque
"Early onset of somatic mutation in
 STRAIN-BALB/CJ;
 DISULFID
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 SIE
 PROSITE; PS50835; IG LIKE; 1.
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
 PIR; JT0503; HVMSRF.
HSSP; P01810; 2FBJ.
 -!- MISCELLANEOUS: THIS SEQUENCE
 NCBI_TaxID=10090;
 61
 20
 80
 μ
 84,
 Similarity
 PDSVKGRFTISRDNAKVTLYLOMSSLRSEDTAMYYCTR 98
 DVKLVESGGGLVKLGGSLKLSCAASGFTFSSYYMSWVRQTPEKRLELVAAINSNGGSTYY 79
 EVQLQESGGGLVKPGGSLKLSCAASGFT8SSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 PDTVKGRFTISRDNAKNTLYLQMSSLKSEDTALYYCAR 117
 20
20
50
55
69
86
41
117
 Conservative
 A
 STANDARD;
 49
54
68
85
117
 67.2%;
85.7%;
 12866
 ¥
 IG HEAVY CHAIN V REGION RF.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
 6
 Pred. No. 5e-37;
 ВУ
 IG HEAVY CHAIN V REGION 7-39. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
 PRT;
 2CE3295F390F725B
 Mismatches
 SIMILARITY
 BELONGS
 S.G., Gearhart P.J.;
immunoglobulin VH genes during
 S.G., Gearhart P.J.;
immunoglobulin VH genes during
 update)
 117
 update)
 Š
 DB 1;
 TO THE VH7183 SUBFAMILY
 TO THE VH7183 SUBFAMILY
 8; Indels
 Length 117
 CRC64
 0
 Gaps
 6
 0
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 STATE
 RESULT 9
HV3C_HUMAN
 믕
 Query Match
Best Local S
Matches 82
Query Match
Best Local Sim
Matches 79;
 GO; GO; 1001575; C:extracellular; MAS.
GO; GO:000352; F:antique bidding activity; MAS.
GO; GO:000352; F:immune response; MAS.
InterFro; IRRO0110; Jg-1ke.
InterFro; IRRO0356; Jg-MC.
InterFro; IRRO0356; Jg-MC.
InterFro; IRRO0356; Jg-MC.
SMART; SMO065; IGV; I.
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; III
JEMART; SMO065; IGV; IIII
JEMART; SMO065; IIIII
JEMART; SMO065; IGV; IIIII
JEMART; SMO065; IGV; IIIII
JEMART; IIIII
JEMART; IIIII
JEMART; IIIIIIIII
JEMART; IIIIIIIIIIIIIIII
 DOMAIN
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 use by non-profit institutions as long as its content in no way modified and this extremat is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an entit to license@isb-sib.ch).
 NON TER
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SEQUENCE
 NEDLINE-81101090; PubMed-6450418;
Matchyseons G., Rabbiter T.H.;
"Structure and multiplicity of genes for the hums
beavy chain variable region."; 7:6561-6565(1980)
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980)
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMRI outstantion the Buropean Bioinformatics Institute. There are no restrictions on its
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 EMBL; J00236; AAA53516.1; -. EMBL; M35415; AAA58735.1; -.
 Homo sapiens (Human).
 21-JUL-1986 (Rel. 01, Create
21-JUL-1986 (Rel. 01, Last s
15-SEP-2003 (Rel. 42, Last a
Ig heavy chain V-III region
 P01764;
 SIGNAL
 Genew; HGNC:5545; IGHV@.
 PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99
 NCBI_TaxID=9606

 -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

 SEQUENCE FROM N.A.
 MAMOH
 80
 51
 20
 щ
 82;
 Similarity
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTR
 EVQLQESGGGLVKPGGSLXLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 PDSVKGRFTISRDNAKNNLYLQMNSLTSEDTALYYCAR
 EVKWVESGGGSVKPGGSLKLSCEASGFTFSNYGMSWVRQTPEKRLEWVASISGGVSYTYY
 20
20
117
117
 117
117
 Conservative
 46695
 Ā
 ζ
 STANDARD;
 68
85
117
 12582 MW;
 66.1%;
83.7%;
 12972
 80.6%;
 Last sequence update)
Last annotation update)
region VH26 precursor.
 Created)
 3
Score 419; DB 1;
Pred. No. 1.3e-35;
8; Mismatches 11
 Ş
 IG HEAVY
 Score 426;
Pred. No. 2
 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
 PRT;
 E826733F1A3CB0F1
 DSCA4167D0F1774F CRC64;
 Mismatches
 activity, NAS.
 117
 CHAIN V-III
 DB
 Š
 . 6e-3
 11;
 human
 86
 Length 117
 Length 117;
 CRC64;
 Indels
 REGION VH26
 immunoglobulin
 0
 79
 60
 0
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Similarity

Conservative

Indels

0

Gaps

0

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RESULT
HV38_MO
ID HV
AC PO
DT 21
DT 21
DT 15
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 Matches
 Query Match
Best Local (
B MOUSE

-HV38 MOUSE

P01808;

21-JUL-1986

21-JUL-1986

15-SEP-2003
 HUMAN
HV3G HUMAN
P01768;
 MOD RES
NON TER
SEQUENCE
 "Manio acid sequence of the variable region of a human location of a possible UH segment." proc. Netl. Acad. Sci. U.S.A. 77:3239-3243(1980). Proc. Netl. Acad. Sci. U.S.A. 77:3239-3243(1980). Proc. Netl. Acad. Sci. U.S.A. 77:3239-3243(1980). A CONTROL OF ACTION OF A CONTROL OF A
 PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic
 NCBI_TaxID=9606;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 21-JUL-1986 (Rel. 01, Create
21-JUL-1986 (Rel. 01, Last &
15-SEP-2003 (Rel. 42, Last &
Ig heavy chain V-III region
 DOMAIN
 HSSP; P01772; 2FB4.
 PIR; A02051; M3HUAM.
 MEDLINE=81013859; PubMed=6774332;
Lehman D.W., Putnam F.W.;
 Homo sapiens (Human)
 121
 121
 61
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 80
 63
 20
 بر
 Similarity
 SS
 SA 122
 ABSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRPLYGBYRAFNYWGQGTLVTV
 QVELVESGGGVVZPGRLRLCAA$GFTF$NYAMHWVRQPPGKGLEWVAVI$YBGBBKYY
 EVQLQESGGGLVXFGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 EVOLUESGGGLUKEGGSLKLSCHASGFTESSTYMSWVRQTEKKLEWVALISGGSSTYY
EVOLUESGGGLUKEGGSLKLSCHASGFTESSTYMSWVRQAEGKGLEWVSAISGSGGSTYY
 GDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK 117
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTR
 122
122 AA,
(Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
 122
 Conservative
 STANDARD;
 STANDARD;
 64.8%;
 13668 MW; A42D0F17D252F1C2 CRC64;
 Last sequence update)
 Created)
 18;
 annotation update)
1 CAM.
 Score 417; DB
Pred. No. 2.2e
18; Mismatches
 PYRROLIDONE CARBOXYLIC ACID
 PRT;
 PRT;
 119
 122
 DB 1;
2.2e-35;
 Š
 25;
 Length 122
 98
 Indels
 PLASMA OF
 2
 chain:
 0;
 Gaps
 120
 120
 60
 79
 60
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RESULT 12
HV3B HUYAN
AC P01763
AC P01763
AC B01767
AC B01767
AC B01767
AC B01767
AC B01767
AC B01767
AC B01767
AC B01767
AC B0177
 S
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 BOOOCARRER TOOOCAR ARREST TOO
 멼
 문
 S
 Matches
 Query Match
Best Local
 Pfam; PRO047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_IKE; 1.
Immunoglobulin V region.
Immunoglobulin V region.
Ill.
 901763)
21-UUL-1996 (Rel. 01, Created)
21-UUL-1996 (Rel. 02, Last sequence update)
15-SEP-2003 (Rel. 42, Last amocation update)
15-SEP-2003 (Rel. 47, Last amocation update)
16-SEP-2003 (Rel. 47, Last amocation WEA,
16-SEP-2003 (Rel. 02, Last sequence update)
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 DOMAIN
NON TER
 Ig heavy chain V region T601.
Mus musculius (Mouse).
Enkayyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkayyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
McBulTaxiD=10090;
[1].
PIR; A02046; M3HUWE
HSSP; P01772; 2FB4.
 (procesin MRA) with antibody activity egainst 3.4-pyruylated galactose in Klabsiella polysaccharides KO and K33."; Proc. Natl. Acad. Sci. U.S.A. 80.4837-4841(1983).

1- MISCELLANEUS; THIS CHAIN MAS OFFANTED FROM A MONOCLONAL ANTIBODY AGAINST 3.4-PYRUYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH MACHINE PROMESS AND ISOLATED FROM A PATIENT WITH MACHINE STANCES AND ISOLATED FROM A PATIENT WITH MACHINE PROMESS AND ISOLATED FROM A PATIENT WITH WITH MACHINE PROMESS AND ISOLATED FROM A PATIENT WITH MACHINE PROMESS AND ISOLATED FROM A PATIENT WITH MACHINE PROMESS AND ISOLAT
 MEDLINE-83273707; PubMed-6410398;
Geni F., Frangione B.,
"Amino acid sequence of the FV region of a human monoclonal
 Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 "Structural evidence for independent joining region gene in immunoglobulin heavy chains from arti-galactan myeloma proteins ties potential role in generating diversity in complementarity checkermining regions;" Foc. Matl. Acad. Sci. U.S.A. 76:2890-2894 (1979).

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 HV3B HUMAN
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 PIR; A02078; AVMST6.
HSSP; P01810; 2FBJ.
 Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
 MEDLINE=79223895; PubMed=111245;
 SEQUENCE
 InterPro;
 nterPro;
 SIMILARITY: Contains 1 immunoglobulin-like domain; A02046; M3HUWE.
 SIMILARITY: Contains 1 immunoglobulin-like domain
 THAT BINDS GALACTAN
 117
 121
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 61 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 83;
 Similarity
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 SA
 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLG----YYGYFDVWGAGTTVTV
 EVOLOESGGGLVKFGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 EVXLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY
 IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
 119 AA;
 122
 Conservative
 119
 STANDARD;
 13169 MW;
 64.6%;
 10;
 Score 416; DB 1;
Pred. No. 2.7e-35;
0; Mismatches 25
 IG-LIKE
 PRT;
 BC38CC84E6EA00E8 CRC64;
 114 AA
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 MOD_RES
 MEDILME-0019926, PubMed-6769593;
Early P., Huang H., Davis M., Celame K., Hood I.
"An immunoglobulin heavy chain variable region
thee segments of DNA: VH, D and JH.";
cell 19:881-992(1980).
 Mus musculus (Mouse).
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 HOUSE
 X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS)
MEDLINE-75065510; PubMed=4330984;
Segal D.M., Padlan B.A., Cohen G.H., I
Davies D.R.;
 "Variable region sequence of the heavy binding myeloma protein."; Biochemistry 13:4033-4038(1974).
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
 00; 00:000576; C:extracellular; NMS:
00; 00:000823; P:antign binding ectivity; NMS:
00; 00:000895; P:immume response; NMS.
InterPro; [PRO03006; 19_MGC.
InterPro; [PRO03006; 19_MG.
InterPro; [PRO03006] 19_MG.
 "The three-dimensional structure of a phosphorylcholine-binding immunoglobulin Fab and the nature of the antigen binding site.", proc. Matl. Acad. Sci. U.S.A. 71:428-4302(1974).
 SEQUENCE OF 1-120.
MEDLINE=75017346; PubMed=4213527;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Ig heavy chain V region M603
 SEQÜENCE
 NON TER
 PROSITE;
 Rudikoff S., Potter M.;
 PROSITE; PS50835; IG LIKE; 1.
[mmunoglobulin V region; Pyrrolidone carboxylic acid
 Local
 BINDS PHOSPHORYLCHOLINE.
SIMILARITY: Contains 1:
B90795; AVMS63.
 1MCP; 15-JUL-92.
2MCP; 15-JUL-92.
 MOUSE
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 ADSVKGRFTISRNBSKNSLYLOMSSLRAEDTAVYYCAR---GWLLN-----WGQGTLVTV
 SS
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 QVQLVDSGGGLVEPGGSLRLSCSASGFTFSANDMWVRQAPGKGLEWLSFIGGSGSTIYY
 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 IPR007110; Ig-like
 6 (Rel. 01,
5 (Rel. 01,
3 (Rel. 42,
 114 AA;
 114
 122
 Conservative
 STANDARD;
 12256 MW; D88294FB418A07B7 CRC64;
 64.1%; Score 413; DB 1; 65.6%; Pred. No. 5.1e-35
 Last sequence u
 Created)
 immunoglobulin-like domain
 19;
 PYRROLIDONE CARBOXYLIC ACID
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 Rudikoff S., Potter M.,
 122
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 Length 114;
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RESULT 14

HV3J_HMGAN STANDARD; PRT; 121 AA.

RC 901771.

RC 21-7UL-1966 (Rel. 01, Created)

RC 21-7UL-1966 (Rel. 01, Last sequence update)

RC 19582-2003 (Rel. 142, Last amporation update)

RC 19582-2003 (Rel. 142, Last amporation update)

RC 19582-2003 (Rel. 142, Last amporation update)

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 Cchiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
*Manion acid seguence of the VH region of human myeloma
cryoimmunoglobulin 19G Hil.*
acryoimmunoglobulin 1
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 Eukaryota; Metazoa;
Mammalia; Eutheria;
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 InterPro; IPR003006; Ig
InterPro; IPR003596; Ig
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
 -!- SIMILARITY: Contains
PIR; A02054; G1HUHL.
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 DOMAIN
 MEDLINE=79124695; PubMed=420800.
 SEQUENCE
 NCBI_TaxID=9606;
 SEQÜENCE
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 Immunoglobulin
 PROSITE; PS50835; IG_LIKE; 1
 PROTEIN
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P01772; 2FB4
 61 EYSASVKGRFIVSRDISQSILYLQMNALRAEDTALYYCARNYYGST--WYFDVWGAGTTV
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 80;
 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGS--ST
 Similarity
 YYPDSVKGRETISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGETVNWYFDVWGAGTLV
 EVKLVESGGGLVQPGGSLRLSCATSGFTFSDFYMEWVRQPPGKRLEWIAASRNKGNKYTT
 IPR003006; Ig_MHC.
IPR003596; Ig_v.
 Conservative
 330
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 V region;
 Chordata;
Primates;
 13626 MW;
 52
 64.5%;
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 3D-structure.
 immunoglobulin-like
 Score 411; DB
Pred. No. 8.8e
17; Mismatches
 IG-LIKE
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H-BOND WITH THE PHOSPHATE GROUP OF
PHORYLCHOLINE.
 Catarrhini; Hominidae; Homo.
 Craniata; Vertebrata; Euteleostomi;
 BA2C864438B64F0F CRC64;
 8.8e-35;
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 Length 122;
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STTTWRUDGE

60

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RESULT 15
HV32_MOUSE
 Overy Match 62.8%; Score 404.5; DB 1; Length 118;
Best Local Similarity 63.7%; Pred. No. 3.8e-94;
Matches 79; Conservative 19; Mismatches 15; Indels 11
 Query March 63.6%, Score 409.5; DB 1; Length 121;
Best Local Similarity 64.8%; Pred. No. 1.2e-94; Marches 79; Conservative 17; Mismatches 25; Indels 1
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SEQUENCE
 MOUSE
 Huy2_MOUSE STANDARD, PRT, 115 AA.
P01801,
121-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last embcation update)
19 heavy chain V-III region J666,
Mis masculus (Mouse)
 MOD_RES
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SEQUENCE
 DOMAIN
 Pfam, PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 PIR; C92811; AVMS06.
HSSP; P01789; 1MCP.
 BINDS INULIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain
 binding proteins.";
J. Immunol. 128:302-307(1982)
 Johnson N., Slankard J., Paul L., Hood L.; "The complete V domain amino acid sequences of two myeloma inulin-
 SEQUENCE
 NCBI_TaxID=10090;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 MEDLINE=82099361; PubMed=6798111;
 120
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 1 EVQLQESGGGLVKPGGSLKLSCAASGETESSYIMSWVRQTPEKRLEWVATISSGGSSTYY 60
1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATI--SSGGSST 58
 PDSVKGRETISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGETVNWYFDVWGAGTLVTV 120
 SS 121
 GDSVKGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARDPDILTA-FSFDYWGQGVLVTV 119
 QVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYY 60
 115 AA; 12810 MW; B67AD6638A121A5F CRC64;
 121 121
121 AA; 13566 MW; 480FC53610BF5DAB CRC64;
 IG-LIKE.
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 59 YYPDSYKORFTISROMAONTLYLOMSSLASBDYANYYCTREGGGFTVNWYFDWGAGTLV 118
61 HYABSVKCRFTISROMSSKSSYVLOMNULABDYGTYYCTTG------PAYWQQGTLV 111
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5: sp_invertebrate:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is th score greater t and is derived is the number of results predicted by chance to have after than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

| 16          | 15         | 14.        | 13         | 12         | 11         | 10         | 9          | 00         | 7          | ø          | U        | 4           | w          | N        | 1          | No.         | Result |
|-------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|----------|-------------|------------|----------|------------|-------------|--------|
| 436         | 437.5      | 438        | 439.5      | 441        | 442        | 443.5      | 450        | 453        | 455.5      | 466.5      | 482.5    | 487         | 493.5      | 515.5    | 521        | Score       |        |
| 67.7        | 67.9       | 68.0       | 68.2       | 68.5       | 68.6       | 68.9       | 69.9       | 70.3       | 70.7       | 72.4       | 74.9     | 75.6        | 76.6       | 80.0     | 80.9       | Match       | O a    |
| 494         | 499        | 573        | 116        | 613        | 118        | 121        | 437        | 473        | 597        | 486        | 480      | 471         | 479        | 119      | 487        | Length DB   |        |
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| Q96K68      | Q8N5K4     | Q8WU38     | Q9UL93     | Q8WUK1     | Q9UL91     | Q9UL71     | Q9R1A4     | Q91Z05     | Q96BB9     | Q91Z07     | Q91XE1   | QSTC77      | Q91WP5     | Q920E7   | Q99KA4     | ID          |        |
| Q96k68 homo | Q8n5k4 hon | Q8wu38 hon | Q9u193 hom | Q8wuk1 hon | Q9u191 hor | Q9u171 hon | Q9r1a4 m   | Q91z05 m   | Q96bb9 hor | Q91z07 m   | Q91xe1 m | Q8tc77 homo | Q91wp5 mus | Q920e7 m | Q99ka4 mu  | Description |        |
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PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWY--FDVWGAGTLV 118 PDNVKGRFTISRDNAKNNLYLQMSHLKSEDTAMYYCARDMGGSPYGGYSRFDYWGQGTTI EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISDGGSYTYY

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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Spring cases. | 11 (22383 | 12. | 00.  | 0.00  |  |
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| 57.5 113 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 2             | . ;       |     | 2 .  | 3 1   |  |
| \$11.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00   10.00                                                                                                                                                                                                                                                  | 960           | :         | 117 | 50.7 | 326.5 |  |
| 87.5 113 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 292           | Ľ         | 143 | 50.8 | 327   |  |
| 25                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Q9u195        | 4         | 125 | 51.5 | 331.5 |  |
| 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Q96qs0        | 44        | 159 | 51.9 | 334   |  |
| 25                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Q9u           | 4         | 112 | 52.1 | 335.5 |  |
| 50 50 50 50 50 50 50 50 50 50 50 50 50 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Q921k1        | Ħ         | 278 | 52.2 | 336   |  |
| 27 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Q91v67        | 11        | 143 | 52.2 | 336   |  |
| 55 S S S S S S S S S S S S S S S S S S                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Q9n0w4        | 6         | 124 | 52.3 | 337   |  |
| 50 50 50 50 50 50 50 50 50 50 50 50 50 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Q9n0w6        | 6         | 124 | 52.6 | 339   |  |
| 55 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Q9u187        | 44        | 104 | 53.0 | 341.5 |  |
| 50 54 54 54 54 54 54 54 54 54 54 54 54 54                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Q9u192        | 4         | 124 | 53.1 | 342   |  |
| 25 67.1 113 4 0 0 25 66.1 112 4 0 0 25 66.1 112 4 0 0 25 66.1 112 4 0 0 25 66.1 113 4 0 0 25 66.1 113 4 0 0 25 66.1 113 4 0 0 25 66.1 113 4 0 0 25 66.1 113 4 0 0 25 66.1 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1 459 113 6 0 25 67.1                                                                                                                                                                                                                                                    | Q924p5        | 11        | 144 | 53.3 | 343.5 |  |
| 50 54.3 110 55 54.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 110 55.3 1                                                                                                                                                                                                                                                   | Q9d814        | 11        | 473 | 53.5 | 344.5 |  |
| 25 67.1 113 4 0 0 20 66.1 112 4 0 0 20 66.1 112 4 0 0 20 66.1 112 4 0 0 20 66.1 112 4 0 0 20 66.1 112 4 0 0 20 66.1 112 4 0 0 20 66.1 112 4 0 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6 0 20 66.1 112 6                                                                                                                                                                                                                                                    | Q             | 11        | 145 | 54.3 | 350   |  |
| 55 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Q8vdc9        | Ľ         | 168 | 54.9 | 353.5 |  |
| 3.5 6.7.5 113 4 Q                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Q8vcx7        | ï         | 613 | 56.4 | 363   |  |
| 32 66.7 113 4 Q 26 66.1 112 4 Q 26 66.1 118 4 Q 27 66.1 118 4 Q 28 66.1 118 4 Q 29 68.3 7 499 4 Q 20 68.3 7 499 4 Q 20 68.3 7 499 4 Q 20 68.3 7 499 11 Q 20 68.3 7 499 11 Q 20 68.3 7 499 11 Q 20 68.3 7 499 11 Q 20 68.3 7 499 11 Q 20 68.3 7 499 11 Q 20 68.3 7 499 11 Q 20 68.3 7 499 11 Q                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Q8vea0        | ۳         | 484 | 57.3 | 369   |  |
| 32 67.1 113 4 Q<br>33 66.8 1122 4 Q<br>34 66.8 112 4 Q<br>17 64.8 112 4 Q<br>17 64.8 112 4 Q<br>18 62.9 493 4 Q<br>18 63.7 493 4 Q<br>18 63.7 493 4 Q<br>18 63.7 493 4 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 493 1 Q<br>18 63.7 4 Q<br>18 63.7 4 Q<br>18 63.7 4 Q<br>18 63.7 4 Q<br>18 6 | Q8n4y9        | a<br>O    | 521 | 59.1 | 380.5 |  |
| 3.5 67.5 113 4 QQ 3.6 66.8 118 4 QQ 3.6 66.8 1112 4 QQ 3.6 68.9 1112 4 QQ 3.7 68.9 19.5 4 QQ 3.7 68.9 19.5 4 QQ 3.8 59.3 46.9 11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 03/Vb60       | 11        | 298 | 59.2 | 381   |  |
| 3.5 67.5 113 4<br>3.6 66.8 1122 4<br>3.6 66.8 1122 4<br>4.7 64.8 11.8 4<br>117 64.8 1112 4<br>1.5 63.7 493 4<br>5.5 62.6 131 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Q8r3v9        | 11        | 469 | 59.3 | 382   |  |
| 3.5 67.5 113 4<br>3.2 67.1 147 4<br>3.0 66.8 122 4<br>2.6 66.1 118 4<br>2.6 64.8 112 4<br>3.5 63.7 493 4<br>3.5 63.9 95 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Q9u188        | 4.        | 131 | 60.6 | 390.5 |  |
| 32 67.5 113 4<br>32 67.1 147 4<br>26 66.8 122 4<br>26 66.1 118 4<br>117 64.8 112 4<br>.5 63.7 493 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Q9ulb6        | 4         | 95  | 62.9 | 405   |  |
| .5 67.5 113 4<br>32 67.1 147 4<br>30 66.8 122 4<br>26 66.1 118 4<br>17 64.8 112 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Q8ncl6        | 4         | 493 | 63.7 | 410.5 |  |
| .5 67.5 113 4<br>32 67.1 147 4<br>30 66.8 122 4<br>26 66.1 118 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Q9hcc1        | 4         | 112 | 64.8 | 417   |  |
| .5 67.5 113 4<br>32 67.1 147 4<br>30 66.8 122 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Q9u172        | 4         | 118 | 66.1 | 426   |  |
| .5 67.5 113 4<br>32 67.1 147 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Q9u184        | 4         | 122 | 66.8 | 430   |  |
| .5 67.5 113 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 097509        | 4         | 147 | 67.1 | 432   |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Q9u190        | 44        | 113 | 67.5 | 434.5 |  |

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InterPro, IPROGNO (3 G-14):e.
InterPro, IPROGNO (4 G-14):e.
InterPro, IPROGNO (5 G-14):e.
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 09804. PRELIMINARY; PRT; 487 AA.
09804. (TrEMELTE). 17. Created)
01.10. 00. (TrEMELTE). 17. Leat sequence update)
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01.10. 200. (TrEMELTE). 17. Leat sequence update)
Hypotherical 2.5. Kba protein.
PREMIONAL CONTROLL
 Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 101;
 Similarity
EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
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 80.9%; Score 521; DB 11; Length 487;
81.5%; Pred. No. 6.2e-45;
tive 5; Mismatches 16; Indels
 7DC8E96DB333077B CRC64;
 ALIGNMENTS
 2;
 Gaps
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Q1-DEC-2001
01-DEC-2001
 091WP5 PRELIMINARY; PRT; 417 AA.
091WP5-201 (TrEMBLICAL 19, Crasted)
01-DEC-2001 (TrEMBLICAL 19, Last seed)
01-MAR-2003 (TrEMBLICAL 23, Last amnotation update)
01-MAR-2003 (TrEMBLICAL 23, Last amnotation update)
 whin JD. Tape A., Jennings I.G., Horatise O., corton "Definition of the Idiotope of Peerin-Mimicking Antibodi in Mammalian Cells" (1900) The BMBL/GenBank/DDBJ databases. BMBL, A300937, AML09421.1; ... InterPro; IPR0071010 19-11ke. InterPro; IPR0071010 19-11ke. InterPro; IPR007306, Ig_MEG. InterPro; IPR003306, Ig_W.
Striquaberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
Submitted (SEP-2001) to the EMBL, GenBank/DDBJ databases
EMBL, ECO11656, AMH3556,1, -
Interpro; IPRO13006, Ig_MHC.
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 Hypothetical 51.6 kDa protein.
Mus musculus (Mouse).
 NON TER
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKB; 1.
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2003 (TrEMBLrel. 22, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable region
 TISSUE=Colon;
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
 Mus musculus (Mouse)
 (Fragment).
 SEQUENCE FROM N.A.
 SEQUENCE
 SEQUENCE FROM N.A.
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 121
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 119
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 61
 _
 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 SA 122
 EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARH-GDYDVG--FAYWGQGTLVTV 117
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 SA 119
 TVSS 143
 TVSA 122
 119 AA;
 119
 80.0%;
llarity 85.2%;
Conservative
 PRELIMINARY;
 13025 MW;
 Jennings I.G., Horaitis O., Cotton R.O
Hiotope of Pterin-Mimicking Antibodies
 3
 Score 515.5; DB 1
Pred. No. 3.9e-45;
3; Mismatches 12
 Craniata, Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
 Sciurognathi; Muridae; Murinae; Mus
 Craniata;
 PRT;
 F6E904044381CA7C CRC64;
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 Vertebrata; Euteleostomi;
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 DB 11; Length
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InterPro; IPB003056; Ig_V.
Pfam; PF0047; Ig_4.
PMSITE; PF08035; IG_LIKE; 4.
PMSITE; PF08035; IG_LIKE; 4.
PMSITE; PF08035; IG_LIKE; 4.
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PERM, PRO0407; 19; 4.
RNSSITE; SM00406; IGV, 1.
RNSSITE; PS50835; IG_MC; 2.
PROSITE; PS00290; IG_MC; 2.
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SEQURNCE 439 AA; 51603 MW;
 087077 PRELIMINARY; PRT; 471 AA.

087077.0 (TrEMBLES) 21, Created)
01-JUN-2002 (TREMBLES) 21, Last sequence update)
01-JUN-2002 (TREMBLES) 23, Last annotation update)
Hyporhetical Protein.
Hyporhetical Facaso, Chocata, Craniata, Vertebrata, Euteleostomi,
Butaryota, Meazoa, Primates, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Q91XE1
 Strausberg R.;
Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; EC024289; AAH24289.1; -.
 Hypothetical protein. SEQUENCE 471 AA; 5
 NCBI_TaxID=9606;
 TISSUE-Spleen,
 SEQUENCE FROM N.A.
 140
 133
 121 SA 122
 121 SA 122
 20
 80 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRQLTSYWYFDLWGRGTLVTV
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 80 SDIMKGRFTISRDNAKSTLYLQMSSLRSEDTAFYYCVRGG----YFDVWGAGTAVTV
 61 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
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 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 92;
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 95;
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 SS 134
 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSMSSSSYIYY
 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 SS 141
 471 AA; 51791 MW;
PRELIMINARY;
 Conservative
 Conservative
 51603 MW;
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 75.6%; Score 487; DB 4;
75.4%; Pred. No. 1.8e-41;
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PRT;
 388F7F4CF588660E CRC64;
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 strauberg R.,

submitted (UHL-2011) to the EMBL/GenBank/DDBJ da
EMBL, BC010324, JAN10324.1; -

InterPro; JRP0071010, 13 JAIRC.

InterPro; JRP003106; 13 JAIC.

InterPro; JRP003106; 13 JAV.

Ffam; PF00047; 33 J.

SAMAT; SM0046; JGP; 1.

SMAT; SM0046; JGP; 1.

SMAT; SM0046; JGP; 1.

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01-DEC-2001 (TERMBLrel. 19, Crea
01-DEC-2001 (TERMBLrel. 19, Last
01-MAR-2003 (TERMBLrel. 29, Last
Hypothetical 18-7 Nob protein.
Mus muscullus (Nouse)
 091Xii, 091Xii
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Exteleostoni, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Murinae, Mus Mammalia, Bukaryota, Rodentia, Sciurognathi, Muridae, Murinae, Mus McDI_TaxID=10090;
 SEQUENCE FROM N.A.
 Substitch (UGL-2001) to the EMBL/GenBank/DDBJ databases.
EMBLI BC010798, ANH0798.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig-MC.
InterPro; IPR003596; Ig-W.
Fram, PF00047; Ig-4.
Fram, PF00047; Ig-4.
FR001712; BS00406; IG-Y.
FR0051712; BS00406; BS00406; BS00406; BS00406; BS00406; BS00406; BS0
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 SEQUENCE
 Strausberg R.,
 rissuz=Colon;
 SEQUENCE FROM N.A.
 Local Similarity
nes 92; Conser
 134
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 DVKLVESGGGLVKPGGSLRLSCAASGFIFSNSYMSWVRQTPEKRLEWVATISNSGYATHY
 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLBWVATISSGGSSTYY
 SS 135
 SA 122
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 72.4%; Score 466.5; DB 11; Length 486;
71.3%; Pred. No. 2.3e-39;
tive 10; Mismatches 14; Indels 13;
 74.98;
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Last annotation update)
 Score 482.5; DB 11;
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 4FEF835125DA870B CRC64;
 20B9234EEF2B41ED CRC64;
 Mismatches
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 Straisberg R.;
Submitted (OGT-2001) to the EME
SMEU; BC019760; AMH5760.1;
InterPro; IRRO03006; Ig_MHC.
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InterPro; IRR003006; Ig_MHC.
InterPro; IRR003006; Ig_MHC.
INTERPRO; SMO016; IGU, I.
SMART; SMO016; IGU, I.
SMART; SMO016; IGU, I.
SMOUNTE; PROSUS; IG_ILTE; SA
Hypothetical protein.
SMOUNTE; PROSUS; AA; 65039 MM;
 Q96BB9;
01-DEC-2001
01-DEC-2001
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091205 (TrEMELTA). 19. Created)
01-DBC-2001 (TrEMELTA). 19. Last sequence update)
01-DBC-2003 (TrEMELTA). 23. Last amnotation update)
Mypothetical 51.9 Abs protectin.
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 AU044919.
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 FISSUE=B-cell
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 140
 118
 134
 114 AGTLVTVSA 122
 80 ADSVKGRFTISRDNSRDTLYLQMNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWGQGTL
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 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYF---DVWGAGTL 117
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 EVOLOESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 VTVSS 144
 VIVSA 122
 EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMMWFQAPGKGLEWVSAISGSGGSTYY
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 QGTTITVSS 142
 EVQLQBSGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 PDNVKGRFTVSRDNAKYTLYLQMSSLKSBDTAMYYCVRPEIPIYYYSGS-----YFDSWG
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 Conservative
 PRELIMINARY,
 65039 MW;
 to the EMBL/GenBank/DDBJ databases
 70.7%; Score 455.5; DE 68.8%; Pred. No. 4e-38;
 18; Mismatches
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 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
 PRT;
 4FCA3AD8ECE263D9 CRC64;
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 Pfam; PF00047; 1g; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS050835; IG LIKE; 4.

PROSITE; PS00290; IG MHC; 1.

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 HSSP, P01842; 7FAB.
HSSP, P01842; 7FAB.
MGD; WG1:96446; Igh-4.
InterFro, FR003016; Ig like.
InterFro, FR003016; Ig WGC.
InterFro, FR003056; Ig WGC.
InterFro, FR003596; Ig WGC.
 OPRIA4 PRELIMINARY;
OPRIA4;
O1-MAY-2000 (TrEMBLrel 13,
O1-MAY-2000 (TrEMBLrel 13,
O1-MAR-2003 (TrEMBLrel 23,
 SEQUENCE
 Nilde K.G., Yu X., Ekramodoullah A.K.M., Misra S.;
"Cinning of cDNAs encoding for anti-white pine bliefer rust monoclonal antibody (Mah 7, its light and heavy chains) and construction of a single chain astitiody (GEV), ", heavy chains) and construction of a single chain astitiody (GEV), ", heavy chains) and construction of a submitted (MAX-1999) to the BMBL/GenBank/DD3J databases.
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 Mus musculus (Mouse).
 Gammal heavy chain of Mab7
 Hypothetical protein. SEQUENCE 473 AA; 51946 MW;
 PROSITE; PS00190; CYTOCHROME
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
 InterPro; IRR000345; CytC, hame bind.
InterPro; IRR007110; Ig-1Tke.
InterPro; IRR003006; Ig-MRC.
InterPro; IRR003506; Ig-MC.
InterPro; IRR003506; Ig-V.
Pfam; PR00047; Ig; 3.
Pfam; PR000406; IGV; 1.
PR001750; NR00406; IGV; 1.
PR001750; NR00406; IGV; 1.
 SEQUENCE FROM N.A.
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 MGD; MGI:2144967; AU044919
 BMBL; BC010327; AAH10327.1; -.
 Submitted
 Strausberg
 134
 119
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 93;
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 90;
 Similarity
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 VQLQESGGGLVKEGGSLKLSCAASGETESSYTMSMVRQTPEKRLEWVATISSGGSSTYFP 61
 TVSS 137
 ADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCARE-----LWLRRIDYWGQGTTI
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWY--FDVWGAGTLV 118
 EVQLQESCGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
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 437
437 AA;
 (JUL-2001) to the EMBL/GenBank/DDBJ databases
 Conservative
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 48142 MW;
 69.9%;
 70.3%;
 (Fragment).
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Last annotation update)
 Score 450; DE
Pred. No. 1e-3
3; Mismatches
 8; Mismatches
 Score 453;
Pred. No.
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 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
 5C3A7BB3EE7D697C CRC64;
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 CF625F008932AF12 CRC64;
 437
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C1-MAY-2000 (TEMBELTel. 11, Created)
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 (Fragment)
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 EMBL; AF035043; AAD56279.1; --
HSSP; P01772; 2EB4.
InterPro; IPR007101; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE;
 SEQUENCE FROM N.A. MEDLINE-98277139; PubMed=9614934; Wu X. Liu B., Van der Merwe P.L., Young D.C.;
 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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 01-MAY-2000 (TERMELrel. 13, Created)
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01-MAR-2003 (TERMELrel. 13, Last sequence update)
01-MAR-2003 (TERMELrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
 Clin. Immunol. Immunopathol. 87:184-192(1998).
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 NCBI_TaxID=9606;
 (Fragment)
 121 SA 122
 113 A 113
 122 A 122
 61 ADSVKGRFTISRDNSKNSLYLOMNSLRAEDTALYYCAK-GKVTTIYDRFDIWGQGTMVTV
 62 DSVXGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTVS
 61 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 85,
 1 VQLQESGGGLVKPGGSLKLSCAASGFTPSSYAMSWVRQTPEKRLEWVASFSSGG-IIYYT
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 DSVKGRFTIYKDKDRNILSLOMSSLRSEDTAMYYCARGD----YSAYWGPGTLVTVS
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121 AA;
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 68.9%; Score 443.5; DB 4
69.7%; Pred. No. 9.4e-38;
tive 14; Mismatches 22
 PRT;
 2F045CCFA5D50736 CRC64;
 Kalis N.N., Berney
 121
 DB 4; Length 121;
 22;
 Indels
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Chordata; Craniata; Vertebrata; Euteleostomi;

region

Catarrhini; Hominidae;

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 Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
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InterPro; IPR003596; Ig_v.
 01-MAR-2002 (TrEMBLrel. 20,
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 Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035023; AAD56259.1; -.
HSSP; P01772; 2FB4.
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 Strausberg R.;
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 NCBI_TaxID=9606;
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 MEDLINE=98277139; PubMed=9614934;
 NCBI_TaxID=9606;
 fetus."
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
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 117
 121 $ 121
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 61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGDSSEA----FDIWGQGTMVTV 116
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
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 86;
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 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Hypothetical protein.

Homo sapient (Human) (Chordata; Chordata; Chorda
 InterPory : PR007110, 1g-like.
InterPory : PR007110, 1g-like.
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01-MAR-2003 (TEMBLIZE). 23, Last anocation update)
Myosin-reactive immunoglobulin heavy chain variable
uPragment).
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 8 EDMBÖ
 Clin. Immunol. Immunopathol. 87:184-192(1998)
BMBL; AF035021; AAD56257.1; -.
HSSP; P01772; 2FB4.
 fetus.";
 MBDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
 Homo sapiens (Human).
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 foung D.C.
 SEQUENCE FROM N.A.
 116 S
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 133
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 62
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 61 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYCA-GGGGLGLGY----WGQGTLVTVS
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 Similarity
 DSVKGRFTISRDNAKNTLYLQMSSLRSEDTAKYYCTREGGGFTVNWYFDVWGAGTLVTVS
 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA
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 PRELIMINARY;
 Conservative
 PRELIMINARY;
 12434 MW;
 68.2%; Score 439.5; DB 4 72.7%; Pred. No. 2.3e-37; tive 10; Mismatches 18
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Last annotation updat
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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 0DA0348154DD6061 CRC64;
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BMBL, BC032249, AMB32349.1;
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BMBL, BC021276, AMH2176.1, "Relative tracero; pro0710; 1g Like.

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R InterPro; PR003506; 1g WRC.

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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 Score
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Mouse antibody MB3
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AAB20435 standard; Protein; 249 A

AAB20435;

21-JUN-2001 (first entry)

Anti-FIX/FIXa antibody 198/AB2 scrv.

Factor IX, FIX, Factor IXa; FIXa; scFy, antibody; procosquiant, Factor VIII codeactor; blood cosquiation disorder; haemophilla h, haemorrhagic diathesis; haemostatic; anidolycle; therapy; mouse.

Chimeric - Mus musculus. Chimeric - Synthetic.

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| 22-MAR-2001. |   | WO200119992-A2. |   |              | Region |            | Protein |                | Peptide |              | Region |            | Protein | Key                 |   |
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 combe present sequence is that of a single chain Fv (ecrv) derivative of antibody 195/Na2, comparising the heavy (MY) and light (UL) chain variable regions of 199/Na2 joined by an artificial, flaxible linker to 199/Na2 in the acrv was obtained by PCR smplification of cubha for 199/Na2 in and UL regions and cloning in vector phap. 199/Na2 is nearly and the record in TRY) for the acre was obtained by PCR smplification of cubha for the comparison of the internal factor in TRY) for the comparison of the comparison
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Matches 122;
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 Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procagalant; Factor VII operator; blood cosquilation disorder; haemophilia h, haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
 New factor IX/factor IXa antibodies and their derivatives useful for increasing embolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
 21-JUN-2001
 AAB20442 standard; Protein; 294 AA
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 Claim 12; Fig 16; 138pp; English
 Anti-FIX/FIXa antibody 198/B1-myc-tag fusion
 Scheiflinger F,
 (BAXT) BAXTER AG
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287..288
 145..159
 /label= Signal_peptide
 Location/Qualifiers
 /label= His_tag
 272..274
 /label= Linker
 /label= scFv
 'note= "encoded
 'label= VH
 abel= Spacer
 abel= Spacer
 Š
 Falkner
 GN.
 'n
 Dorner
```

New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic disthesis

Example 18; Fig 34; 138pp; English

Coleader, a single chain Pv (serv) derivative of antibody 199[h] coopprising the heavy (VM) and 140ht (VM) chain variable regions of comprising the heavy (VM) and 140ht (VM) chain regions of the popular and the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the proce The present sequence is that of a fusion protein comprising: PelB

Sequence 294 AA;

```
Query Match
Best Local S
Matches 118
 Similarity
 Conservative
 96.9%;
Score 624; DB 22;
Pred. No. 1.5e-52;
2; Mismatches 2;
 Length 294;
 Indels
 0
Gaps
```

0

23 EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60 82

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S
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 N-PSDB; AAF30728.
 WPI; 2001-290358/30
 (BAXT) BAXTER AG.
 14-SEP-1999;
 13-SEP-2000; 2000WO-EP08936
 WO200119992-A2
 Peptide
 Protein
 Protein
 Peptide
 Misc-difference
 Misc-difference
 Region
 Peptide
 Misc-difference
 Region
 Protein
 Chimeric -
 Chimeric -
 Chimeric -
 bivalent antibody; plasmid pZip-198AB2#102
 Factor IX; FIX; Factor IXa; FIXa; miniantibody; procegniant; Factor VII coffactor; blood cospulation disorder; haemophilia a; haemorrhagic disthesis; haemostatic; amidolytic; therapy; mouse;
 AAB20438;
 Protein
 Peptide
 Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody
 21-JUN-2001
 AAB20438 standard; Protein; 325 AA.
 143
 121
 83
 61
 SS 144
 SA 122
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTSVTV 142
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVNGAGTLVTV
 Escherichia coli.
 Mus musculus.
Synthetic.
 (first entry)
 99AT-0001576.
 166
 320
 145..159
 Kerschbaumer R,
 /label= Helix
 /note= "encoded by
 /label= Mature_protein
23..271
 /label= Signal_peptide
/note= "PelB leader"
 Location/Qualifiers
 . 091
 note= "encoded
 /label= VH
 label= Spacer
 note= "encoded
 label= VL
 label= Linker
 label= scFv
 319
 284
 271

 Hinge

 His_tag
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 Falkner F,
 GGN
 TON
 TNT
 Dorner
 120
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RESULT 4 AAB20437 묽

143 SS 144

AAB20437 standard; Protein; 732 AA

New factor IX/factor IXa antibodies and their derivatives useful for

Peptide Misc-difference Region Protein Key

Proteir Peptide Chimeric Chimeric alkaline

23..144 /label= VH 145..159

note= "encoded by

GGN

/label= scFv /label= Mature\_protein 23..271 /label= Signal\_peptide 23..732 Location/Qualifiers

Chimeric - Mus musculus.

phosphatase.

1.1

Escherichia coli. Synthetic Factor IX; FIX; Factor IXa; FIXa; scPv; antibody; procagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia a; haemorrhagic diathesis; haemostatic; amidolytic; therapy; moust, haemorrhagic diathesis;

amidolytic; therapy; mouse;

Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion

21-JUN-2001 AAB20437;

(first entry)

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 Query Match
Best Local &
Matches 118
 The present sequence is that of a bivalent miniantibody comprising a fall leader spitide, the single chain by (seft) frament of and a C-terminal fifth red, The protein was expressed in ructure and a C-terminal fifth red, The protein was expressed in the case of the state of the protein red expressed in the case of the first set
 Seguence
 increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic disthesis
 activity.
 Example 16; Fig 28; 138pp; English.
 121 SA 122
 83
 23
 118;
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYEDVWGAGTLVTV
 1 BVQLQBBGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 Similarity
 PDSVKGRFTISRDNAKUTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTSVTV
 EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 325
 Conservative
 AA,
 96.9%;
 Score 624; DB 22;
Pred. No. 1.6e-52;
2; Mismatches 2
 Length 325,
 Indels
 0
 Gaps
 142
 120
 82
 60
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0

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RESULT 5
AAB20436
ID AAB2
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 Matches
 Query Match
Best Local Similarity
 The present sequence is that of a fusion protein comprising; a Pells leader; a single chain Fv (scFv) dortvative of antibody 19/81 comprising the heavy (WH) and light (WL) chain variable regions of 199/81 joined by an artificial. flexible linker apptide, a spacer; Escherichia coli alkaline phosphatese; and a C-terminal 6His efficient yeal. 199/81 is an example of anti-human factor IX (FIX)/activated Factor IX (FIX) antibodies of the invention.

MRI-FX/FIX antibodies and their carivatives; including serv
 AAB20436 standard; Protein; 249
 regments, have FVIIIa cofactor activity or FIXa activating activity. Administration leads to an increase in the processpalant activity of FIXa, even in the presence of FVIII inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitors patients. FVIII or Composition for treating patients with blood coagulation disorders, especially hampophilia A and themocrapid distribution disorders, especially hampophilia and themocrapid distribution disorders, especially hampophilia and themocrapid distribution disorders, especially hampophilia A and themocrapid distribution disorders.
 New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
 Sequence
 Example 16; Fig 26; 138pp; English.
 WPI; 2001-290358/30.
 Scheiflinger F, Kerschbaumer R,
 14-SEP-1999;
 13-SEP-2000; 2000WO-EP08936
 22-MAR-2001.
 WO200119992-A2
 Peptide
 (BAXT) BAXTER
 Peptide
 Protein
 Region
 121 SA 122
 83
 23
 بر
 PDSVKGRFTISRDNAKUTLYLQNSSLRSEDTAMYYCTREGGGFTVNMYFDVMGAGTSVTV
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 EVQLQESGGGLVKPGGSLKLSCAASGFTESSYTMSWVRQTDEKRLEWVATISSGGSSTYY
 SS 144
 732 AA;
 Conservative
 99AT-0001576
 272..275
/label= Spacer
 276..725
 /label=_Alkaline_phosphatase
 'label= His_tag
 /label= VL
 'label= Linker
 96.9%;
 .732
 Score 624; DB 22;
Pred. No. 4.2e-52;
2; Mismatches 2;
 Falkner F,
 Dorner
 2; Indels
 Length 732;
 0,
 Gaps
 142
 120
 82
 60
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Misc-difference
 Misc-difference
 Protein
 Peptide
 Region
 Key
 Chimeric - Mus musculus.
Chimeric - Synthetic.
 Factor IX, FIX, Factor IXa, FIXa, scFv, antibody, procagulant, Factor VIII cofactor; blood cosgulation disorder, haemophilia h, haemorrhagic diathesis; haemoscatic; amidolytic; therapy; mouse.
 Anti-FIX/FIXa antibody 198/A1 scFv
 21-JUN-2001
 AAB20436;
 Protein
 (first entry
 224
 123..136
/label= Linker
 Location/Qualifiers
 /note= "encoded by GCN"
 /labe:
 note= "encoded by
 label= VL
 .abel= CDR3
 abel= CDR3
 HV ≡
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WO200119992-A2

13-SEP-2000; 2000WO-EP08936

14-SEP-1999; 99AT-0001576

(BAXT ) BAXTER AG

Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F

N-PSDB; AAF30726. 2001-290358/30.

New factor IX/factor IXa antibodise and their derivatives useful for increasing andobytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic disthesis

Example 10; Fig 17; 138pp; English.

com the present sequence is that of a single chain FV (actV) derivative of antibody 198/AL, comparising the heavy (W1) and light (VI) chain variable regions of 198/AL joined by an artificial, flexible linker to peptide. The actV was obtained by PCR amplification of chasa for 198/AL yellows and cloning in vector phys. 198/AL is at bomple of anti-linmant factor XI XIVI) act varied Factor XI (VIX) and the process of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr diathesis.

Sequence 249

Query Match
Best Local Similarity
Matches 114; Conserv Conservative 94.6%; Score 609; DB 22; pred. No. 3.4e-S1; 5; Mismatches 3 22; Length 249; Indels 0, Gaps

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 The invention relates to a novel monoclonal antibody having the identifying characteristics of, or that is a monoclonal antibody 1473. An antibody of the invention has osteopathic, antirhamatic, antiarchiritic, antiarchiritic, antirinflammatory, cytostatic, antirinflammatory, the polymucleotides encoding the antibodies and neuroprotective activity. The polymucleotides encoding the antibodies of the invention may have a use in gene therapy. The antibodies and polypeptides are useful for treating or preventing osteopathic diseases, such as rhemmatocia, archiritis, osteoppools, metastatic, and primary bone
 cancer,
 Disclosure; Page 8; 51pp; English
 New monoclonal antibody having the characteristics of a monoclonal antibody 1473, useful for treating or preventing osteopathic diseases e.g., rheumatoid arthritis, or osteoporosis, and immune diseases e.g.
 WPI; 2003-156758/15.
N-PSDB; ABV99887.
 18-MAY-2001; 2001US-292031P
 03-MAY-2002; 2002WO-US14246
 Region
 Region
 Mus musculus
 multiple sclerosis; heavy chain variable region; complementary determining region; CDR.
 Nouse, monocloral antibody; 1493, osteopathic; antishematic; antiathematic; antiathematic; antidebatic; antion antiathematory; cytoetatic; antiqueoriatic; antidebatic; neuroprotective; gene therapy; theirmatoid arthritis; osteopocosis; bone eance; osteolysis; osteopathinis; immune disease; psoriasis; insylin-dependent diabetes; inflammatory bowel disease;
 Murine antibody 14F3 heavy chain variable region.
 21-MAR-2003
 ABP60555
 WO200295012-A1
 ABP60555 standard; protein; 134 AA
 (SMIK) SMITHKLINE BEECHAM PLC
 Region
 121
 121
 13
 61
 wear debris induced osteolysis or osteoarthritis, and immune
 SMITHKLINE
 SS 122
 PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYHCTREGGGYYVNWYFDVWGAGTTLTV
 EVQLQESGGGLVKPGGSLKLSCAASGFIFSSYIMSWVRQTPEKRLEWVATISSGGSSTYY
 UNITED TO SECONDARY OF THE SECONDARY OF
 SA 122
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 or diabetes -
 Tornetta
 (first entry
 /label= CDR2
99..110
/label= CDR3
 /label=
 Location/Qualifiers
 BEECHAM
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 CDRI
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 120
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 Query Match
Best Local S
Matches 104
 N-PSDB;
 WPI;
 Region
 (BAXT) BAXTER
 14-SEP-1999;
 22-MAR-2001
 WO200119992-A2
 Proteir
 Chimeric
 21-JUN-2001
 AAB20434;
 AAB20434
 Sequence
 (CDR's)
 121
 120
 61
 104;
 61
 ,
 AAF30724.
 SA 122
 PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCARL-DGYNYRWYFDVWGTGTTVTV
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diseases such as psoriasis, insulin-dependent diabetes, inflammatory bowel disease or multiple sclerosis. The present sequence represents the heavy chain variable region of the murine monoclonal autilogy 1473 of th invention. The sequence contains three complementary determining regions
 the
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### 134 B

```
Similarity
 Conservative
 85.24;
 Score 538.5;
Pred. No. 1.:
 Mismatches
 1.2e-44;
 DB 24;
 Indels
 Length
 134;
۲,
Gaps
```

#### PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV EVQLVESGGDLVKPGGSLKLSCNASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSYTYY **EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY** 120 60 60

119

#### SS 121

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standard; Protein;
249 AA.
```

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(first entry)
```

Anti-FIX/FIXa antibody 193/K2 scFv

Factor IX, FIX, Factor IXa; FIXa; scFv, antibody; proceapulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A, haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

## Chimeric - Mus musculus. Synthetic.

| Peptide                  | Region                | Protein            | Key                 |  |
|--------------------------|-----------------------|--------------------|---------------------|--|
| 122135<br>/label= Linker | 98110<br>/label= CDR3 | 1121<br>/label= VH | Location/Qualifiers |  |

136..249 /label= VL 230..238 /label= CDR3

13-SEP-2000; 2000WO-EP08936

99AT-0001576

Kerschbaumer R, Falkner ٦ Dorner Ŧ

# 2001-290358/30

New factor IX/factor IXa antibodies and their derivatives useful for increasing andolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis

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RESULT A RESULT A RESULT AND LIAR AND L
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 The present sequence is that of a single chain by (soft) derivative of sinkey 193/EZ; comparising the heavy artificial 194 (No. 1944). In the variable regions of 193/EZ (sinked by sex) artificial 194 (No. 1944). In the comparising the property of the serve was obtained by PCR amplification of cDNs from the comparison of the serve was obtained by PCR amplification of cDNs from the comparison of the serve was not denoted by PCR amplification (PVIII a) of an example of anti-human Factor X (FIX)/Assistance X (FIX) (PVIII a)
 Query Match
Best Local S
Matches 105
 Nouse, antibody ZM, heavy chain variable region, osteopathic, pesciasis,
cytostatic, antihidamatory, osteopocosis, bone cancer; immune disease;
inflammatory bowel disease; multiple sclerosis; osteopenic disease;
rheumatoid arthritis; diabetes.
 26-MAY-2000; 2000US-207628P
 24-MAY-2001; 2001WO-US16865
 WO200191793-A1
 Region
 Region
 Region
 Mus sp
 Mouse antibody 2A4 heavy chain variable region.
 AAE16426 standard;
 Sequence
 Claim
 119
 120
 105;
 10;
 61
 61
 Similarity
 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSS--FDYWGQGTTLT
 VSA 122
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGG-GFTVNWYFDVWGAGTLVT 119
 EVOLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
 VSS 121
 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEXRLEWVATISSGGSSTYY
 Fig 15; 138pp;
 249
 Conservative
 (first entry)
 AA;
 /note= "Complementarity determining region"
 /note= "Complementarity determining region"
 Location/Qualifiers
 'note= "Complementarity determining region'
 /label= CDR
 /label= CDR
 Protein; 121 AA
 110
 83.5%;
 English.
 8,
 Score 537.5; DB
Pred. No. 3e-44;
8; Mismatches
 7;
 22;
 Indels
 Length
 249;
 3,
 Gaps
 118
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RESULT 7
ABG774241
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 Ş
 Matches 103; Conservative
 Query Match
 7-cell receptor; cytostatic; dermatological; neuroprotective; immunostimulant; 031; ganglioside antigen; MB.5; pSMM, tumour; DB; 4D4; 3B21; prostate-specific newbrane antigen; zeta signalling chain; CD841pha hinge; cancer; melanome; neuroendocrine tumour; prostate cancer; small cell lung cancer; heavy chain variable region; mouses.
 The invention relates to anti-NANK monoclonal antibodies which has the identifying characteristics of monoclonal antibody AM. The antibody or polypeptide is useful for treating or preventing ose-eopenic diseases (e.g., rhewardoid arthritis, ost-eopenies, metastatic and primary bone cancer, wear debris induced ost-eolygis or ost-eolythitis) or immure diseases (e.g., poprisais, insulin dependent disheres, inflammatory bowel disease or multiple sclerosis). The antibody is also useful for treating and disgnosing conditions mediated by the NANK ligand. The present sequence is mouse entitlody 2A4 heavy Chain variable region.
 30-NOV-2000; 2000US-250087P
 10-DEC-2001; 2001US-0006773
 19-SEP-2002
 US2002132983-A1
 Mus sp
 Mouse antibody MB3.6 heavy chain variable region.
 22-APR-2003
 ABG74241;
 ABG74241 standard; Protein; 140 AA
 Sequence
 or multiple sclerosis)
 New anti-RANK ligand monoclomal antibodies, useful for treating or preventing offeropenic diseases (e.g. arthitis, osteoporosis or bone cancer) or immune disease (e.g. psoriasis, inflammatory bowel disease
 (SMIK)
 Claim 6; Page 9; 50pp; English
 N-PSDB; AAD26948.
 WPI, 2002-122040/16
 Local Similarity
 120
 121 SA 122
 62
 61
 SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC.
 SS 121
 PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCARL-DGYNYRWYFDVWGTGTTVTV
 PDSVKGRETISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 EVQLVESGGDLVKPGGSLKLSCAASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSYIYY
 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 121 AA;
 Sweet RW,
 (first entry)
 82.7%;
 Taylor AH,
 Score 532.5; DB
Pred. No. 4e-44;
4; Mismatches
 Wattam TA;
 DB 23;
 14;
 Indels
 Length
 121;
 ۳,
 Gaps
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120 60 60

119

(JUNG/) JUNGHANS R P

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RESULT 10
ANU72814
ID ANU72814
XX
AC ANU72
XX
C 26-FE
XX
TUMAN
THAME
XX
THAME
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TRAILI
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 or The invention relates to a chimaeric modecule comprising the gof 3 cc (ganglioside antigen) binding domain of antibody Mmg 36, with any of 3 cvariable gene sequences, or the SBMA (prostate-specific membrach antigen) cc binding domain of antibody 308, 404 and 381, with variable gene sequences, the zeta signalling chain of the Toell receptor and an interventing (Osalpha hange in which cystelia residues have been mutated. The second of the second sequences of the company of the control of the con
 Matches 103;
 Query Match
Best Local
 WO200183560-A1
 Tumour nocrosis factor-related apoptosis-inducing ligand receptor, TRAII, TRAII receptor DB5, cytostatic; apoptosis; cell proliferation; autoimmune disease; systemic lugus erythemateous; Hashimotor's disease; rhemated arthritis; 5jogren's syndhome; Chnori disease; services and addison disease; scleroderma; coodpacture's syndroms; setralization, addison disease; scleroderma; coodpacture's syndroms; setralization; westighe scleroders; Beschor's disease; dibetes; altergy; arterioscieness; myocarithis, certificationally; of the set of th
 08-NOV-2001
 Synthetic
 AAU72814;
 Humanised mouse TRA-8 anti-human DR5 antibody #4.
 26-FEB-2002
 AAU72814 standard; Protein; 119 AA
 Sequence
 chain variable region.
 Disclosure; Page 9; 35pp; English.
 New chimeric molecule useful in treating patients with disorders, such as melanoma, neuroendocrine disorders, protette and small cell lung cancer comprises GD3 and/or PSMA binding domains of antibody -
 Junghans RP
 136
 118 VTVSA 122
 2003-208946/20
 80
 61
 20
 Similarity
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREG----GGFTVNWYFDVWGAGTL
 VTVSS 140
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTALYYCARPGYDRGA----
 EVVVVESGGGFVKPGGSLKLSCAAAGFTFSRYAMSWVRQTPEKRLEWVATISSGGSHTYY
 BVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 140 AA,
 Conservative
 (first entry
 81.9%;
 Pred. No. 1.4e-43
 antibody; chromosome 8p21-22; TRA-8
 Mismatches
 DB 24;
 10;
 Indels
 Length 140;
 -WFFDVWGAGTT 135
 7;
 Gaps
 117
 79
 60
 RESULT 11
AAU72801

 S
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 S
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 B
 Matches
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WPI; 2002-049338/06
 Zhou T,
 (UABR-)
 02-MAY-2000; 2000US-201344P
 02-MAY-2001; 2001WO-US14151
 UAB RES FOUND
 Ichikawa K,
 Kimberly RP,
 Koopman WJ
```

Movel antibody specific for tumour necrosis factor-related apoptosis-inducing ligand, useful for inhibiting cell proliferation in

Example 26; Page 212-213; 229pp; English

Commentation describes a novel antibody which recognizes a tumour controls factor (TME) related application to the describe and the described factor (TME) related application to the described factor (TME) related application to activity to a cell expressing DBS in vivo. It is also useful for properties of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the described factor of the describ

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Query Match
Best Local
 Sequence
 Similarity
 119 AA;
80.7%;
Score 519.5; DB 2
Pred. No. 7.1e-43;
 DB 23;
 Length
 119
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61
 102;
 ۲
PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISGGSYTYY
 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 Conservative
 Mismatches
 Indels
 ω
 Gaps
 120
 60
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61

PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITT----DYWGQGTTLTV

AAU72801 standard; Protein; 464 AA

AAU72801;

26-FEB-2002 (first entry

heavy chain.

Twoour necrosis feator-related approasis inducing ligand receptor, TRAII, TRAII receptor DES, cytostatic, apotposis, poll proliferation; attoinmune disease, systemid lugue explanatoons; disease, of disease, rhematecid attrictis, syogen's syndroms; Chan is seases lateral relations, addison disease; scleroderms, coodpasture; syndroms, setzility, mysathenia gravis; multiple scleroderis; Basedows disease; diabetes; allergy; atteriosclerosis, mycoarddits, cardiomypathy;

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RESULT 12
AAW57576
ID AAW5'
XX
AC AAW5'
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 The invention describes a novel antibody which recognises a tumour concernes feator (TNE) related approvals inducting ligand (TRAII) receptor DES (located on chromosome 8p21-22). The antibody has apoprosits inducting cattivity to a cell expressing pES in vivo. It is also useful for property a therapeutic for selective apoprosis of abnormal or comparing a therapeutic for selective apoprosis of abnormal or cell, grant and for inhibiting cell proliferation in a cell, present and the proliferation of a cell, carefully a human breast, ovary, colon, haematopolestic, prostate, colon carefully a human breast, ovary, colon, haematopolestic, prostate, carefully a language of the carefully a carefully a human breast, ovary, colon, haematopolestic, prostate, carefully may carefully a language of the carefully may carefully a language of the carefully may carefully a carefully a carefully a carefully may carefully a c
 Query Match
Best Local S
Matches 102
 03-SEP-1998
 AAV.57576 standard;
 Claim 26; Page 198-199; 229pp; English.
 Novel antibody specific for tumour necrosis factor-related apoptosis-inducing ligand, useful for inhibiting cell proliferation in
 Sequence
 02-MAY-2000; 2000US-201344P
 02-MAY-2001; 2001WO-US14151.
 08-NOV-2001.
 Mus musculus.
 glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8
 Zhou T,
 (UABR-)
 2002-049338/06
 137
 al Similarity
102; Conserv
 61
 80 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITT----DYWGQGTTLTV
 UAB RES FOUND
 SA 122
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 Ichikawa K,
 SS 138
 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY
 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLBWVATISSGGSSTYY
 464 AA;
 TRA-8 are shown
 Conservative
(first entry)
 protein; 118 AA
 80.7%;
 Kimberly RP,
 5
 Score 519.5; DB 23;
Pred. No. 3.5e-42;
2; Mismatches 15;
 AAU72799 and AAU72800
 Koopman WJ;
 DB 23;
 Indels
 Length 464;
 3,
 136
 79
 RESULT 13
AAW89627
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 S
 14-APR-1999
 AAW89627;
 Sequence
 Sato K,
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Query Match
Best Local Simi
Matches 102;
 New antibodies have been developed which are specific for human parathormone ratated peptides (horper). The antibodies comprise chimeric Land/or H chains, where the C region is of human and L region of mouse, origin. The persent sequence represents a specifically claimed region of an antibody of the invention. Host cells, transformed with vectors containing DNA encoding antibodies of the invention, can be used to produce the antibodies of the invention, containing DNA encoding antibodies and be used to treat produce the antibodies. The antibodies may be used to treat produce the antibodies of the invention, or cancers of hypercalcamen a sepecially that due to a malignancy, e.g. cancers of hypercalcamen as packed by the composition of malignancy is produced. They hadder, womb or prosess or malignancy is produced. They was also be used for treatment of hypophosphaenia such as that due to marked one or treatment of hypophosphaenia such as that due to marked one or treatment of hypophosphaenia such as that due to marked one or treatment of hypophosphaenia such as that due to
 New chimeric antibodies against human parathormone related peptide(s) - useful for, e.g. treatment of hypercalcaemia i disorders caused by malignant neoplasm(s)
 Chimeric; antibody; human parathormone related peptide; hPTRP; mouse
L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
bypopbosphaemia; pathogen; vitamin D resistance; V region; C region; humanised.
AAW89627 standard; Protein; 118 AA.
 pathogens or to vitamin D resistance.
 Claim 5; Page 111-112; 182pp; Japanese
 24-JUL-1997;
26-SEP-1996;
 24-SEP-1997;
 02-APR-1998
 WO9813388-A1.
 Chimeric - Homo
 Synthetic.
 Chimeric H chain SEQ ID NO:46 for an antibody against hPTRP
 (CHUS) CHUGAI SEIYAKU KK
 Chimeric -
 117 SA 118
 121 SA 122
 61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMFYCARQ----TTMTYFAYWGQGTLVTV
 61 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 1 EVOLOESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 Similarity
 Wakahara Y,
 EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWIRQTPDKRLEWVATISSGGSYTYY
 S
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 118 AA;
 Conservative
 s sp.
sapiens.
 97JP-0214168
96JP-0255196
 97WO-JP03382
 80.6%;
 Yabuta N
 Score 519; DB 19;
Pred. No. 7.9e-43;
 Mismatches
 hypercalcaemia and other
 11;
 Length 118;
 Indels
 4;
 Gaps
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(first entry)

60 60

Mouse humanised antibody #23-57-137-1 heavy chain mature protein.

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RESULT 14
AAY77502
ID AAY77
XX
AC AAY77
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DT 26-AI
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KW Hypei
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 Query Match
Best Local S
Matches 102
 cachexia containing a substance which inhibits the binding of a parathyroid homeone related peptide (PEHP) to its receptor, as an active component. This substance may be an antagonist to the receptor, or an antibody (preferably monoclonal) or antibody fragment recognising PHHP: The antibody is preferably humanised or chimeric. The preferably humanised or chimeric may preferably humanised or chimeric may preferably humanised or chimeric may preferably humanised or chimeric may be compared by hybridoma 23:5-137-1 (ESW) BP-5631). The composition is used for by hybridoma 23:5-137-1 (ESW) BP-5631). The composition is
 Mus sp.
Synthetic.
 Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP; tumour
 26-APR-2000
 AAY77502 standard; Protein; 118 AA
 Sequence
 the treatment of cachexia arising in connection with diseases such as
cancer, threshy improving the quality of life of the patiant. The
present sequence represents mouse humanised antibody heavy chain from
#23-57-137-1 from the present invention.
 cancer or other diseases
 Human; parathyroid hormone related protein; PTHxP; cachexia; cancer;
inhibitor; humanised.
 Peptide seg ID No: 46.
 AAY77502
 The present invention describes compositions for the treatment
 Example 2; Page 72-73; 125pp; Japanese.
 Inhibitors of binding of parathyroid hormone related peptide to its
 WPI; 1999-070101/06.
 Ishii K,
 (CHUS) CHUGAI SEIYAKU KK.
 18-JUL-1997;
15-MAY-1997;
 13-MAY-1998;
 19-NOV-1998
 WO9851329-A1
 117 SA 118
 121 SA 122
 102;
 61
 61
 ,_
 ,,
 Similarity
 PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMFYCARO----TTMTYFAYWGQGTLVTV
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWIRQTPDKRLEWVATISSGGSYTYY
 EVQLQESGGGLVKFGGSLKLSCAASGETESSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 Sato K,
 useful for, e.g. treatment of cachexia arising from
 118 AA;
 Conservative
 (first entry)
 97JP-0194445
97JP-0125505
 98WO-JP02116
 Tunenari T;
 83.6%;
 Score 519; DB 20;
Pred. No. 7.9e-43;
5; Mismatches 11
 Length 118;
 Indels
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RESULT 15
ANG63392
TID ANG63392
XX XX ANG62
XX XX PACS1
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 δ
 Matches 102;
 Query Match
 AAG63382;
 Sequence
 The invention relates to a method of treatment of hypercalcenic orisis.

A composition for the treatment of hypercalcenic crisis contains as
active component a substance which inhibite the binding of parathyroid
hommone related peptide (PTHFP) to its receptor. The inhibitor is used
for the treatment of hypercalcenic orisis, such as that associated with
 Treatment of hypercalcemic crisis with a substance inhibiting binding of parathyroid hormone related peptide to its receptor
 WPT; 2000-117115/10.
 WO200000219-A1
 Mus musculus
 25-JAN-2000; 2000JP-0083034
 14-DEC-2000; 2000WO-JP08875
 02-AUG-2001.
 WO200154725-A1
 Mus musculus
 Parathyroid hormone-associated peptide; PTHrP; dental disease
 Amino acid sequence of a murine polypeptide.
 15-OCT-2001
 AAG63382 standard; Protein; 118 AA
 Sato K,
 26-JUN-1998;
 25-JUN-1999;
 06-JAN-2000.
 Example 2; Page 87-88; 120pp; Japanese.
 (CHUS)
 Local Similarity
 malignant tumour.
 117 SA 118
 121 SA 122
 61
 61 PDSVKGRFTISRDNAKUTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
 1 EVQLQESGGGLYKPGGSLKLSCAASGFTFSSYTMSWVRQTPBKRLEWVATISSGGSSTYY
 CHUGAI SEIYAKU KK
 Tsunenari T;
 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMFYCARQ----TTMTYFAYWGQGTLVTV
 EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWIRQTPDKRLEWVATISSGGSYTYY
 118 AA;
 Conservative
 (first entry)
 98JP-0180143
 99WO-JP03433.
 83.6%;
 5;
 Score 519; DB 21;
Pred. No. 7.9e-43;
 Mismatches
 Length 118;
 Indels
 4.
 Gaps
 120
 60
 60
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Kato A,

Suzuki M,

Sugimoto T;

(CHUS )

CHUGAI SEIYAKU KK.

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Page 1
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Search completed: November 7, 2003, 07:27:02
Job time : 52.6115 secs
 Query Match 80.6%; Score 519, DB 22; Length 118; Best Local Similarity 83.6%; Pred No. 7.96-43; Matches 102; Conservative 5; Mismatches 11; Indels 4
 The specification describes a treatment for dental diseases. The treatment comprises a substance that inhibits binding between parathyroid homome associated poptide and its receptor. The present sequence represents a murine protein, which is used in the course of the invention.
 WPI; 2001-465459/50.
 Sequence
 Parathyroid hormone-associated peptide binding inhibitors useful for treating dental disease
 Disclosure; Page 102-103; 140pp; Japanese.
 121 SA 122
 117 SA 118
 61 PDS.VIGGRETISRDNARNTLYLONGSLÆSEDTAMYYCTREGGGETVINNYEDVIGAGGTLVTV 120
61 PDS.VIGRETISRDNARGYTLYLONGSLÆSEDTAMPYCARG---THMTYFAXWOQGTLVTV 116
 1 BYQLUESGGLINKEGGSLKLSCAASGFTESSYTASWIRQTEXRLEWIATISSGGSYTYY 60
 118 AA;
 4
 Gaps
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# GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: OM protein - protein search, using sw model November 7, 2003, 07:30:19; Search time 107.015 Seconds
(without alignments)
195.799 Million cell updates/sec

Perfect score: sequence: Title: US-09-661-992B-86\_COPY\_1\_122 644 1 EVQLQESGGGLVKPGGSLKL.....FTVNWYFDVWGAGTLVTVSA 122

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

published Application An.

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| Com2.5 (prodate.// pubpas/1907 MR PUB pep.\*
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| Com2.5 (prodate.// pubpas/1905 MR PUB pep.\*)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| 15                | 14               | 13               | . 12              | 11                | 10                | 9                 | 8                 | 7                 | 0                 | s                 | 4                 | ω                 | ы                 | -                 | Result         |
|-------------------|------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|----------------|
| 517.5             | 519              | 519              | 519               | 519               | 519               | 519               | 519.5             | 519.5             | 519.5             | 519.5             | 519.5             | 519.5             | 527.5             | 529.5             | Score          |
| 80.4              | 80.6             | 80.6             | 80.6              | 80.6              | 80.6              | 80.6              | 80.7              | 80.7              | 80.7              | 80.7              | 80.7              | 80.7              | 81.9              | 82.2              | Query<br>Match |
| 144               | 137              | 137              | 118               | 118               | 118               | 118               | 464               | 462               | 462               | 119               | 119               | 119               | 140               | 123               | Length I       |
| 9                 | 12               | 10               | 15                | 15                | 12                | 70                | 12                | 12                | 12                | 12                | 12                | 12                | 14                | 10                | B              |
| US-09-881-823-12  | US-10-337-981-76 | US-09-423-800-76 | US-10-169-003-46  | US-10-182-018-46  | US-10-337-981-46  | US-09-423-800-46  | US-10-275-180A-23 | US-10-286-132A-23 | US-10-281-479A-23 | US-10-286-132A-61 | US-10-275-180A-61 | US-10-281-479A-61 | US-10-006-773-4   | US-09-144-886-60  | ID             |
| Sequence 12, Appi |                  |                  | Sequence 46, Appl | Sequence 46, Appl | Sequence 46, Appl | Sequence 46, Appl | Sequence 23, Appl | Sequence 23, Appl | Sequence 23, Appl | Sequence 61, Appl |                   | Sequence 61, Appl | Sequence 4, Appli | Sequence 60, Appl | Description    |

밁 Ś 문 8 용

| 5                | 44                | 43               | 42              | 41                | 40                | 39                | 38               | 37               | 36               | 35                | 34                | w<br>W            | 32                | 31               | 30               | 29                | 28                | 27                | 26               | 25               | 24               | 23              | 22                | 21                | 20                | 19               | 18              | 17              | 16              |
|------------------|-------------------|------------------|-----------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|-----------------|-------------------|-------------------|-------------------|------------------|-----------------|-----------------|-----------------|
| 489.5            | 489.5             | 489.5            | 490             | 491.5             | 491.5             | 491.5             | 492              | 493              | 493              | 494.5             | 494.5             | 494.5             | 494.5             | 495              | 496              | 496.5             | 496.5             | 496.5             | 500              | 502              | 504              | 510             | 513.5             | 513.5             | 513.5             | 514.5            | 515.5           | 517.5           | 517.5           |
| 76.0             | 76.0              | 76.0             | 76.1            | 76.3              | 76.3              | 76.3              | 76.4             | 76.6             | 76.6             | 76.8              | 76.8              | 76.8              | 76.8              | 76.9             | 77.0             | 77.1              | 77.1              | 77.1              | 77.6             | 78.0             | 78.3             | 79.2            | 79.7              | 79.7              | 79.7              | 79.9             | 80.0            | 80.4            | 80.4            |
| 252              | 125               | 125              | 443             | 119               | 119               | 119               | 116              | 116              | 116              | 119               | 119               | 119               | 117               | 116              | 118              | 119               | 119               | 119               | 118              | 116              | 116              | 124             | 119               | 119               | 119               | 123              | 140             | 165             | 155             |
| 12               | 12                | 12               | 9               | 12                | 12                | 12                | 12               | 12               | 12               | 12                | 12                | 12                | 12                | 12               | 10               | 12                | 12                | 12                | 10               | 12               | 12               | 11              | 12                | 12                | 12                | ö                | ٥               | 12              | 12              |
| US-10-169-351-49 | US-10-169-351-102 | US-10-169-351-31 | US-09-917-410-4 | US-10-286-132A-31 | US-10-275-180A-31 | US-10-281-479A-31 | US-10-169-351-35 | US-10-169-351-47 | US-10-169-351-39 | US-10-286-132A-59 | US-10-275-180A-59 | US-10-281-479A-59 | US-10-078-757B-56 | US-10-169-351-45 | US-09-144-886-62 | US-10-286-132A-56 | US-10-275-180A-56 | US-10-281-479A-56 | US-09-144-886-63 | US-10-169-351-37 | US-10-169-351-43 | US-09-518-737-2 | US-10-286-132A-60 | US-10-275-180A-60 | US-10-281-479A-60 | US-09-144-886-61 | US-09-286-240-4 | US-10-077-624-4 | US-10-077-624-7 |
|                  |                   |                  |                 |                   |                   |                   |                  |                  |                  |                   |                   |                   |                   |                  |                  |                   |                   |                   |                  |                  |                  |                 |                   |                   |                   |                  |                 |                 |                 |
| Sequence         | Sequence          | Sequence         | Sequence        | Sequence          | Sequence          | Sequence          | Sequence         | Sequence         | Sequence         | Sequence          | Sequence          | Sequence          | Sequence          | Sequence         | Sequence         | Sequence          | Sequence          | Sequence          | Sequence         | Sequence         | Sequence         | Sequence        | Sequence          | sequence          | Sequence          | sequence         | sequence        |                 | Sequence        |
| 49               |                   | 31               | 4.              | н                 | 3                 | ω                 | ü                | 47               | 3                | 59                | 5                 | 5                 | 56                | 45               | 62               | 56                | 56                | 5                 | 6                | 37               | 4                | 2               | 60                | 000               | ,6                | Ę                | *               |                 | ٠,              |
| , Appl           | Z, App            | Appl             | riddy           | Appi              | e 31, Appl        | Appl              |                  |                  |                  | Appl              | Appl              | App1              | Appl              |                  |                  |                   | - Appl            | Appl              | Appl             |                  | Appı             | Appli           | Tddv              | Appr              | rddy              | rddy             | ridd            | riddy           | Appli           |

#### ALIGNMENTS

| 7 MO                                                                                                                                             | 8-11-11                                                                                                                                                                                        | B 6000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | RES     |
|--------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------|
| Query Match 82.2%; Score 529.5; DB 10; Lengt: Best Local Similarity 80.5%; Pred. No. 4.6e-42; Matches 99; Conservative 10; Mismatches 11; Indels | TYPE: PRT ORGANISM: Ar FEATURE: OTHER INFORM OTHER INFORM OTHER INFORM OTHER INFORM                                                                                                            | IS-09-144-896-60 IS-09-144-896-60 Patent No. U820020155114A1 GENERAL INFORMATION: APPLICANT: Marke, James D APPLICANT: Marke, James D APPLICANT: Marke, James D TITLE OF INVENTION: Therapeutto Monoclonal Antibodies That Neutralize TITLE OF INVENTION: Therapeutto Monoclonal Antibodies That Neutralize TITLE OF INVENTION: Modera: U8/09/144,886 CURRENT APILING DATE: 1998-08-31 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMERE SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUBMER SEG ID NGS: 98 SUB | KKCCL I |
| 8 C 34                                                                                                                                           | ER<br>ER<br>44-                                                                                                                                                                                | AL RECAL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | _       |
| al tch                                                                                                                                           | INF                                                                                                                                                                                            | OBSTRATES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |         |
| Sim                                                                                                                                              | TYPB: PRT  NGANISM: Artificial Sequence  REMITHE:  REMITHE:  OTHER INFORMATION: Description of Artifici  OTHER INFORMATION: IAl region VH epitope 2  9-144-886-60                              | Ma:<br>Ma:<br>Ma:<br>Ma:<br>Ma:<br>Ma:<br>Ma:<br>Ma:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |
| Co                                                                                                                                               | ATI C                                                                                                                                                                                          | oplion<br>0020<br>cks<br>erse<br>NTI<br>NTI<br>SAT<br>1D                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |         |
| rity                                                                                                                                             | ON:                                                                                                                                                                                            | In Very No.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |         |
| γ <sub>a</sub>                                                                                                                                   | Des<br>1A1                                                                                                                                                                                     | mes<br>er,<br>The<br>Bott<br>NUM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |         |
| 82<br>1ve                                                                                                                                        | icri<br>re                                                                                                                                                                                     | A1 D Pe rap uliuling                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |
| . 22 N                                                                                                                                           | pt i                                                                                                                                                                                           | /09                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |         |
| 8<br>10;                                                                                                                                         | ng e<br>√.                                                                                                                                                                                     | 1441<br>Nei<br>Nei<br>31                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |         |
| med.                                                                                                                                             | e de la                                                                                                                                                                                        | 9/14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |
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| 82.2%; Score 529.5; DB 10;<br>80.5%; Pred. No. 4.6e-42;<br>bive 10; Mismatches 13;                                                               | Pe                                                                                                                                                                                             | ns nal                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |         |
| 8 6                                                                                                                                              | 2 2                                                                                                                                                                                            | š                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |         |
| -42<br>1                                                                                                                                         | So<br>o                                                                                                                                                                                        | tib.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |
| 10;                                                                                                                                              | gues                                                                                                                                                                                           | odie                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |
| Inc.                                                                                                                                             | Ce                                                                                                                                                                                             | ñ.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |         |
| Length 123;<br>indels 1;                                                                                                                         | <br>6                                                                                                                                                                                          | hat.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         |
| " j                                                                                                                                              | /Trac                                                                                                                                                                                          | N O                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |         |
| 23;                                                                                                                                              | A<br>C                                                                                                                                                                                         | utr                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |         |
| ရှ                                                                                                                                               | YIPE: IPT<br>ORGANISH: Artificial Sequence<br>PRATURE:<br>PRATURE: INPORMATION: Description of Artificial Sequence: BONT/A clone<br>OTHER INPORMATION: 1Al region VR epitope 2<br>9-144-885-60 | a 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |         |
| Gaps                                                                                                                                             | (p                                                                                                                                                                                             | 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |         |
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; ORGANISM: Mus sp
US-10-006-773-4
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 RESULT 2
US-10-006-773-4
 CURRENT AFPLICATION NUMBER: 69/20/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR FAPPLICATION NUMBER: 69/391,478
PRIOR FILING DATE: 2003-66-24
PRIOR PELING DATE: 2003-66-24
PRIOR PELING DATE: 2003-66-24
PRIOR PELING DATE: 2003-11-01
PRIOR REPLICATION NUMBER: 60T/901/14151
PRIOR PELING DATE: 2003-05-02
PRIOR FELING DATE: 2003-05-02
PRIOR FELING DATE: 2003-05-02
 US-10-281-479A-61
 GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
 Sequence 4. Application U8/10066773
Publication No. U82000013293A1
GENERAL INFORMATION: U82000013293A1
APPLICANT: JUNGAMAT, Richard P.
TITIE OF INVENTION: Artibodies as Chimeric Effector Cell Receptors Against Tumor Ant
 Sequence 61, Application US/10281479A Publication No. US20030133932A1
 Query Match
Best Local Similarity
 SEQ ID NO 4
LENGTH: 140
 NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
 Matches 103; Conservative
 FILE REFERENCE: 003
CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT PILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
PRIOR APPLICATION NUMBER: 600/250,089
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 19
 APPLICANT: LOBUGISO, Albert S.
APPLICANT: BUGBBAUM, DORALI J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUNOR NECROSIS
TITLE OF INVENTION: CACCOLOR-SELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THEI
TITLE OF INVENTION: AGENTS
TILE REFERENCE: 2:1055.00356
 SOFTWARE: PatentIn version 3.1
 APPLICANT:
 TYPE: PRT
ORGANISM: artificial sequence
 TYPE: PRT
 LENGTH: 119
 118 VTVSA 122
 136 VTVSS 140
 80
 61 PDSVKGRETISRDNAKNTLYLQMSSLRSEDTAMYYCTREG---GGETVNWYEDVWGAGTL 117
 20 EVVVVESGGFVKPGGSLKLSCAAAGFTPSRYAMSWVRQTPEKRLEWVATISSGGSHTYY
 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 Ichikawa, Kimihisa
Kimberly, Robert P.
Koopman, William J.
Oshumi, Jun
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAIYYCARPGYDRGA----WFFDVWGAGTT
 81.9%;
 Score 527.5; DB 1
Pred. No. 8 le-42;
 Mismatches
 DB 14;
 10;
 Indels
 Length
 140;
 7;
 79
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Sequence 61, Application US/10286132A
Publication No. US200198637A1
GENERAL INFORMATION
APPLICANT: Edour Tony
APPLICANT: Kamberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Loshuglio, Albert S.
APPLICANT: buchsbaum, Donald J.
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 ; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932Ale = US-10-281-479A-61
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 OTHER IMPORMATION: Description of Artificial Sequence:/No. US20030190687Ale = 'OTHER IMPORMATION: Synthetic Construct US-10-275-180A-61
 US-10-275-180A-63
 US-10-286-132A-61
 RESULT 5
 Ś
 REPLICANT: ICDÁRANA (KIMÍMEA)
APPLICANT: KOMBATÍ, NODEST P.
APPLICANT: KOOMBAN, WILLIAM PROCETTY POR A TUMOR NECEDOSIS FACTOR-RELATED APOPT
TITLE OF INVENTION: A NATIGODY SELECTIVE FOR A TUMOR NECEDOSIS FACTOR-RELATED APOPT
TITLE OF INVENTION: A NATIGODY SELECTIVE FOR AND USES THEREOF
FILE REFERENCE: 1.0085.002.005
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT PILINE DATE: 2002-10-31
UNMERIO OF SEQ LID NOS: 102
SOPTMARE: PERTANE.
SEC LID NO 6:
LID NO 6:
LID NO 6:
LID NO 6:
ATTIFICATION OF SEQ LID NOS: 102
ORGANISMIT
ORGANISMIT
ORGANISMIT
APPLICATION ATTIFICIAL SEQUENCE
 GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
 Sequence 61, Application US/10275180A Publication No. US20030190687A1
 Query Match
 Query Match
Best Local &
 Matches 102; Conservative
 FEATURE:
 Local Similarity
 Match 80.7%;
Local Similarity 83.6%;
 118 $$ 119
 118 SS 119
 121 SA 122
 121 SA 122
 61
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITT----DYWGQGTTLTV 117
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITT---DYWGQGTTLTV 117
 61 PDSVKGRFTISRDNAKVILYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVÄTISSGGSSTYY
 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY 60
 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPBKRLBWVATISSGGSYTYY 60
 Conservative
 83.6%;
 Score 519.5; DB 12; Length Pred. No. 3.8e-41; 2; Mismatches 15; Indels
 Score 519.5; DB 1
Pred. No. 3.8e-41;
2; Mismatches 19
 DB 12; Length 119;
 Indels
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US-10-281-479A-23

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 CUREERMY APPLICANTION NUMBER: US/10/281,479A
CUREERMY FILING BATE: 2003:01-28
RECOR FILING BATE: 2003:01-28
RECOR FILING BATE: 2003-65-24
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RECOR FILING BATE: 2003-65-24
RECOR FILING BATE: 2003-65-22
RECOR FILING BATE: 2003-65-22
RECOR FILING BATE: 2003-65-22
RECOR FILING BATE: 2003-65-22
RECORES: 05-20 ID-MSS: 1923-65-22
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 PILE REPERSICS: 2.1065.00.29U7

CURRENT PELLONG DATE: 2003-01-22

CURRENT PILLING DATE: 2003-01-22

PRIOR REPLICATION WINDER: US 60/346,402

PRIOR PILLING DATE: 2001-11-01

PRIOR REPLICATION WINDER: POT/US01/14151

PRIOR PILLING DATE: 2001-05-02

PRIOR APPLICATION WINDER: US 60/201,344

PRIOR PILLING DATE: 2000-05-02

PRIOR PILLING DATE: 2000-05-02

MUMBER: 09 580 1D NOS: 102 -02

MUMBER: 09 580 1D NOS: 102
 US-10-281-479A-23
 RESULT 6
 US-10-286-132A-61
 SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 462
 Sequence 23, Application US/10281479A Publication No. US20030133932A1 GENERAL INFORMATION:
 Query Match 80.7
Best Local Similarity 83.6
Matches 102; Conservative
 SEQ ID NO 61
 PREJICANT: JOBUSTIO, Albort S.
APPLICANT: BECHEVARIO, PLORED S.
APPLICANT: BECHEVARIO, PROPRIATIONS OF ANTIBODIES SELECTIVE FOR A TIMOR NECROSIS
TILLE OF INVENTION: CASCING-SELATED APOPTOSIS-INDUCING LICAND RECEPTOR AND OTHER THEN
TILLE OF INVENTION: ASSISTANCE APOPTOSIS-INDUCING LICAND RECEPTOR AND OTHER THEN
TILLE OF INVENTION: ASSISTANCE APOPTOSIS-INDUCING LICAND RECEPTOR AND OTHER THEN
TILLE OF INVENTION: ASSISTANCE APOPTOSIS-INDUCING LICAND RECEPTOR AND OTHER THEN
TILLE OF INVENTION: ASSISTANCE APOPTOSIS APPROPRIEST APPROPR
 APPLICANT:
 APPLICANT:
 APPLICANT: The UAB Research Foundation
 SOFTWARE: PatentIn version 3.0
 TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
 FILE REFERENCE: 21085.0029U6
 PEATURE: OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637Ale = Synthe
 LENGTH: 119
TYPE: PRT
ORGANISM: artificial sequence
 ORGANISM: artificial sequence
 TYPE: PRT
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
 118
 121
 61
 61 PDSVKGRETISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 SS 119
 SA 122
 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATTSSGGSSTYY 60
 Koopman,
Oshumi,
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCARRGDSMITT---DYWGQGTTLTV
 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY
 Ichikawa, Kimihisa
Kimberly, Robert P.
Koopman, William J.
 Zhou, Tong
 Jun
 80.7%;
 Score 519.5; DB 1
Pred. No. 3.8e-41;
 Mismatches
 DB 12;
 Length 119;
 3
 117
 60
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 US-10-286-132A-23
 RESULT 8
 US-10-286-132A-23
Sequence 23, Application US/10275180A
Publication No. US20030190687A1
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
 Matches
 PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
 APPLICANT: Zhou, 1
APPLICANT: Kimber
APPLICANT: Koopma
APPLICANT: LoBugl
 GENERAL INFORMATION:
 Sequence 23, Application US/10286132A Publication No. US20030198637A1
 Matches 102;
 Query Match
Best Local Similarity
 Query Match
 APPLICANT: BUCHSEAND, DOALD J.

TITLE DE INVENTION: AM ANTIDON' SELECTIVE FOR A TUNOR RECROSIS FACTOR-RELATED
TITLE DE INVENTION: APOPROSIS-INDUCING LICAND RECEPTOR AND USES THEREOF
FILE REFERENCE; 2.1085, 01291.
CHERENT PELLOATION NUMBER: US 1/20/266,132A
CHERENT FILHE DATE: 2.001-0.1-22
FRICOR PELLOATION NUMBER: US 6/346,402
FRICOR APPLICATION NUMBER: US 6/346,402
FRICOR APPLICATION NUMBER: PCT 1/20/2414151
FRICOR APPLICATION NUMBER: PCT 1/20/2414151
FRICOR APPLICATION NUMBER: PCT 1/20/2414151
FRICOR APPLICATION NUMBER: PCT 1/20/2414151
FRICOR APPLICATION NUMBER: US 6/701,344
 TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637Ale =
 ENGTH: 462
 Local Similarity
les 102; Conserv
 137 SS 138
 121 SA 122
 137 88 138
 121 SA 122
 80 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITT---DYWGQGTTLTV 136
 61 PDSVKGRFTISRDNAKWTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 20 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY
 80
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSBDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 20 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY
 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 1 EVOLOESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITT----DYWGQGTTLTV 136
 Kimberly, Robert P.
Koopman, William J.
LoBuglio, Albert S.
 Conservative
 Conservative
 Research Foundation
 80.7%;
 80.7%;
 2; Mismatches
 Score 519.5; DB 1
Pred. No. 1.6e-40;
 Score 519.5; DB 1
Pred. No. 1.6e-40;
2; Mismatches 19
 DB 12;
 DB 12;
 15;
 Indels
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 Length 462;
 Length 462;
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 OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
; OTHER INFORMATION: Synthetic Construct
US-10-275-180A-23
 US-09-423-800-46
 US-09-423-800-46
 APPLICAMY: Kimberly, Robert P.
APPLICAMY: Kimberly, Robert P.
APPLICAMY: Koppman, William J.
TITLE OF INVANTION: NO MODITAL SELECTIVE FOR A TUMOR NECESCOSIS FACTOR-RELATED APOPTOS
TITLE REPERBUCE: 21.085.00.2195
CIRERET APPLICATION NOMERS: US/10/275,180A
CURRENT PILLIO DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 120.105.03.0
SEQ ID NOS: 2007-10-31
LEMETH: 664
LEMETH: 664
 Query Match
Best Local Similarity
 Best Local Similarity
Matches 102; Conserv
 SOFTWARE: 1
SEQ ID NO 46
 GENERAL INFORMATION
 Sequence 46,
 Matches 102;
 Patent No. US20020165363A1
 APPLICANT:
 PRIOR APPLICATION NUMBER: JP
PRIOR FILING DATE: 1997-07-18
 FILE REPRENCE: 0483-0036
CURRENT APPLICATION NUMBER: US/09/423,800
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: DCT/JP98/02116
PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1997-05-15
 APPLICANT: TSUNENARI, T
APPLICANT: ISHII, KIMIE
TITLE OF INVENTION: CAC
 APPLICANT: SATO, KOH
APPLICANT: TSUNENARI,
 NUMBER OF SEQ ID NOS:
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Artificial Sequence
 TYPE: PRT
 LENGTH: 118
 FEATURE:
 137
 121
 20
61 PDSVKGRETISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 80
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 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
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 PatentIn Ver. 2.1
 SS 138
 SA 122
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 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSMVRQTPEKRLEMVATISSGGSYTYY
 EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWIRQTPDKRLEWVATISSGGSYTYY
 Application US/09423800
 Conservative
 Conservative
 Tong
 CACHEXIA REMEDY
 80.6%;
 80.7%;
83.6%;
 Kimihisa
 87
 TOSHIAKI
 JP 194445/1997
 Score 519; DB 10;
Pred. No. 4.1e-41;
5; Mismatches 11;
 2
 Score $19.5; DB 1
Pred. No. 1.6e-40;
 Mismatches
 DB 12;
 Length 118;
 Indels
 Indels
 Length 464;
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 79
 60
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 RESULT 10
US-10-337-981-46
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 US-10-182-018-46
 US-10-182-018-46
 US-10-337-981-46
Query Match 80.6%;
Best Local Similarity 83.6%;
Matches 102; Conservative
 Sequence 46, Application US/10182018
Publication No. US20030049211A1
GENERAL INFORMATION:
 Matches
 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
 Sequence 46, Application US/10337981
Publication No. US20030138424A1
 SEQ ID NO 46
 Query Match
Best Local Similarity
 GENERAL INFORMATION
 CURRENT APPLICATION NUMBER: US/10/182,018
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: US 2000-83034
PRIOR FILING DATE: 2000-01-25
 PERIOR REPLICATION NUMBER: PCT/JF98/02116
PRIOR PRILING DERE: 1996-05-1
PRIOR PRILING DATE: 1997-05-1
PRIOR PRILING DATE: 1997-05-1
PRIOR PRILING DATE: 1997-07-18
PRIOR PRILING DATE: 1997-07-18
NUMBER: OF SRI IN NOS: 87
NUMBER: OF SRI IN NOS: 87
 SOFTWARE: PatentIn Ver. 2.0
 APPLICANT: CHUGAI SETYAKU KABUSHIKI KAISHA
TITLE OF INVENTION: THERAPEUTIC AND FREVENTIVE AGENTS FOR DENTAL DISEASES
FILE REFERENCE: PH-1052-PCT
 FILE REFERENCE: 04853-0036
CURRENT APPLICATION NUMBER: US/10/337,981
CURRENT FILING DATE: 2003-01-08
 APPLICANT: TSUNENARI, TOSHIAKI
APPLICANT: ISHII, KIMIE
TITLE OF INVENTION: CACHEXIA REMEDY
 APPLICANT: SATO,
APPLICANT: TSUN
 NUMBER OF SEQ ID NOS: 75
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Mus musculus
 TYPE: PRT
 LENGTH: 118
 ENGTH: 118
 117 SA 118
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 121 SA 122
 121 SA 122
 102;
 61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMFYCARQ----TTMTYFAYWGQGTLVTV 116
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 61 PDSVKGRPTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
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Score 519; DB 15;
Pred. No. 4.1e-41;
5; Mismatches 11;
 Score 519; DB 12;
Pred. No. 4.1e-41;
 Mismatches
 Length 118;
 Length 118;
 Indels
 4
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Indels

4 Gaps 1,

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 US-09-423-800-76
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 RESULT 12
US-10-169-003-46
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 FILE REPERSICE: 04853-0036
CURERNY APPLICATION NUMBER: US/09/423,800
CURERNY FILING DATE: 1999-11-12
PRICE APPLICATION NUMBER: CC/12986/02116
PRICE RILLING DATE: 1999-05-13-25505/1997
PRICE RILLING DATE: 1999-05-15
PRICE FILING DATE: 1999-05-15
PRICE FILING DATE: 1979-07-18
PRICE FILING DATE: 1979-07-18
 US-10-169-003-46
 밁
 Sequence 76, Application US/09423800 Patent No. US20020165363A1 GENERAL INFORMATION:
 NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
 GENERAL IMPORMATION:
APPLICANT: GUIDAL ESTYAKU KASUSHIKI KAISHA
TITLE OF INVENTION: Stabilized Antibody Composition and Pharmaceutical Preparation for INVENTION: Injection
FILE REPERANCE: PH-1033-PCT
 Matches 102;
 Best Local Similarity
 Query Match
 Sequence 46, Application US/10169003
Publication No. US20030124119A1
NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
SEQ ID NO 76
 APPLICANT: TSUNENARI, TOSHIAKI
APPLICANT: ISHII, KIMIE
TITLE OF INVENTION: CACHEXIA REMEDY
 APPLICANT:
 CURRENT APPLICATION NUMBER: US/10/169,003
CURRENT FILING DATE: 2002-06-26
 PRIOR APPLICATION NUMBER: JP 11-375203
PRIOR FILING DATE: 1999-12-28
 LENGTH: 118
TYPE: PRT
ORGANISM: Mus musculus
 117 SA 118
 121
 117 SA 118
 121 SA 122
 61
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 PatentIn Ver. 2.1
 SA 122
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 SATO, KOH
 Conservative
 . 1997-07-18
ROS: 87
 83.6%;
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Pred. No. 4.1e-41;
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 Indels
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RESULT 15 US-09-881-823-12

Sequence 12, Application US/09881823 Patent No. US20020068066A1 GREERAL IMPORMATION:

APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE

MAXWELI

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 ; ORGANISM: Homo sapiens
US-10-337-981-76
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 ; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-76
 APPLICANT: SATO, KOH
APPLICANT: TSUNENALI, TOSHIAKI
APPLICANT: ISHII, KHMIB
TITLE OF INVENTION: CALEXIA REMEDY
FILE REFERENCE: 04853-0036
CURRENT APPLICATION UNDER: US/10/337,981
CURRENT APPLICATION WHORES: UC/1090/02116
PRIOR APPLICATION WHORES: UC/1090/02116
PRIOR ETLING DATE: 1998-05-13
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 GENERAL INFORMATION
 Sequence 76, Application US/10337981
Publication No. US20030138424A1
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 NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.1
 PRIOR APPLICATION NUMBER: JP 125505/1997
PRIOR TILING DATE: 1997-05-15
PRIOR APPLICATION NUMBER: JP 194445/1997
PRIOR FILING DATE: 1997-07-18
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nes 102; Conservanting
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136 SA 137
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 Score 519; DB 12;
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5; Mismatches 11;
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 Score 519; DB 10;
Pred. No. 4.9e-41;
 Length 137;
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 Gaps
 Gaps
 135
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APPLICANT: MINS. LATTIAN
APPLICANT: MINS. LATTIAN
APPLICANT: CHEM, LI
TITLE OF INVENTION Method for the Treatment and Prevention of Dental Caries
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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 Total number of hits satisfying chosen parameters:
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 Perfect score:
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 Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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505.5
502
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Gapop 10.0 , Gapext 0.5
 Match
 Issued Parents An:

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3. /cgn2 6/pcodara/1/iaa/6B_COMB.pep:*

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5. /cgn2 6/pcodara/1/iaa/6B_COMB.pep:*

6. /cgn2 6/pcodara/1/iaa/backflas1.pep:*
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 November 7, 2003, 07:21:18; Search time 17,9172 Seconds
(without alignments)
288.098 Million cell updates/sec
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 2 Sequence 3 Sequence 3 Sequence 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 10, Appl<br>21, Appl<br>22, Appl<br>23, Appl<br>24, Appl<br>25, Appl<br>26, Appl<br>27, Appl<br>28, Appl<br>29, Appl<br>21, Appl<br>21, Appl<br>21, Appl<br>22, Appl<br>23, Appl<br>24, Appl<br>25, Appl<br>26, Appl<br>26, Appl<br>27, Appl<br>28, |

Query Match

79.4%; Score 511.5;

DB 5;

Length 247;

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밁
 RESULT 2
US-08-875-674A-1
 밁
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 Patent No.
GENERAL I
 Best Local Similarity 82.0%; Pred. No. 8e-47; Matches 100; Conservative 5; Mismatches 14;
 Sequence
 TELEPAX: (914)-723-430
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 Amino acid
 MOLECULE NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
ANTI-SENSE: NO
TYPE: -N Terminal fragment.
 COMPUTER READABLE PORM:
MEDIUM TYPE: Eloppy disk 3.5' (1.4 MB).
COMPUTER: Compatible PC 1BM (80486, 8 M Ram).
OPERATING SYSTEM: Mindows 55.
OPERATING SYSTEM: Windows 55.
CURBERT APPLICATION DATA:
CURBERT APPLICATION DATA:
 TOPOLOGY: Un
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CU96/00004
FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
 TELECOMMUNICATION INFORMATION:
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 APPLICANT:
 IMMEDIATE SOURCE:
 APPLICANT: TORMO BRAVO,
 APPLICANT:
 APPLICANT: MONTERO CASIMIRO, J.
 APPLICATION NUMBER: US/08/875,674A
FILING DATE: 17-July-1997
CLASSIFICATION: 530
IDENTIFICATION METHOD: Experimental, OTHER INFORMATION: Sequence corresponding to the variable region
 ORGANISM: Mice Balb/C
INDIVIDUAL ISOLATE: ic
 NAME: HENRY A. MARZULLO, JR.
REGISTRATION NUMBER: 20,910
REFERENCE/DOCKET NUMBER: P-12
 STATE: New York
COUNTRY: U.S.A.
 TISSUE TYPE: Murine hibridoma
 STRANDEDNESS:
 TELEPHONE:
 CITY: Scarsdale
 ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C. STREET: One Chase Road
 137 88 138
 121 SA 122
 61
 INFORMATION:
 80 PDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYHCARGG---VRRGYFDVWGAGTTVTV 136
 20 EVHLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSMVRQTPEKRLDMVAYISSGGGTYY 79
 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 10583
 Amino acid.
 Application US/08875674A
 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 Sub-clone ior tlA
 P REZ RODR GUEZ, R. SIERRA BL ZOILE?
 119 Amino acid residues.
 (914) -723-4301
 Unknown.
 (914) 723-4300
 Unknown.
 Anti-CD6 monoclonal antibodies and their uses
 Indels
 3
 Gaps
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 8
 밁
 ; Patent No. 6572857
; OTHER INFORMATION:
; OTHER INFORMATION:
 US-08-579-378A-16
 US-08-875-674A-1
 Sequence 16, Application US/08579378A
Patent No. 6210671
 Matches 100; Conservative
 Query Match
 PRIOR MEPLICATION NOTES: 1.255.8

APPLICATION NUMBERS: BE 95112895.8

PRIOR APPLICATION NUMBERS: BE 95114696.8

PRIOR APPLICATION NUMBERS: BE 95114696.8

PRIOR APPLICATION NUMBERS: DE 95114696.8

APPLICATION NUMBERS: 10-50.9

REGISTRATION NUMBERS: 37.505.

REGISTRATION NUMBERS: 11623-0022
 CLASSIFICATION: 424
BRIDE APPLICATION NUMBER: US 08/160,074
FILING DATE: 00-1007-1993
PRIOR APPLICATION BATH: 00-07/983,946
FILING DATE: 01-08C-1992
FILING DATE: 01-08C-1992
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO
 ZIP: 94105
COMPUTER EXAMBLE FORM:
MEDIUM TYBE: Flopy disk
COMPUTER: ELOPY disk
COMPUTER: ELOPY CODENTING
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTMARE: PC-DOS/NS-DOS
SOFTMARE: PC-DOS/NS-DOS
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 27-DEC-19
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One MarketPlaza, Stevart Tower, Suite 2000
 APPLICANT: Co, Man Sung
TITLE OF INVENTION: Hum
TITLE OF INVENTION: L-S.
MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
 NUMBER OF SEQUENCES:
 TOPOLOGY:
 TELEPHONE:
 COUNTRY:
 CITY: San Francisco
STATE: California
 Match 78.5%;
Local Similarity 82.0%;
 118 SS 119
 121 SA 122
 61
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 1 EVOLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 : 135 amino acids
amino acid
 PDSVKGRFTISRDNVKNTLYLOMSSLRSEDTAMYYCARRDYDLD---YFDSWGQGTTLTV 117
 EVQLVESGGGLVKPGGSLKLSCAASGFKFSRYAMSWVRQTPEKRLEWVATISSGGSYIYY
 415-326-2422
 USA
 linear
 27-DEC-1995
 L-Selectin
 Humanized Antibodies Reactive with
 of the heavy chain of the monoclonal antibody recognizing h designated as sub-clone for tlA.
 US/08/579,378A
 16:
 11823-002220
 Score 505.5; DB 4;
Pred. No. 1.4e-46;
2; Mismatches 17;
 17, Indels
 Length 119;
 3
 60
```

Query Match Best Local 9 Matches 98

h 78.0%; Score 502; DB 3; Length 135; Similarity 80.3%; Pred. No. 3.8e-46;

Mismatches

9; Indels

6;

N

Conservative

1 EVOLOESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60

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 US-08-875-674A-3
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 밁
 Sequence 3, Application US/08875674A Patent No. 6572857
 PRIOR APPLICATION DATA.

APPLICATION UNDERS. PCT/CU96/00
PILING DATS: 10 -NOV-1996
APTORNEY/AGREY INFORMATION:
NAME: HINEY A. MAZGULLO, JR.
REGISTRATION MUMBER: 2-0,910
REGISTRATION GOCKET MUMBER: 9-10
 GENERAL INFORMATION:
 TELEPHONE: (914) 723-4300
TELEPAX: (914)-723-4301
INFORMATION FOR SEQ ID NO: 3:
 ANTI-SENSE, NO
FRAGMENT TYPES, -N Terminal fragment.
ORIGINAL SOURCE:
TISSUE TYPES. Animal cells.
CELL LINE: NSO " SP 2/0 " CHO
 ZIP: 10583
COMPUTER READABLE FORM:
MEDIUM TYPE: FlopyH.
COMPUTER: Compartible PC IBM (80486, 8 M Ram).
OMPUTER: Compartible PC IBM (80486, 8 M Ram).
OPERATING SYSTEM: Windows 95.
CURBENT APELLOXICIO DATA:
CURBENT APELLOXICIO DATA:
FEATURE: IDENTIFICATION METHOD: By similarity with known sequence.
 IMMEDIATE SOURCE:
 HYPOTHETICAL:
 MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION:
 CORRESPONDENCE ADDRESS:
 RPIICANT: LOWBARDESO VALLADARES, J.
APPLICANT: PERZ RORS GHEZ, R.
APPLICANT: SIERAN BL ZOUES, P.
APPLICANT: TITLE OF INVENTION: Anti-CD5 monoclonal antibodies and their uses
 NUMBER OF SEQUENCES:
 APPLICANT:
 STREET:
CITY: S
 STATE: 1
 APPLICATION NUMBER:
FILING DATE: 17-Jul
CLASSIFICATION: 53
 CLONE: Sub-clone ior tlA
 LENGTH: 119 Amino acid residues.
TYPE: Amino acid.
 TOPOLOGY:
 STRANDEDNESS:
 ADDRESSEE:
 134 SS 135
 121 SA 122
 61 PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 20 EVKLVESGGGLVKPGGSLKLACAASGFTFSTYAMSWVRQTPEXRLEWVASISTGG-STYY 78
 Scarsdale
 New York
 PDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCARDYDG----YPDYWGQGTTLTV 133
 One Chase Road
 Unknown.
 MONTERO CASIMIRO, J.
 Lackenbach Siegel Marzullo Aronson & Greenspan, P.C
 No
 17-July-1997
 Protein
 Unknown.
 PCT/CU96/00004
 US/08/875,674A
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 ; MOLECULE TYPE: protein US-08-475-000-16
 RESULT 5
US-08-475-000-16
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 Patent No. 6572857
OTHER INFORMATION:
OTHER INFORMATION:
 US-08-875-674A-3
 Query Match 77.7%, Score 500.5; DB 2
Best Local Similarity 79.5%, Pred. No. 4.7e-46;
Matches 97; Conservative 10; Mismatches 12;
 COUNTRY: USA
ZIP: 94652-8097
ZIP: 94652-8097
ZIP: 94652-8097
ZOMETUTER READARLE FORM:
MEDIUM TIPE: Floppy disk
COMMUTER: IIAM PC compatible
COMMUTER: IIAM PC compatible
COMMUTER: IIAM PC compatible
COMMUTER: IIAM PC compatible
COMMUTER: STERNE PC FORMATION
FOR FORMATION: 428
APPLICATION: 428
AP
 Sequence 16, Application US/08475000
Patent No. 5811267
BRIGHT NO. 5811267
BRIGHAL IMPORMATION: AMPLICAN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: AMPLICAN-BINDING SITES OF AMPLICAN-BIN
 Matches 100; Conservative
 Query Match
Best Local Similarity
 TELEPHONE: (510) 601-2585
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIMOL CORPORATION
STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
 TELEPHONE: (510) 601-2585
 NUMBER OF SEQUENCES:
 LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
 CITY: Emeryville
 118 SS 119
 121 SA 122
61 PDSVKGRETISRDNAKNTLYLØMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 61 PDSVKGRFTISRDNVKNTLYLQMSSLRSEDTAMYYCARRDYDLD---YFDSWGQGTLVTV 117
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 1 EVQLQESGCGLVKPCGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 1 EVOLVESGGGLVKPGGSLKLSCAASGEKFSRYAMSWVRQAPGKRLEWVATISSGGSYIYY 60
 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 EVKVVESGGVLVRPGGSLKLSCAASGFTFSRYTMSWVRQTPEKKLEWVATISSGGGNTYY 60
 ç
 Application US/08475000
 77.9%;
 18
 Sequence corresponding to the humanized
 variant of sub-clone ior tlA recognizing human CD6, particuto the variable region of its heavy chain.
 1; Mismatches
 Score 501.5; DB 4;
Pred. No. 3.7e-46;
 18;
 Length 119;
 Indels
 Length 119;
 3
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 Gaps
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 Query Match
Best Local Similarity
Watches 97; Conserve
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 US-08-484-508-16
 RESULT 7
 US-08-483-199-16
 RESULT 6
US-08-483-199-16
 S
 Sequence 16, Application US/08484508 Patent No. 5948647
 NAME: SAVEREIDE, PAUL
REGISTRATION WIMBER: 36,914
REFERENÇE/COCKET NUMBER: 0850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 655-3542
INFORMATION FOR SEQ ID NO: 156
 GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: MOLECT
TITLE OF INVENTION: MOLECT
 Patent No.
 GENERAL INFORMATION:
 ZIP: 94662-8097
COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,199
 NUMBER OF SEQUENCES:
 MOLECULE TYPE: protein
 SEQUENCE CHARACTERISTICS:
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
 APPLICANT: RING, DAVID B.
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
 ADDRESSEE: CHIRON CORPORATION
 NUMBER OF SEQUENCES:
 LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
 FILING DATE: 07-JUN-1995
 COUNTRY:
 STREET:
 118 SA 119
 121 SA 122
 121
 61
 118 SA 119
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 Н
 1 EVQLQESGGGLVKPGGSLKLSCAASGETFSSYTMSHVRQTPEKRLEHVATISSGGSSTYY
 I: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
Emeryville
 584987
 PDSVKGRFTVSRDNAMSSLYLQMSSLRSEDTALYYCARYGAG---DAWFAYWGQGTLVTV
 .
SA
 ç
 PDSVKGRFTVSRDNAMSSLYLQMSSLRSEDTALYYCARYGAG---DAWFAYWGQGTLVTV 117
 Application US/08483199
 USA
 Conservative
ANTIGEN-BINDING SITES OF ANTIGODY MOLECULES SPECIFIC FOR CANCER ANTIGENS: 18
 77.7%; Score 500.5; DB 2
79.5%; Pred. No. 4.7e-46;
ative 10; Mismatches 12
 0850.009
 DB 2;
 12;
 Indels
 Length 119;
 3 J
 Gaps
 60
 6
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US-08-326-362-2
 RESULT 8
 밁
 S
 밁
 US-08-484-508-16
 ATTONNEY/AGENT INFORMATION:
NAME: SAFTEREIDS, PAUL
REGISTRATION INVESES: 9.944
REFERENCY, DOCKET NUMBER: 0.950
TELEPOMENICATION INFORMATION:
TELEPOME: ($10) 655-25-25
TELEPOMETICAN CORRESSO IN NO: 14:
SPOURNCE CHARACTERISIES:
 Patent No. 5730981
 Sequence
 Query Match
 Matches
 GENERAL INFORMATION:
 ZIP: 20005-3115
COMPUTER READABLE FORM:
MEDIUM TYPE: $10ppy disk
COMPUTER: EM PC compatible
OMPUTER: FLOREY PC-2005/NS-DOS
DEEMATING SYSTEM: PC-2005/NS-DOS
DEEMATING SYSTEM: PC-2005/NS-DOS
 APPLICANT: Bossièt, Klaus
APPLICANT: Besand, Gerhard
APPLICANT: Bippold, Molfgang
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
PITLE OF INVENTION: Its Preparation and Use as a Tumorthexapeutic Agent
INVESE OF SUPERIOCES: 4
CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 MOLECULE TYPE: protein
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 ADDRESSEE: CHIRON CORPORATION
 TYPE: amino acids
TYPE: amino acid
TOPOLOGY: line...
LECTR
 STREET: 1300 I St
CITY: Washington
STATE: D.C.
 Local Similarity 79.5%;
nes 97; Conservation
 COUNTRY:
 ADDRESSEE: Finnega
ADDRESSEE: Dunner
 APPLICATION NUMBER: US/08/484,508
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
 STREET: INITIAL COUNTY: Emeryville
 118 SA 119
 121 SA 122
 6,
 61 PDSVKGRETISRDNAKUTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 1 EVQLQESGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 94662-8097
 Application US/08326362
 PDSVKGRFTVSRDNAMSSLYLQMSSLRSEDTALYYCARYGAG---DAWFAYWGQGTLVTV 117
 EVKVVESGGVLVRPGGSLKLSCAASGFTFSRYIMSWVRQTPEKRLEWVATISSGGGNTYY 60
 1300 I Street, N.W., Suite 700
 INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
 USA
 Finnegan, Henderson, Farabow, Garrett &
 10;
 Score 500.5; DB:
 0850.008
 Mismatches
 DB: 2;
 12;
 Indels
 Length 119;
 ω,
 Gaps
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 US-08-579-378A-20
 , MOLECULE TYPE: peptide
US-08-326-362-2
 Sequence 20, Application US/08579378A Patent No. 6210671
 Matches
 Query Match
Best Local
APPLICATION NUMBER: US/08/579,378A
FILTMS DATE: 37-D8C-1955
CLASSIFICATION APPLA
FILTON DATE: 08/160,074
FILTMS DATE: 30-M071-193
APPLICATION NUMBER: US 09/983,946
FILTMS DATE: 30-M071-193
APPLICATION DATE: 192
FILOW APPLICATION DATE: 192
FILOW APPLICATION DATE: 39-9112895.8
 GENERAL INFORMATION:
APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Rev
TITLE OF INVENTION: Selectin
UMBER OF SEQUENCES: 20
CORRESONNENCE ADDRESS: do Townsend and Crew
ADDRESSEE: Townsend and Townsend and Crew
 TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
 ZTP: 94105

COMPUTER REALDALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PASCELLE RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
 SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
TOPOLOGY: linear
 FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Elimandi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE DOCKET NUMBER: 02.
TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/032,863
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: DE P 42 08 795.3
 STREET: One MarketP)
 Local Similarity
 COUNTRY:
 TELEPHONE:
 CLASSIFICATION:
 APPLICATION NUMBER: US/08/326,362
 117 SS 118
 121 SA 122
 61 RDSVKGRFTISRDNAKNTLYLOMSSLRSEDTANYYCARGGSRYAM-----DYWGQGTTVTV 116
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVXMYFDVMGAGTLYTV 120
 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVXQTPEKKLEWVATISSGGSSTYY 60
 97;
 1 QVQLQQSGGGLVKPGGSLTLSCAASRFTPSTYAMSWVRQTPAKRLEWVAYISSGGASTYY 60
 California
 One MarketPlaza, Steuart Tower, Suite 2000
 USA
 Conservative
 202-408-4000
 76.7%;
79.5%;
 Humanized Antibodies Reactive with
 US/08/579,378A
 7; Mismatches
 02481-1276-00000
 Score 494; DB 1; Length 118;
Pred. No. 2.3e-45;
 14; Indels
 Gaps
 1;
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 S
 В
 US-08-579-378A-20
 PCT-US96-13152-4
 Sequence 4, Application PC/TUS9613152
GENERAL INFORMATION:
 Matches
 Query Match
 TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
KEGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: EP 95 112 895.8

FILING DATE: 17-AUG-95

APPLICATION NUMBER: EP 95 114 969.9

FILING DATE: 119-08p-95

APPORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 30,946
 COMPUTER FEADABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC-ompatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: NSCII
CURRENT APPLICATION DATA:
 APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fa
 TOPOLOGY: linear MOLECULE TYPE: protein
 TELEPHONE: 415-326-2400
 APPLICATION NUMBER: EP 95114696.8 FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: 27-Dec-95
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 TYPE: amino acid
 APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
 STREET: 805 Third Avenue
CITY: New York
STATE: New York
 Local Similarity
 NAME: Liebescheutz, Joe O. REGISTRATION NUMBER: 37,50
 COUNTRY:
 ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson
 LENGTH:
 REFERENCE/DOCKET NUMBER:
 134 SS 135
 121 SA 122
 79 PDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCARDYDG----YFDYWGQGTLVTV 133
 61 PDSVKGRFTISBDNAKNTLYLOMSSLRSEDTAMYYCTREGGGPTVNWYFDVWGAGTLVTV 120
 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVASISTGG-STYY 78
 10022
 1 EVOLOESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 96; Conservative
 135 amino acids
 U.S.A.
 76.1%; Score 490; DB 3; Length 135; 78.7%; Pred. No. 7.2e-45;
 08/578,953
 PCT/US96/13152
 37,505
 10; Mismatches
 11823-002220
 10;
 indels
 Gaps
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(212) 688-9200

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8
 S
 B
 US-08-553-497A-18
 PCT-US96-13152-4
 Seguence 18,
 Matches
 Query Match
Best Local !
 GENERAL INFORMATION:
 TELEFAX: (212) 836-3684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 tent No.
APELICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIAMA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
 MEDIUM YVDE: Ploppy disk
COMPUTER: IR NP C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PS-EAST HE MEDIAGE HIO, VETSION #1.30
LOBELT-TOTTON MANAGED. HIO. ACCES ACCES
ADDITIONTON
 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
 FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 CORRESPONDENCE ADDRESS
 APPLICANT:
 APPLICANT:
APPLICANT:
 PRIOR APPLICATION DATA:
 APPLICANT:
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 APPLICANT:
 MOLECULE TYPE: protein
 APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
 APPLICATION NUMBER: FILING DATE: 16-MAR
 STREET: 2200 CLA
CITY: ARLINGTON
 COUNTRY:
 ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C
STREET: 2200 CLARENDON BLVD. SUITE 1400
 Local Similarity
 TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
 LENGTH: 443
 115
 121 SA 122
 60
 61
 96;
 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 2220
 SS 116
 PDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCARDYDG----YFDYWGQGTLVTV 114
 PDSVKGRFTISRDNAKWTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVASISTGG-STYY
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 Application US/08553497A
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 PIULATS, JAUME
VENTION: ANTI-EGER SINGLE-CHAIN FVS AND ANTI-EGER
VENTION: ANTIBODIES
 ROSELL, ELISABET
BLASCO, FRANCESC
 MITJANS, FRANSESC
ROSELL, ELISABET
 ADAN
 GUSSOW, DETLEF
 Conservative
 KETTLEBOROUGH, C.
 JAUME
 76.1%; Score 490; DB 5; Length 443; 78.7%; Pred. No. 3.3e-44; rative 10; Mismatches 10; Indels
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 WO PCT/EP95/00978
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 US-08-356-272-3
 US-08-553-497A-18
 Patent No. 576694
 Matches
 Query Match
 Best Local Similarity
 INFORMATION FOR SEQ ID NO: 3:
 GENERAL INFORMATION:
 APPLICATION DATE: 17-TUN-1992

APPLICATION DATE: 10-TUN-1992

APPLICATION BUTNER: No PCT/EP93/01533

FILING DATE: 16-TUN-1993

ATTORNEY/AGENT IMPORMATION:

BANG: Battle Carl
 CLASSIFICATION: C12N5/
CLASSIFICATION: G01N33
CLASSIFICATION: G01N33
CLASSIFICATION: A61K39
PRIOR APPLICATION DATA:
 TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 TELEPHONE: (201) 503-8177
TELEPHONE: (201) 503-8807
TELEFAX: (201) 503-8807
 OMPUTER READMANE FOOM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAPELL/TION BATH:
URERET APPLICATION BATH:
 CORRESPONDENCE ADDRESS:
 APPLICANY: Cianfriglia Dr., maurizio
TITLE OF INVENTION: Monoclonal Antibodies to glycoprotein P
 TOPOLOGY: linear
MOLECULE TYPE: protein
 SEQUENCE CHARACTERISTICS
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
 REFERENCE/DOCKET NUMBER:
 NAME: Battle, Carl W.
REGISTRATION NUMBER: 30,731
 CLASSIFICATION:
 FILING DATE:
 APPLICATION NUMBER: US/08/356,272
 CITY: East Hanover STATE: N. J.
 ZIP: 07936
 COUNTRY:
 STREET: 59 Route 10
 ADDRESSEE: Patent and Trademark Department, Sandoz
 TYPE: amino acid
 LENGTH:
 117 VSS 119
 120 VSA 122
 61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARLETGDYAL----DYWGQGTTVT 116
 61 PDSVKGRPTISRDNAKNTLYLOMSSLRSEDTAMYYCTR-EGGGFTVNWYFDVWGAGTLVT 119
 99;
 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 Application US/08356272
 EVKLQESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLESVATISSGGAYIYY 60
 240867
 239 amino acids
 U. S. A.
 Conservative
 703-243-6333
 15-DEC-1994
 C12N5/20
G01N33/574
G01N33/577
 76.0%;
 461K39/29S
 18:
 118-8040
 7; Mismatches
 Score 489.5; DB 2
Pred. No. 1.7e-44;
 DB 2;
 12;
 Indels
 Length 239;
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 Gaps
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 TOPOLOGY: linear
, MOLECULE TYPE: protein
US-08-356-272-3
 US-07-934-373C-4
 US-07-934-373C-4
 RESULT 13
 Sequence 4, Application US/07934373C
Patent No. 5821337
 Matches
 Query Match
 Matches
 Query Match
 CLASIFICATION: 530
PEIGR APPLICATION DATA,
APPLICATION UNMBER: CCT/US
PILING DATE: 15-UN-1992
PRICE APPLICATION UNMBER: 07/715
FILING DATE: 14-UN-1991
ATTORNEY/AGENT INFORMATION:
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 GENERAL INFORMATION:
 APPLICANT: Paul J. Carter
APPLICANT: Peonard G. Presta
TITIE De INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: A
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
 CURRENT APPLICATION DATA:
 Local Similarity
 NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378
 APPLICATION NUMBER:
FILING DATE: 21-Aug
 COUNTRY:
 STREET:
 TYPE:
 TOPOLOGY:
 LENGTH:
 CITY: South San Francisco
 ADDRESSEE:
 Local Similarity
 LENGTH: 123 amino acids
 118 VTVSS 122
 118 VTVSA 122
 94; Conservative
 61 FPDSVKGRFTISRDNAKNTLYLQVSSLKSEDTAMYYCARPAEFRGYS---WFAYWGQGTT 117
 60 YPDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTR--EGGGFTVNWYFDVWGAGTL 117
 1 QVQLQESGGDLVXDPGGSLXLSCAASGFTFSRYGMSWVRQTPDKRLEWVATISGGGSYTY 60
 1 EVQLQESGGGLVK-PGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTY 59
 99;
1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
 94080
 : 120 amino acids
Amino Acid
 amino acid
 California
 1 DNA Way
 USA
 Conservative
 WinPatin (Genentech)
 Linear
 Genentech, Inc.
 21-Aug-1992
)N: 530
 75.5%;
 75.8%;
79.2%;
 07/715272
 PCT/US92/05126
 US/07/934,373C
 9; Mismatches
 9, Mismatches
 P0709P2
 Score 488; DB 1; Length 123; Pred. No. 1e-44; 9; Mismatches 11; Indels
 Score 486; DB 2; Length 120;
Pred. No. 1.7e-44;
 Indels
 2; Gaps
 6
 Gaps
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61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNMYFDVMGAGTLVTV 120

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 US-08-437-642B-4
 RESULT 14
 US-08-437-642B-4
Matches
 Sequence 4, Application US/08437642B Patent No. 6054297
 Query Match
 GENERAL INFORMATION:
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
 FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
 COMPUTER READABLE RORM:
MEDIUM TYPES 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OREBATING SYSTEM: PC COMS/MS-DOS
SOFTWARE: WinFatin (Genentech)
 APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITUE OF INVENTION: Immunoglobulin Variants
 TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 TYPE: Amino Acid
 APPLICATION NUMBER: 07/715272
 APPLICATION NUMBER: 08/146206
 CLASSIFICATION:
 STREET: 1 DNA Wa
 Local
 TOPOLOGY:
 TELEPHONE:
 REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: PO
 FILING DATE: 15-JUN-1992
 APPLICATION NUMBER:
 FILING DATE:
 APPLICATION NUMBER:
 COUNTRY:
 ADDRESSEE:
 119 SS 120
 121 SA 122
 61 POSVICARETISROMANYTLYLONSSLASEDTAMYYCTREGGGFUVNWYEDVIGAGTUVTV 120

61 ADSVIKARETISRODSKATLYLONSSLASEDTAMYYCTREGGGAVS--YEDVIMOQGTLVTV 118
 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYAMSWVRQAFGKGLEWVAVISENGSDTYY 60
 94; Conservative
 Similarity
 California
 1 DNA Way
 USA
 Linear
 650/225-1994
 Genentech, Inc.
 09-May-1995
 14-JUN-1991
 Francisco
 75.5%;
77.0%;
 PCT/US92/05126
 US/08/437,642B
9; Mismatches 17;
 P0709P2C1
 Score 486; DB 3; Length 120;
Pred. No. 1.7e-44;
 Indels
 2;
 Gaps
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 В
 Š
 US-08-146-206C-4
 PILING DATE: 11-1/UN-1991
ATTORNEY AGENT INFORMATION:
NAME: Lee, Wenty M.
REGISTRATION UNBER: 40,370
REFERENCY DOCKET MANDER: 970
REFERENCY DOCKET MANDER: 970
REFERENCY DOCKET MANDER: 970
REFERENCY DOCKET MANDER: 970
REFERENCY DATE: 970
REFERENCY
 RESULT 15
US-08-146-206C-4
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 Omery March 75.5%, Score 466; DB 4; Length 120; Best Local Similarity 77.0%; Bred No. 1.7e-44; Length 120; Matches 94; Conservative 9; Mismatches 17; Indels 2; Gaps
 Sequence 4, Application US/08146206C Patent No. 6407213
GENERAL INFORMATION:
 ZIP: 94090

ZIP: 94090

COMPUTER RADARLE PORM:

WEDILM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: ISM PC compactible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: HATPACIN (Genantech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/146,206C

PLIANG DATE: 17-Mo. 6407213-1993

CHANG DATE: 07.05272

PRELICATION BATH: 07.15272

PRELICATION BATH: 07.15272
 APPLICANT: Carter, Paul J.
APPLICANT: Frasta Leonard G.
TTTUE OF INVENTION: Method for Making Humanized Antibodies
UNMBER OF SEQUENCES: 26
COREESCONDENCE ADDRESS:
 COUNTRY:
 ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
119 88 120
 121 SA 122
 119 SS 120
 121
 61 ADSVKGRFTISTDDSKNTLYLQVMSLRAEDTAVYYCARDRGGAVS--YEDVWGQGTLVTV 118
 61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
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 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYAMSWVRQAPGKGLEWVAVISENGSDTYY 60
 1 EVOLOESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKELEWVATISSGGSSTYY 60
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 SA 122
 USA
 P0709P1
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Search completed: November Job time: 17.9172 secs

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Post-processing: Minimum Match 0%
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 Title:
Perfect score:
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 Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| 102    | 102    | 110    | 91     | 111    | 108    | 109    | 95     | 111    | 111    | 111    | 111    | 111    | 110    |
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| PH1079 | PH1076 | S24288 | S25462 | S09966 | KVMS54 | PH0093 | S25177 | 809969 | 809963 | PL0081 | KVMS50 | KVMS80 | KVMS10 |
|        |        |        |        |        |        |        |        |        |        |        |        |        |        |
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| light  | light  | kappa  |
| chain  | chain  | chain  | chain  | chain  | chain  | Chain  | chain  | chain  | chain  | chain  | chain  | chain  | chain  |
| ۲.     | < <    | r :    | azď.   | V-7    | < ·    | ۲.     | ۷.     | V-7    | V-1    | ۷,     | 4      | ۷ ۲    | ۷ ۲    |

#### ALIGNMENTS

| RiStation 1 accord, A.J. RiStation 114, Catcon, A.J. J. Edg. Med. 114, 613-624, 1991 A.Title: Antibodies that are specific for a single amino acid interchange in a protein A.Tette: Antibodies that are specific for a single amino acid interchange in a protein A.Reference number: 826309; MOID:91341421; PMID:1908510                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| RESULT 2<br>355434 chain V region - mouse<br>535434 chain V region - mouse mouse)<br>C Short 13-Jun-195541 feedemouse revision 13-Jun-1995 #text_change 20-Jun-2000<br>C Noteseijan 55643 feedemouse_revision 13-Jun-1995 #text_change 20-Jun-2000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| GY 63 PARESGSGSKTDFIL/TIMPYEADDYMYYCQQSMEDPYTFOGGTRLEIK 111 Db 63 PARESGSGSKTDFIL/TIMPYEADDYMYYCQQSMEDPYTFOGGTRLEIK 111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| OY SUCCESSALAVSLOCANTISCESSESUDEXCHIPMENCOLTEOGREGULTERASHILESCI 62 Db SULTOSENSLAVSLOCANTISCESSESUDEXCHIPMENCOLTEOGREGULTERASHILESCI 62 Db SULTOSENSLAVSLOCANTISCESSESUDEXCHIPMENCOLTEOGREGULTERASHILESCI 62                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| Ouery Match 91.1%; Score 532; DB 1; Length 111; Best Local Samilarity 94.5%; Pred No. 1.66-41; Length 111; Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| A.Residues: 1-111 cMCTs. C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k nain dismlide bonds. In some cases, such as LpA and JpM, the subunits associate into C:Superfamily: immunoglobulin v region; immunoglobulin bomology F:16-94/Domain: immunoglobulin bomology <-IMM> F:16-94/Domain: immunoglobulin bomology <-IMM> F:16-94/Domain: immunoglobulin bomology <-IMM>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| RiMcKean, D.J., Ball, M.; Rotter, M. Proc. Matl. Acad. Sci. U.S.A. 5, 3913-3917, 1978 A.Title: Mechanisms of antibody diversity; multiple genes encode structurally related A.Reference number: A93822, MUD:79012520, PMID:99744 A.Contents: Till A.Contents: Till A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, MUD:79012520, PMID:99744 A.Accession: A93822, PMID:99012520, PMID:9901 |
| A/Tille: Rearrangement of genetic information may produce immunoglobulin diversity. A.Reference number: A93004 NUID:79073152, PMID:103003 A.Contents: PC3741 A.Acontents: PC3741 A.PACACESSION: A93204 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSION: PC5741 A.PACACESSI |
| (house mouse)  mence revision 0  material property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the prop |
| RESULT 1<br>KM837<br>Ig kappa chain V regions (PC3741, Tll1) - mouse                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |

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C:Keywords: heterocutramer, and composition for class F;15-93/Domain: immunoglobulin homology <IMM>
 C;Accession: S26344
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
 olverdaguer, N.; Mateu, M.G.; Bravo, J.; Domingo, B.; Fita, I.
1. Mol. Biolog booket to accommodate the cell attachment Arg-cly-Asp motif in a neutral placetience number: 863596; MUID:96174482; PMID:9594203
A; Accession: 863596
A; Scause: preliminary; not compared with conceptual translation
A; Scause: preliminary; not compared with conceptual translation
A; Scause: preliminary; not compared with conceptual translation
A; Scause: preliminary; not compared with conceptual translation
 A;Crose-references: RMBL/XS9209 NID;52336; FIDN:CAA41939 1; FID;91334074 C;Superfaakly; immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin ...
 A; Molecule type: mRNA
A; Residues: 1-107 <STA>
 A.Tille: Antibodies that are specific for a single amino acid interchange in A.Reference number: 826309; MUID:91341421; PMID:1908510
A.Accession: 826344
 Ig kappa chain V region - mouse
C.Spacies: Nu musculus (house mouse)
C.pacie: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C.pacession: 563596
R.Yerdsquer; M.; Mateu, M.G.; Bravo, J.; Domingo, B.; Fita, I.
J. Mol. Biol. 256, 364-376, 1996
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 A;Residues; 1-115 <VER>
A;Cross-references: GB:881196; NID:gl336821; PIDN:AAB36171.1; PID:gl336822
C;Superfamily; immunoglobulin V region; immunoglobulin homology
F;16-94/Domain: immunoglobulin homology <IPM>
 A; Status: preliminary
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 A;Cooss-réterences: RMBL:X59207; NID:952334; PIDM:ChA41917.1; PID:91334073
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IDM>
 A;Accession: S26343
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <STA>
 Ig kappa chain V region -
 Species: Mus musculus (house mouse)
Pats: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 Query Match
Best Local :
 Query Match
Best Local (
 Matches
 63
 63 PARFSGSGSRTDFTLTINPVBADDVATYYCQQSNBDPLTFGTGTRLBIKR 112
 62
 63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRL 108
 ψ
 w
 N
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIFGQPFKLLIYRASNLESGI
 98,
 Similarity
 Similarity
 PDRFSGSGSRTDFTLTIDEVBADDVATYYCQQSNBVPLTFGAGTKLDLKR
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 VLTQSPASLAVSLGQRATISCRASESVDSSGHSFMHWYQQKPGQPPKLLIYRASNLESGI
 PARPSGSGSRTDFTLTINEVEADDVATYYCQQSNEDPFTFGSGTKL
 VMTQTPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGI
 Conservative
 Conservative
 38.0%;
 88.5%;
 mouse
 5
 Score 517; DB
Pred. No. 3.5e
5; Mismatches
 Score 514;
Pred. No. 7
 Mismatches
 1; DB 2;
. 3.5e-40;
 7e-40;
 DB 2;
 5
 Length 115
 Length 107
 Indels
 107
 0
 Gaps
 Gaps
 62
 62
 62
 61
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 0
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Best Local Similarity
Matches 98; Conserva
 62
 63
 N
 3 VLTQSPASLAVSLGQRATISCRASBSVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
PARESGSGSRIDETLITINEVEADDVATTYCOOSNEDPYTEGGGTKL 107
 PARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDPLTFGTGTRL 108
 VMTQTPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGI
 Conservative
 92.5%;
 Pred. No. 8e-40;
4; Mismatches
 Indels
 0
 Gaps
 61
 0,
```

CSpecies: Mus musculus (house mouse)

C)Date: 07-Mpr-1902 Hecquence revision 02-Apr-1902 #text change 21-Jan-2000

C)Accession: B90412; B90174; B3922; C93822; C93204; D93204; PH1078; A01915

R; Burstein, Y; Schechter, I.

Biochemistry IT, 2392-360, 1978

A;Title: Primary structures of N-terminal extra pepride segments linked to 1 Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) -

variabl

segments linked to the

A; Reference number: A90412; MUID: 78235887; PMID: 98179 expression of immunoglobulin genes.

A; Accession: B90412 A; Contents: M63

A; Molecule type: protein A; Residues: 1-35 <BUR>

R.Worken, D.; Dotter, M.; Hood, L. Biochennistry 12, 760-771, 1973 AFTILE: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains A.Reference number: A50374; NUID:73140225; PMID:4691517

A; Accession: B90374

A, Molecule type: protein
A, Meaidues 21.6, 07, 48-53, 'B', 55-57, 'Z', 59-86,' P', 88-131 < NCKS
A, Mote: this sequence has since been revised in reference A99822
R, McKean, D.J., Bell, M, Potter, M,
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A, Title: Mechanisme of antibody diversity; multiple genes encode structurally related
A, Meterence number: A99822; NUID:79012520; PMID:99744

A; Accession: B93822

A; Molecule type: protein A; Residues: 1-53;69-107 -A; Accession: C93822 <MC2>

A; Molecule type: protein A; Residues: 21-119, 'Y', 121-131 <MC3>

R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, Nature 276, 785-790, 1978 J.; Hood,

Ratune 276, 785-790, 1978
A-Tille: Rearrangement of generic information may produce immunoglobulin diversity.
A-Reference number: A93204, MUID:79073152; PMID:103003
A-Concents: PC2945; PC4050
A-Accession: C93204

A; Molecule type: protein A; Residues: 21-119,'Y',121-131 <WEI>

A;Accession: D93204

A.Woldenie type: protein
A.Woldenie type: protein
A.Residues: 21:119 /L/,121-123,/A/,125-129,/L/,131 <W82>
R.Tillman, D.M., JOU, N.T., Hill, R.J., Marion, T.N.

J. Exp. Med. 116, 761-779, 19921
A.Fitle: Both 1gM and 1gG and 1DMA antibodies are the products of clonally selective
A.Reference number: PHO971; MUID:92301444; PMID:1812540
A.MCCESSION: PHIO78

A;Status: nucleic acid sequence not shown

Alkesiduse. 1908.
Alkesiduse. 1912. CTIL.
Alkesiduse. 2120. CTIL.
Alkesiduse. 2120. CTIL.
Alkesiduse. 2120. CTIL.
COMMENT: The NGS preductor sequence is shown.
COCOMPLANT A immunoglobulin heteroterizamer subunit consists of two identical light haid districts bonds. In some cases, such as 194 and 194, the subunits associate int Cysperizanily: immunoglobulin V region; immunoglobulin homology
Cysperizanily: immunoglobulin v region; immunoglobulin homology
Cysperizanily: immunoglobulin sequence sericus experimental <SIG>
F)1-20/Domain: signal sequence sericus experimental <SIG>

Query Match '

87.8%;

Score 513;

DB 2,

Length 107

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C;Keywords: nece
F;16-94/Domain:
 A. Cross-references. BMEL:X51833, NID:95394, FIDM:CDA36146.1, FID:9930230
C.Superfamily, immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer, immunoglobulin.
 Ig kappa chain V-J region (106-108) - mouse (fragment)
C:Species: Ma musculus (house mouse)
C:Patce: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C:Paccesion: 90965
S:Reininger, L., Shibata, T.; Osaki, S.; Shirai, T.; Jaton, J.C.; Izni, S.
Bur, J. Immunol. 20, 771-777, 1990
N:Pitler Variable region sequences of pathogenic anti-mouse red blood cell autoantibodi, N. Marker (1988) MUD190568328; PMID:3347362
 RESULT 7
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 A:Status; preliminary; not compared with conceptual translation A:Molecule type; nucleic acid A:Peasimon; 1-111 - CSTM; A:Peasimon; 1-111 - CSTM; A:Peasimon; 1-111 - CSTM; A:Peasimon; 1-111 - CSTM; A:Peasimon; 1-111 - CSTM; A:Peasimon; 1-111 - CSTM; A:Peasimon; 1-111 - Immunoglobulin V region; Ammunoglobulin homology (JKeywords: 9)ycopyrotein (JKeywords:
 anti-glycoprotein H monoclonal entibody light-chain variable domain (Nab 109) - mouse (f
Cippere 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
CiAccession: DE722
FSimpoon, 15-190-195, 1993 Monoclonal antibodies that distinguish three antigenic sites on hu
A.Tetie: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A.Reterence number: A47722 MUID:93.00833; PMID:7677958
A.Reterence number: A47722 MUID:93.00833; PMID:7677958
 A; Molecule type: mRNA
A; Residues: 1-111 < REI>
 A; Accession: 809965
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 F:21-111/Bomain: Ig kappa chain precursor V region #status experimental <MAT>
F:35-114/Domain: immunoglobulin homology <LMM>
F:43-114/Disulfide bonds: #status predicted
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 43-112/Disulfide bonds: #status predicted
 Matches
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 96;
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 96;
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 98;
 Similarity
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIFGQPPKLLIYRASNLESGI
 Similarity
 Similarity
 vltospaslavsroqratiscrasesvdsycksfmimyqqkfqqppklliylasnibsgv
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
 PTRFSGSGSRTDFTLTIDPVEADDAATYYCOOMNEDPRTFGGGTKLEIK 111
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNBDPLTFGTGTRLEIK 111
 vltospaslavsligoratiscrasesvdsygnsfmhwyooxpgoppkiliylasniesgv
 immunoglobulin homology < IMM>
 Conservative
 Conservative
 Conservative
 84.6%;
 85.8%; Score 501; DB 2.
88.1%; Pred. No. 1e-38;
 87.5%;
 Score 494; DB 2;
Pred. No. 4.4e-38;
6; Mismatches 7
 5; Mismatches
 Score 511; DB 1;
Pred. No. 1.5e-39;
 Mismatches
 DB 2;
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 Length 111;
 Length 111;
 Length 131
 Indels
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 62
 62
 82
 62
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 Ig kappa chain V and J regions, monoclonal antibody OHP 482.2.1 - mouse (fragment) CiSpecies: Mus musculus (house mouse) CiPace: 02-May-1994 flacence_revision 18-Nov-1994 fleext_change 20-Jun-2000 CiAccession: 853285 R. Sawada, J. Mizusawa, S., Terao, T., Naito, M., Kurosawa, Y. Mol. Immunol. 28, 1063-1072, 1991
A: Title: Molecular characterization of monoclonal anti-steroid antibodies:
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 RESULT 9
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 A; Accession: A90373
 묽
 Matches
 Query Match
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 96;
 63
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F;1-20/Domain: signal sequence #status predicted F;21-132/Product: Ig kappa chain V regions (MODC F;36-114/Domain: immunoglobulin homology almos F;43-112/Disulfide bonds: #status predicted
 C/Complex: An immunoglobulin heterortetramer subunit consists of two identical light bain disulfide bonds. In ome cases, such as 19 and 19M, the subunits associate int C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Superfamily: immunoglobulin V region; immunoglobulin homology
 A;Accession: A90374
A;Molecule type: protein
A;Residues: 21-131 <MC2>
 A, Title: Mouse immunoglobulin chains. Pattern of sequence A, Paterence munber: A90374; MUID:73140225; PMID:4691517 A; Contents: TEPC 124
 A;Note: the partial sequence of R;McKean, D.; Potter, M.; Hood, Biochemistry 12, 760-771, 1973
 A/fitle: Mouse immunoglobulin chaine. Partial amino acid
A;Faterence number: A90373; NUID:73140224; PMID:4120629
A;Contents: MOPC 321
 Ig kappa chain precursor V regions (MOPC 321, TEPC 124) - mouse (tentative CiSpecies: Mus muschise (house mouse) CiDates 31-May-1979 #sequence_revision 31-May-1979 #text_change 31-Mar-2000 CiAccession: A0412, Mo1073, Mo1074, Mo1933 CiAccession: A0412, Mo1073, Mo1074, Mo1933 Moleculary, J. Schochter, I. Biochteri, V. Schochter, I. Biochteri, V. Schochter, I. 392-400, 1978 Biochteri, V. Schochter, I. 392-400, 1978
 A;Note: the sequence is compatible with that of MOPC 321 except in having 47-Glx, 51-TC_Comment: The MOPC 321 sequence is shown.
 A; Molecule type: protein
A; Residues: 21-132 < MCK>
 R;McKean, D.; Potter, M.; Hood,
Biochemistry 12, 749-759, 1973
 A; Molecule type: protein
A; Residues: 1-37 < BUR>
 expression of immunoglobulin genes.
A;Reference number: A90412; MUID:78235887; PMID:98179
A;Contents: MOPC 321
 A; Note: this precursor was synthesized in a cell-free
 A, Accession: A90412
 Local Similarity
 63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNBDPLTEGTGTRLEIKR
 ω
 VLTQSPASLAVSLGQRATISCRASKSVNTYGNSFMZWYZZKPGZPPKLLIYRASNLZSGI
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
PARESGSSRTBETLTIBPUZABDVATYFCZZSBZBPWTFGSGTKLBIKR
 PARPSGSGSTTDFTLTINPVEADDVASYFCQQSNEYPWXFGGGTKLEIK 111
 PARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 VLTQSPASLAVSLGQRATISCRASESVDSFDNSFMHWYQQKPGQPPQLLIYRASNLESGI
 Conservative
 83.9%;
78.2%;
 20;
 the
 Score 490; DB 1;
Pred. No. 1.2e-37;
 a
 Mismatches
 region of this Bence
 <SIG>
 Length 132;
 TEPC 124) #status
 system directed by
 Indels
 sequence
 variation
 Jones
 (tentative sequence)
 132
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 protein was also
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 among kappa chains
 Gaps
 kappa
 predicted <MAX
 mRNA isolated
 82
 62
 the variabl
 0
 into
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primary

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Ig kapps chain v region (PC7043) - mouse (Eragment)
Cispacies Mus musculus (Nouse mouse)
Cipacies (1.5ep-1981 Recquence revision 01.5ep-1981 Hext. change 21-Jan-2000
CiAccession Adul937; 842187; 842149 442199; 842199; 842187; 842192
Ribeigert, M. Getmatean L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 2790, 1978
A.Fütle: Rearrangement of Genetic information may produce immunoglobulin diversity.
A.Fütle: Rearrangement of Genetic information may produce immunoglobulin diversity.
A.Fütle: Rearrangement of Genetic information may produce immunoglobulin diversity.
A.Fütle: Rearrangement of Genetic information may produce immunoglobulin diversity.
A.Fütle: Rearrangement of Genetic information may produce immunoglobulin diversity.
A.Fütle: Rearrangement of Genetic information may produce immunoglobulin diversity.
A.Fütle: Rearrangement of Genetic information may produce immunoglobulin diversity.
A.Fütle: Rearrangement of Genetic information may produce immunoglobulin diversity.
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A.Fütle: Rearrangement of Genetic information may
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 A; Molecule type; protein
A; Mesidues: 1.11.1 (MEI).
A; Residues: A1.11.4 (MEI).
A; Residues: A1.11.4 (MEI).
A; Residues: A1.11.4 (MEI).
A; Complex: An immunoglobulin beterotetramer subunit consists of two identical light (karlished bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfenily: immunoglobulin vegion; immunoglobulin homology
C; Superfenily: immunoglobulin vegion; immunoglobulin
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F; 33-9()Densilis: immunoglobulin homology carefey
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F; 34-9()Densilis: Superfenily: Superfenily: immunoglobulin homology
F; 34-9()Densilis: Superfenily: S
 Cispecies: Mus musculus (house mouse)
Cispecies: Au-un-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
Cispacesion: BO1937, A01937
Cispacesion: BO1937, A01937
R;Melgert, M., Ostenatian, L.; Loh. E.; Schilling, J.; Hood, L.
Mature 276, 785-790, 1978
Mature 276, 785-790, 1978
Mature 276, 785-790, 1978
A;Milte: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Melternoe number: A9204; NWID:79073153; PWID:103003
A;Motoession: B01937
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 and their pH-reactivity profiles.
A;Reference number: A53285; MUID:92017897; PMID:1922102
A;Accession: E53285
 KVMS43
 Ig kappa chain V region (PC7183) - mouse
 A; Status: preliminary
 Query Match
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Matches 90
 Query Match
Best Local S
Matches 92
 63
 63 PARFSGSGSRTDFTLTINPVBADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 63
 63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 3 VITQSPASIAVSIGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 90;
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 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIPGQPPXLLIYRASNLESGI
 Similarity
 Similarity
 PARESGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPLTFGAGTKLELK
 VLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGI
 PARFSGSGSRTDFTLTIDPVEADDAATYYCQQNIEDFFTFGSGTQLEIK 111
 VVTQSPASLAVSLGQRATVSCRASESVDRYGNNPIHWYQQXEGQPPQLLIYFASNLXSGV
 Conservative
 Conservative
 83.7%; Score 489; DB 2;
84.4%; Pred. No. 1.3e-37;
 80.1%;
 Mismatches
 9; Mismatches
 Score 468; DB 1
Pred. No. 1e-35;
 DB 1,
 10;
 Length 111;
 Length 111
 Indels
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A.Noolecule type: protein
A.Noolecule type: protein
A.Noolecule: 1-111 (481)
A.Rescidues: An immunoglobulin heteroretramer subunit consists of two identical light ()
hin disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
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 A; Molecule type: DNA
 A; Accession: S42189
 A; Accession: S42194
 A; Accession: S42187
 Matches
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 63
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Ig kappa chain V region (PCS308) - mouse
C:Species: Num maculus (house mouse)
C:Pace: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: 0.01997; Au1397 L.; Loh, E.; Schilling, J.; Hood, L.
RiPeigert, M.; Garmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 795, 790 . 1918
A:Tille: Rearrangement of genetic information may produce immunoglobulin dis
A:Beference number: A3204; MUID:79073152; PMID:103003
A:Beference number: A3204; MUID:79073152; PMID:103003
A:Accession: C01937
 A;Crose-references: EMBL:225454; NID:9407842; PIDN:CAA80941.1; PID:9407843
A;Motes: V-kappa-218; anti-collagen
C;Complex: An immunoglobulin heteroretramer subunit consists of two identical light (A
hain disulfied bonds: In some cases, such as 150; and 150; the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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 A./Rolecule type: DNA
A./Rolecule: 1199 - MOY>
A./Cross-réferences: BMBL:225452; NID:9407840; PIDN:ChA80939.1; PID:9407841
A./Mote: V-kappa-21B; anti-collagen
A./Accession: 542132
 A; Molecule type: DNA
A; Residues: 10-99 < MOO>
 A;Residums: 12-99 -4062>
A;Cosas-references: EMBL:225446; NID:9407834; FIDN:CAM80933.1; FID:9407835
A;Note: V-kapps-21E; anti-collagen
A;Notes: V-kapps-21E; anti-collagen
 A.Crose.references: EMGL.225449; NID:9407836; PIDN:CAA80935.1; PID:9407837
A.Wote: V-kappa-21E; anti-collagen
A.Wocession: S41188
 A.(Cross-references: EMBL:225458, NID:9407844; PIDN:CAA00945.1, PID:9407845
A.)Mote: V-Kappa-21E; anti-collagen
A.)Accession: 542150
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A;Residues: 10-99 <MOJ>
A;Cosso-references: EMBB: 225444; NID:9407832;
A;Note: Y-kappa-21E; anti-collagen
 A; Molecule type: DNA
A; Residues: 15-99 < MOA>
 A; Woldeule type: DNA
A; Reackdues: 13-90 - MODS
A; Cross-references: RMBL: 225450; WID:9407838; PIDN:CAA80937.1; PID:9407839
A; Woter V-Axpp2-212; anti-collagen
 A; Molecule type: DNA
A; Residues: 12-99 < MOW>
 A; Title: Variable region gene selection of A; Reference number: S42176; MUID: 94009207;
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 63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPXLLIYRASNLESGI
 90;
 VLTQSPASLAVSLGQRATISCKASQSVDYDGDSYNNWYQQKPGQPPKLLIYAASNLESGI
 PARFSGSGGTDFTLNIHPVEEEDAATYYCQQSNEDPFTFGSGTKLEIK 111
 Conservative
 80.0%;
82.6%;
 9,
 Score 467; DB 1;
Pred. No. 1.2e-35;
 Mismatches
 immunoglobulin G-expressing B cells with PMID:7691608
 PIDN: CAA80931.1;
 Length 111;
 Indels
 PID:g407833
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immunoglobulin diversity

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A; Molecula type; protein
A; Meadidues: 1.11 (*MID.
A; Readidues: 1.11 (*MID.
A; Readidues: A111 (*MID.
A; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds: In some cases, such as Igh and IgM, the subunits associate into it
C; Superidanily: immunoglobulin V region; immunoglobulin homology
C; Serwords: heterotetramer; immunoglobulin
C; As *A) Demain; immunoglobulin homology 41Meb
F; 35 *3/ Demain; immunoglobulin homology 41Meb
F; 35 *3/ Demain; immunoglobulin homology 41Meb
 Ig kappa chain V region (PC7175) - mouse (centative sequence)
CiSpecies: Mus muschius (house muse)
CiSpecies: Mus muschius (house muse)
CiPace: 30-Jun-1993 #sequence-revision 30-Jun-1993 #text_change 31-Mar-2000
CiPacession: D01398, M01393 #sequence
R/Weignert, M.; Garmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Mature 276, 785-790, 1978
Mature 276, 785-790, 1978
Mylicle: Nebrzangement of genetic information may produce immunoglobulin diversity.
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Mylicle: Nebrzangement of genetic information may produce immunoglobulin diversity.
Mylicle: Nebrzangement of genetic information may produce immunoglobulin diversity.
Mylicle: Nebrzangement of genetic information may produce immunoglobulin diversity.
 AyGross-references: RMELX85994, NID:952290, FIDM:GAM46222.1, FDD:952291
C;Superfamily: mumuoglobulin V region; immunoglobulin bomology
C;Koywords: heteschetramar; immunoglobulin
C;Koywords: heteschetramar; immunoglobulin
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <WEI>
 A; Description: Structural characterization of CD4 mAb
A; Reference number: $19963
A; Accession: $19972
 RESULT 14

RESULT 14

RESULT 17

Gl kappa, Chain V region (M-T321) - mouse (fragment)

Gl kappa, Chain V region (M-T321) - mouse (fragment)

Gl kappa, Chain V region (M-T321) - mouse (fragment)

GLPates (64-Pèb-1955 #sequence_revision 06-Pèb-1995 #text_change 21-Jan-2000

GLPates (64-Pèb-1995 #sequence_fragment)

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 C;Keywords: heterotetramer; immunoglobulin F;16-94/Domain: immunoglobulin homology <IMM> F;23-92/Disulfide bonds: #status predicted
 R; Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P. submitted to the EMBL Data Library, March 1992
 Matches
 Query Match
Best Local
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 Query Match
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 Local Similarity
 63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 63 PARFSGSGSGTDFTLNIHPVBEEDAATYYCQHSRELPLTFGAGTKLELK 111
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 63 PARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPWTFGSGTKLEIK 111
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
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n 78.8%;
Similarity 80.9%;
89; Conservative
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
 Similarity
 VLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYTASNLESGI
 VLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQXPGQPPKLLIYLASNLESGV
 Conservative
 Conservative
 79.1%;
 79.6%;
 9; Mismatches
 9;
 Score 465;
Pred. No. 1
 Pred. No. 5.4e-35;
 Score 462; DB 1;
Pred. No. 3.5e-35;
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Coomplex: An immunoglobulin heteroretramer subunit consists of two identical light (k bain disulfide bonds. In some cases, such as 154 and 169, the subunits associate into C.Superfamily. immunoglobulin V region, immunoglobulin homology C.Superfamily. immunoglobulin V region; immunoglobulin homology C.Keywords: heteroretramer, immunoglobulin monology c.J.S. 29, 29, 20 and 1: immunoglobulin bonology c.J.MN>
 RiWeigert, M.; Garmairan, L.; Loh, B.; Schilling, J.; Hood, L.
Nature 276, 798-790, 1978
Nature 276, 798-790, 1978
A.Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A.Reference number: A33204; NUID:79073152; PNID:103003
A.Reference Audiogram A.Reference and A.Referenc
 Ig kappa chain V region (PC7769) - mouse
CiSpactes: Mus musculus (house mouse)
CiPates 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 21-Jan-2000
CiPates 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 21-Jan-2000
CiPatesession: E019373, A01936
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 A; Residues: 1-111 <WEI>
 F;23-92/Disulfide bonds: #status predicted
 RESULT 15
 Matches
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 Query Match
 Local Similarity
63 PARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPWTFGSGTKLEIK 111
 63
 63 PARFSGSGSGTDFTLDIHPVBEEDAATYYCQQSSEDFYTFGGGTKLEIKR 112
 63 PARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDFLTFGTGTRLEIKR 112
 3 VLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKVLIFAASNLESGI
 88;
 3 VLTQSPASLAVSLGQRATIFCRASQSVDYNAISYMHWYQQKPGQPPKLLIYAAANLESGI
 3 VITQSPASLAVSLCQRATISCRASESVDSYGYNFMHWYQQIPGQPPKILIYRASNLESGI
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIPGQPPKLLIYRASNLESGI
 PARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDPLTFGTGTRLEIX 111
 Conservative
 78.4%; Score 458; DB 1;
80.7%; Pred. No. 8.2e-35;
tive 11; Mismatches 10
 DB 1; Length 111;
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Maximum Match 100%
Listing first 45 s
 Total number of hits satisfying chosen parameters:
 Pred. No. is the number of results predicted by chance to have a score greates than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 US-09-661-992B-86_COPY_138_249
 November 7, 2003, 07:21:18; Search time 8.07477 Seconds (Without alignments) 552.278 Willion cell updates/sec
 127863 seqs, 47026705 residues
 ENVLTQSPASLAVSLGQRAT.....QQSNEDPLTFGTGTRLEIKR 112
 GenCore version
Copyright (c) 1993 - 2003
 Gapext 0.5
 KY31 MOUSE
KY3E MOUSE
KY3E HUMAN
KY4C HUMAN
KY4C HUMAN
KY4E HUMAN
KY1H HUMAN
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 KV3T MOUSE
KV3P MOUSE
KV3A MOUSE
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KV3H_MOUSE
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 InterPro; IPR007110; I
InterPro; IPR003006; I
InterPro; IPR003596; I
InterPro; IPR003596; I
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1
 DOMAIN
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SEQUENCE
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 Immunoglobulin
DOMAIN
 MEDLINE-9012520; bubbed-99744;
McKenn D.J., Bell M., Potter M.;
McKenn D.J., Bell M., Potter M.;
McKenniems of antibody diversity; multiple genes encode structurally
related mouse kappa variable regions."
proc. Marl. Acad. Seti U.S.A. 75.3913-3977(1978).
1 MISCRILANDUS; PHE BC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
11 MISCRILANDUS; MES DC 3741 AND TEPC 111 SEQUENCES ARE JOENTICAL.
HEST. POSTON, ANDERS.
 KV3H MOUSE
P01660;
21-JUL-1986
 DOMAIN
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 MEDLINE-79073153, PubMed=10003;
Wedgert M., Garmattan L., Lob E., Schilling J., Hood L.E.,
"Rearrangement of genetic information may produce immunoglobulin
 DOMAIN
 PROSITE;
 Nature 276:785-790(1978).
 diversity."
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Mus musculus (Mouse)
 21-VIL-1986 (Rel. 01, Created)
21-VIL-1986 (Rel. 01, Last sequence update)
15-VIL-1999 (Rel. 38, Last annotation update)
15-VIL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-III region PC 3741/TEPC 111.
 SEQUENCE (TEPC 111).
 SEQUENCE (PC 3741).
 NCBI_TaxID=10090;
 350.5
348.5
348.5
344.5
342.4
342.5
342.5
 103;
63 PARFSGSGSRTDFTLTINFVBADDVATYYCQQSNEDPLTFGTGTRLBIK 111
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 Similarity
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 ULTOSPASLAVSLGORATISCRASBSVDSYGNSPMHWYQOXDGQPPKLLIYRASNLSSGI
 PS50835;
 1
24
39
54
61
61
93
102
23
111
111
AA,
 Conservative
 59.0
59.8
59.2
59.2
59.2
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59.2
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59.3
59.4
 1 V region.
1 23
24 38
39 53
64 60
92
101
101
102
111
102
92
 STANDARD;
 Gv; 1.
IG_LIKE;
 12099 MW;
 91.1%;
 Ig-like.
Ig_MHC.
Ig_v.
 PRAMENORY.

COMPLEMENTATY - DETERMINING-1.
PRAMENORY.

COMPLEMENTATIY - DETERMINING-2.
PRAMENORY.

COMPLEMENTATIY - DETERMINING-3.
PRAMENORY.

BY SITHLARTIY.

BY SITHLARTIY.
 2;
 Score 532; DB 1;
Pred. No. 1.6e-49;
2; Mismatches 4
 KY3D HUMAN
KY1Y HUMAN
KY1Y HUMAN
KY1A MOUSE
KY1Y HUMAN
KY1D HUMAN
KY1D HUMAN
KY1D HUMAN
KY1B HUMAN
KY1B HUMAN
KY1B HUMAN
KY1B HUMAN
KY1B HUMAN
KY1B HUMAN
 EC46C9D2S9213BE4 CRC64;
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 ALIGNMENTS
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 Length 111;
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 P01622
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P803636
P803680
P01680
P01607
P01607
P01617
P01517
P01524
P01524
P01534
P01534
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Result

Score

Query

Length D8

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Database

SwissProt\_41:\*

Minimum DB Maximum DB

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length: 0 length: 2000000000

Searched:

Scoring table:

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AC P01662;
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DT 21-7UL-1996
DT 15-7UL-1999
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 RESULT 2

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 Query Match
Best Local S
Matches 98
 POLOGIA:
11-JUL-1986 (Rel. 01, Created)
11-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last amotation update)
15-JUL-1999 (Rel. 38, Last amotation update)
15-JUL-1999 (Rel. 38, Last amotation update)
15-JUL-1999 (Rel. 38, Last amotation update)
16-Venna chain V-11
SEQUENCE (ABPC 22).
MEDLINE-7901-520; PUMPEd-99744;
MCMean D. J., Bell M., Potter M.;
"Mechanisms of anthoby diversity: multiple
related mouse kappa variable regions.";
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
 NON_TER
 DOMAIN
DOMAIN
DOMAIN
 HSSP; P01679; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 NCBI_TaxID=10090;
 "Rearrangement of genetic information may produce diversity.";
 SEQUENCE
 Pfam, PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
 Nature 276:785-790(1978).
 Immunoglobulin
 MEDLINE=79073152; PubMed=103003;
 NCBI_TaxID=10090;
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 Mus musculus (Mouse)
 P01663;
21-JUL-1986
 KV3K_MOUSE
 15-JUL-1999
 kappa chain V-III region
 63
 63
 ω
 ω
 98;
 Similarity
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYPASNLESGI 62
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYLASNLESGV
 PARFSGSGSRTDFTLTIDFVEADDAATXYCQQNNEDPLTFGAGTKLELK
 111 AA;
 Conservative
 24
54
54
93
23
 (Rel.
 1 V region.

1 23

24 38

39 53

60

61 92

111

101

101

102

111
 STANDARD,
 STANDARD;
 01, Last sequence update)
38, Last annotation updat
[II region PC 4050]
 12005 MW;
 89.5%;
 Created)
 FRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
FRAMEMORK-2.
FRAMEMORK-2.
FRAMEMORK-3.
COMPLEMENTARITY-DETERMINING-2.
COMPLEMENTARITY-DETERMINING-3.
 Pred. No. 5.20
5; Mismatches
 Score 517;
Pred. No. 6
 FRAMEWORK-4
BY SIMILARIT
 PRT;
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
 39D87619313453CB CRC64;
 SIMILARITY
 111
 111
 update)
 A
 DB 1;
 Å
 genes encode structurally
 Ş
 Length 111;
 Hood
 Indels
 immunoglobulin
 Euteleostomi,
 Murinae; Mus
 F
 0
 Gaps
 62
 0
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 Query Match
Best Local
 Matches
 SEQUENCE
 SEQUENCE (EC 2227)
MEDLINE=99073152; PubMed=103003;
MGCTART M. Gatmaitan L., Loh E.,
 Nature
 diversity."
 Weigert M., Gatmaitan L., Loh E., Schi
Rearrangement of genetic information
 SEQUENCE (PC 9245)
 Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978)
[2]
 63
 63
 3 VLTQS$ASLAVSLGQRATISCRASESVDSYGYNEMHWYQQIPGQPFXLLIYRASNLESGI
 98;
 276:785-790(1978)
 Similarity
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK
PARFSGSGSRTDFTLTIDPVEADDAATYYCOONNEDPYTFGGGTKLEIK 111
 VLTQSPASLAVSLOQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYLASNLESGV
 111
111 AA;
 Conservative
 12041 MW;
 87.7%;
 FRAMEMORK.1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEMORK-3.
FRAMEMORK-4.
FRAMEMORK-4.
FRAMEMORK-4.
FRAMEMORK-3.
 5
 Score 512;
Pred. No. 2
 D7DF0609303453CE CRC64;
 Mismatches
 SIMILARITY.
 Schilling J., Ho
 PC9241 SEQUENCES ARE IDENTICAL
 DB 1;
1.1e-47;
 6.
 Length 111,
 Hood L.E.;
 Indels
 immunoglobulin
 0;
 Gaps
 62
 62
 0
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PARENT REPRESENTATION OF THE PROPERTY OF THE P
 RESULT
KV3 I_MC
 21-JUL-1986
21-JUL-1986
15-JUL-1999
 MEDILINE-7314025; PabMod-489151;
McKean D.J. Pocter M. Hood L.B.,
"Mouse immunoglobulish chains. Pattern of sequence variation
kappa chains with limited sequence differences.",
Biochemistry 12:760-771(1973).
 SEQUENCE OF 1-35.

MEDLINE-78218807 phiMed=98179;

MEDLINE-78218807 phiMed=98179;

Burstein Y., Schechter I.;

reminal extra peptide segments linked primary structures of N-terminal extra peptide segments linked the variable and commetant regions of immunoglobulin light chain the variable and constant regions of manual controlled expression of manual controlled expression of manual controlled expression of manual controlled expressions of manual controlled expressions of manual controlled expressions.
 MEDLINE=79012520;
McKean D.J., Bell
 REVISIONS
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 KV3I MOUSE
P01661;
 MOUSE
 SEQUENCE OF 21-131.
 Mus musculus (Mouse)
 Ig kappa chain V-III region
 NCBI_TaxID=10090;
 (Rel. 01, Created)
(Rel. 01, Last sequence update)
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ain V-III region MOPC 63 precurs
 STANDARD;
PubMed=99744;
M., Potter M.
 Rodentia;
 Chordata;
 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
 PRT;
 63 precursor
 131 AA.
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 RESULT 5
 Query Match
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Matches 98
RESIDUES.

PIR; A90412; KVMS32.

HSSP; P01679; 2FBJ.

InterPro; IPR007110;
 ssourance of 1-17.

MEDILINE-MR31858); PubMed-88179;

MEDILINE-MR31858); PubMed-88179;

Burstein Y., Schochter I.;

"Primary structures of M-terminal extra peptide segments linked to
"Primary structures of M-terminal extra peptide segments light chain
precursors: (mylications on the organization and controlled
expression of immunoglobulin genes.";
 InterPro; irr...; 1; 1.
pfam; pF00047; ig; 1.
sMART; SM00406; IGv; 1.
pROSITE; P85083; IG_LIKE; 1.
lmmurglobulin V region; Signal.
 NON TER
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridac; Murinae; Mus
 P01658;
21-JUL-1986
 SSDOW
 BIOODEMISETY 12:749-759(1973).

1- MISCELLANSCOIS THE PATTIAL SEQUENCE OF THE C REGION OF THE SENCE-COMES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT RESPORTED WAS MADE MOVED FOR C.2 COMU. IN THE TRANSPOSITION OF THO MERREY
 "McKean D.J., Potter M., Hood :
"Mouse immunoglobulin chains.
 MEDLINE=73140224; PubMed=4120629;
 SEQUENCE OF 21-132.
 NCBI_TaxID=10090;
 Mus musculus (Mouse)
 21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region MOPC 321 precursor.
 KV3F
 DISULFID
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 InterPro; IPR003006; Ig_WH
InterPro; IPR003596; Ig_v.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
 HSSP; P01679; 2FBJ.
 veldanisma of antibody diversity; milityle genes encode structurally
related mouse bepps variable regions "lityle genes encode structurally
reco. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
ETR, 380411; KVMSNG.
 MOUSE
 83
 63
 23
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 186
 Similarity
 PARFSGSGSRTDFTLTIDFVEADDAATYYCOONNEDPWTFGGGTKLEIK 131
 VLTQSPASLAVSLGQRATISCRASBSVDSYGYNFMHWYQQIPGQPPKLLIYRASNLBSGI 62
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKFGQPPKLLIYLASNLESGV
 679; 2FBJ.
IPR007110;
 131 AA;
 Conservative
 (Rel. 01, Created)
 STANDARD;
 43
58
73
80
112
121
131
 87.5%;
 14291 MW;
Ig-like
 Hood i.E.;
hains. Partial amino acid sequence of a kappa
 ر
ب
 Score 511;
Pred. No. 3
 IG KAPPA CHAIN V-III REGION MOPC 63. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
 FRAMEWORK-4
 COMPLEMENTARITY-DETERMINING-3
 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
 FRAMEWORK-
 PRT;
 D212EC9F08DC880A CRC64;
 Mismatches
 SIMILARITY.
 132 AA
 DB 1;
 Length 131;
 Indels
 0,
 Gaps
 62
 0;
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RESULT 6
KV3G_MOUS
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Query Match
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Matches 86
 Matches
 Query Match
Best Local :
 Prem; Pro047; 19; 1.

SMART; SM00406; IGV; 1.

FROSTTE; PS50835; IG_LIKE; 1.

Immunoglobulin V region; Bence
 KV3G_MOUSE
 DISULFID
NON_TER
 P01659;
21-JUL-1986
21-JUL-1986
 NON TER
 Mus müscilus (Mouse).
EMbaryota; Metazos; Chordata; Craniata; Vertebrata; Eureleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 CHAIN
 SEQUENCE
 kappa chains with limited sequence Biochemistry 12:760-771(1973).
 DISULFID
 DOMAIN
 InterPro; IPR003006;
InterPro; IPR003596;
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 PROSITE; PS50835;
Immunoglobulin V 1
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGV;
 Interpro; IPR007110
 "Mouse
 McKean D
 MEDLINE=73140225; PubMed=4691517;
 NCBI_TaxID=10090;
 21-UU-1986 (Rel. 01, Created)
21-UU-1986 (Rel. 01, Last sequence update)
15-UU-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region TEPC 124.
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 nterPro;
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 a-73.4022s; runned L.B.;
D.J., Potter M., Hood L.B.;
immunoglobulin chains. Pattern of sequence variation
immunoglobulin chains. Pattern of sequence variation
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 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 Similarity
 Similarity
 VLTQSPASLAVSLGQRATISCRASKSVNTYGNSFMZWYZZKPGZPPKLLIYRASNLZSGI
 IPR003596;
 IPR003006;
 IPR007110;
 112 AA;
 Conservative
 Conservative
 STANDARD;
 region.
 38
53
60
92
101
 112
121
131
 12339 MW;
 83.9%;
78.2%;
 Ig_w.C.
 82.7%;
 Ig_NHC.
 14523 MW;
 Bence-Jones protein; Signal.
 20;
18;
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 FRAMEWORK-3.
COMPLEMENTARITY-
FRAMEWORK-4.
 Score 490;
Pred. No. 5.
 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
 IG KAPPA CHAIN V-III REGION MOPC 321.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
 Pred. No. 2.5e-44
 Score 483;
 BY SIMILARITY
 COMPLEMENTARITY-DETERMINING-2
 BY SIMILARITY
 COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-4.
 FRAMEWORK-
 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
 PRT;
 9F3B809BB773FBE9 CRC64;
 7CFD328DBE8E9D71 CRC64;
 Mismatches
 Mismatches
 112 AA.
 DB 1; Length 112;
 DB 1; Length 132;
 -DETERMINING-3
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RESULT 8
KV3M MOUSE
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AC P01665
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DT 15-JUL
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 p01655;
21-VUL-1996 (Rel. 01, Created)
21-VUL-1996 (Rel. 01, Last sequence update)
15-VUL-1996 (Rel. 28, Last amoutation update)
15-VUL-1996 (Rel. 38, Last amoutation update)
16 kuppa chain V-III region PC 7043.

Mamanian Macacous, Pouseo , and Macacou
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 DOMAIN
 DOMAIN
 InterPro; IPR007110;
InterPro; IPR003006;
 PIR; B01937; KVMS83.
HSSP; P01679; 2FBJ.
 SEQUENCE.
MEDLINE=79073152; PubMed=103003;
MEDLINE=79073152; PubMed=103003;
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 Ig kappa chain V-III region
Mus musculus (Mouse).
 P01666;
21-JUL-1986
 MOUSE
 DOMAIN
 Nature 276:785-790(1978).
 diversity.
 Rearrangement of genetic information may produce immunoglobulin
 NCBI_TaxID=10090;
 15-JUL-1999
 21-JUL-1986
 KV3N MOUSE
 HOUSE
 63
 63
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 63
 63
 90,
 Similarity
 PARFSGSGSRTDFTLTINPVBADDVATYYCQQSNBDPLTFGTGTRLEIK 111
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNEMHWYQQIPGQPPKLLIYRASNLESGI
 PARPSGSGSGTDPTLNIHPVBEEDAATYYCQQSNEDPLTFGAGTKLELK 111
 VLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLIYAASNLESGI
 PARFSGSGSRTBFTLTIBFVZABDVATYFCZZSBZAPWTFGSGTKLEIKR
 PARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDFLTFGTGTRLEIKR
 Conservative
 (Rel.
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 STANDARD;
 STANDARD;
 01, Last sequence update)
38, Last annotation update)
III region PC 7183.
 38
53
60
92
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111
 11952 MW;
 82.6%;
 80.1%;
 Created)
 9;
 Score 468; DB 1;
Pred. No. 9.5e-43;
 ΒY
 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
 FRAMEWORK-4
 COMPLEMENTARITY-DETERMINING-1
 FRAMEWORK-1.
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
 PRT;
 PRT;
 2058BB50CE306D31 CRC64;
 Mismatches
 SIMILARITY
 Schilling J.,
 111
 111
 B
 A
 10;
 Length 111;
 Hood L.E.;
 Indels
 0
 112
 Gaps
 62
 62
 0
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RESULT 9
KV30_MOUSE
 S
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 Query Match
Best Local S
Matches 90
 PROSTTE, PSSURS, PSSUR
 DOMAIN
DOMAIN
DOMAIN
DOMAIN
 NON TER
 Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
 InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
 21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
 PROSITE;
 PIR; C01937; KVMS08.
HSSP; P80362; 1WTL.
 Nature 276:785-790(1978).
 diversity.
 MEDLINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E.,
 NCBI_TaxID=10090
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 Mus musculus (Mouse)
 21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
Ig kappa chain V-III region PC 6308.
 P01667;
 KV30_MOUSE
 "Rearrangement of genetic
 SEQUENCE
 SEQUENCE
 SMART; SM00406; IGV;
 Pfam; PF00047; 19;
 InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 HSSP; P80362; 1WTL.
 diversity
 MEDLINE=79073152; PubMed=103003; Schi
Weigert M., Gatmaitan L., Loh E., Schi
"Rearrangement of genetic information
 PIR; A01937; KVMS43.
 Nature 276:785-790(1978).
 SEQUENCE
 NCBI_TaxID=10090
 63
 S
 w
 w
 90;
 ; PS50835;
lobulin V r
 Similarity
 PARFSGSGSGTDFTLN1HPVEBEDAATYYCQQSNEDPFTFGSGTKLEIK
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK
 VLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGI
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIPGQPPKLLIYRASNLESGI
 PS50835; IG_LIKE;
 111 AA;
.Gv; 1.
.; IG_LKB; V region.
1 23
24 38
39 53
60
 54
54
 Conservative
 STANDARD;
 01, Created)
 ; Ig-like.
; Ig_MHC.
; Ig_v.
 80.0%;
 12002 MW;
 information may produce immunoglobulin
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
 Score 467; DB 1;
Pred. No. 1.2e-42
 COMPLEMENTARITY-DETERMINING-3 FRAMEWORK-4.
 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2
FRAMEWORK-3.
 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
 PRT;
 7A5FCB586C306D29
 Mismatches
 SIMILARITY.
 Schilling
 Schilling J., Ho
 111
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 A
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 Hood
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21-UU-1996 (Rel. 01; Created)
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15-UU-1996 (Rel. 38; Last amnotation update)
15 kappa chain V-III region PC 7175.
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 SEQUENCE
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
 Mus muscullus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinse; Mus.
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 Immunoglobulin
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 InterPro;
 PIR; B01938; KVMS75.
HSSP; P01679; 2FBJ.
 Nature 276:785-790(1978).
 diversity.";
 Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
 MEDLINE=79073152; PubMed=103003;
 SEQUENCE
 NCBI_TaxID=10090;
 KV3S MOUSE
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 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 Similarity
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 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNEWHWYQQIPGQPPKLLIYRASNLESGI 62
 PARREGEGEGETETINIHPVEEEDAATYYCQQSNEDPWTFGSGTKLEIK 111
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 VLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLIYTASNLBSGI
PARFSGSGSGTDFTLNIHPVEBEDAATYYCOHSRELPLTFGAGTKLELK 111
 VLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGV
 PS50835; IG_LIKE; 1.
 IPR007110, Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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 STANDARD;
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12071 MW;
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 FRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEMORK-3.
COMPLEMENTARITY-DETERMINING-3.
 9;
 9; Mismatches
 PRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
PRAMEWORK-4.
BY SIMILARITY.
 Score 462; DB 1; Length 111;
Pred. No. 4.1e-42;
 FRAMEWORK-4
BY SIMILARI
 Score 465; UB .
No. 2e-42;
 F041E89AA7858523 CRC64;
 PRT;
 7A4ADE4D6C2S6D29 CRC64;
 Mismatches
 SIMILARITY.
 111 AA
 DB 1; Length 111;
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 10; Indels
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RESULT 11

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RESULT 12
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P01669;
 REDLINE-901250; PubMed-9974;
McXean D.J., Bell M., Potter M.;
Webcharieme of antibody diversity; multiple genes encode structurally
related nouse Asppa variable regions ",
Proc. Natl. Acad. Sei. U.S.A. 75,3911-3917(1978).

1- MISCRLANBOUS: "HIS CIAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PERS, MAISOS; KWRGCL.
 Bükaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostoni,
Mammalis, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TarD=10090;
 901664, 101.1986 (Rel. 01, Created)
21.-UL-1986 (Rel. 01, Last sequence update)
15.-UL-1996 (Rel. 38, Last amnotation update)
15.-UL-1996 chain V-III region CBPC 101.
Make maccoluse (Wouse).
 MOUSE
 Pfam; PP00047; ig; 1.
SMART; SM00406; IGv;
PROSITE; PS50835; IG
 Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus
 21-UII-1986 (Rel. 01, Created)
21-UII-1986 (Rel. 01, Last sequence update)
15-UII-1996 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7769.
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 Mus musculus (Mouse).
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 InterPro;
 HSSP, P80362; 1WTL.
 Nature 276:785-790(1978).
 "Rearrangement
 Weigert M.,
 MEDLINE=79073152; PubMed=103003;
 NCBI_TaxID=10090;
 InterPro:
 InterPro, IPR007110;
P80362; 1WTL
 63
 63 PARFSGSGSRTDFTLTINEVEADDVATYYCQQSNBDPLTFGTGTRLBIK 111
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 88;
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIPGQPPKLLIYRASNLESGI
 Similarity
 PARFSGSGSTDFTLNIHPVESEDAATYYCQQSNEDPWTFGSGTKLEIK 111
 VLTQSPASLAVSLGQRATISCKASQSVDYDGDSYNNWYQQKPGQPFKVLIFAASNLESGI
 IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
 111 AA;
 Gatmaitan L., Loh E., Schilling J., Hood L.E.; ent of genetic information may produce immunoglobulin
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 Conservative
 V region.
 STANDARD;
 STANDARD;
 IG_LIKE; 1.
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 12011 MW;
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 11; Mismatches
 Score 458; DB 1;
Pred. No. 1.1e-41;
 COMPLEMENTARITY-DETERMINING-1.
FRAMMORK-2.
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
 FRAMEWORK-4.
BY SIMILARITY.
 FRAMEWORK-1.
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 6FAA345279356829 CRC64;
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InterPro: IPR00306; Ig_wK:
InterPro: IPR00356; Ig_w
Pfam: PF0047; Ig-
93MRT: SM00406; IG-1.
PR0SITE; PS5083; IG_LIKE; 1.
Immunoglobulati, V region.
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 MEDIINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh B., Schillin "Rearrangement of genetic information may
 Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
 PIR; A01938; KVMS84.
HSSP; P80362; 1WTL.
 diversity."
 "Rearrangement of genetic
 21-ULI-1986 (Rel. 01, Created)
21-ULI-1986 (Rel. 01, Last sequence update)
15-ULI-1999 (Rel. 38, Last annotation updat
Ig kappa chain V-III region PC 6684.
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
 Nature 276:785-790(1978).
 NCBI_TaxID=10090;
 InterPro;
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 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
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 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 VLTQSPASLAVSLGQRATISCKASQSVDYTGESYMNWYQQNPGQSPKLLIYAASNLESGI
 PARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPYTFGGGTKLEIK 111
 IPR003006;
 IPR007110;
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 Chordata;
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 Score 456; DB 1;
Pred. No. 1.8e-41;
8; Mismatches 13
 FRAMEWORK-3.
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 FRAMEWORK-4.
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 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
 FRAMEWORK-1
 1E46988341858526 CRC64;
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RESULT 15

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Bukaryota; /Metazoa; Chordata; Craniata, Yertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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 diversity.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 HSSP; P80362; 1WTL.
 PIR; C01938; KVMS40.
 Vature 276:785-790(1978)
 NCBI_TaxID=10090;
 Mus musculus (Mouse)
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 PARFSGSGSGTDFTLNIHPVEBEDAVTYYCOHSRELPFTFGGGTKLEIK
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 VLTQSPASLAVSLGQRATISCRASKSVSAFGYSYMHWYQQXPGQPPKLLIYLASNLESGV
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 PARFSGSGSGTDFTLNIHPVEBEDAATYYCQHSRELPRTFGGGTKLEIK
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNBDPLTFGTGTRLEIK
 VLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGV
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIFGQPFKLLIYRASNLESGI
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FRAMEMORK. 2.
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FRAMEMORK. 3.
COMPLEMENTARITY DETERMINING-3.
 Score 456; DB 1;
Pred. No. 1.8e-41
 FRAMEWORK-4.
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Page 7
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 InterPro; PRO07110, 1g-1kke.
InterPro; PR007110, 1g-1kke.
InterPro; PR0013066, 1g-wc.
InterPro; PR0013966, 1g-wc.
Pfam; PR00017; 1g-1.
PR005171; PR005395, 1d_LTKE; 1.
PR005171; PR005171; 1d_LTKE; 1.
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 Nature 276:785-790(1978).
1- MISCELLANEOUS: THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.
FIR, A01939; KYNASS.
1858P; P01679; 2FBJ.
 NEDITHER-9073152; bubMed=103003; Medjert M., Gathaitlan L., Joh E., Schilling J., Hood L.E.; Weigert M., Gathaitlan L., Joh E., Schilling J., Hood L.E.; Startangement of genetic information may produce immunoglobulin diversity.";
 NCBI_TaxID=10090;
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 63 PARESGSGSRTDFTLTINPVEADDVATYYCQQSNEDDLTFGTGTRLEIK 111
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 7 VLTQSPASLAVSLOQRATISCRASESVDSYVNPRAMKYQQIPQQPPKLLIYRASNLESGI 62
 PARFSGSGGTDFTLNIQPVEBEDAAIYYCQHSRELFLTFGAGTKLELK 111
 111 AA;
 11986 MW; BF38CS9AA7858467 CRC64;
 Score 450; DB 1; Length 111;
Pred. No. 7.6e-41;
9; Mismatches 14; Indels
 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
 BY SIMILARITY.
 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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 Minimum DB seq length: 0
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### SUMMARIES

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| 0.4.0       | 3              | 343.5       | 344.5      | 345         | 345.5      | 347.5      | 349.5       | 350.5      | 352.5      | 356    | 357    | 357.5       | 358    | 358.5  | 412        | 457        | Score       |
| 00./        | 1              | 58.8        | 59.0       | 59.1        | 59.2       | 59.5       | 59.8        | 60.0       | 60.4       | 61.0   | 61.1   | 61.2        | 61.3   | 61.4   | 70.5       | 78.3       | Query       |
| TOR         |                | 239         | 114        | 108         | 112        | 238        | 107         | 112        | 238        | 234    | 108    | 107         | 108    | 109    | 103        | 111        | Length      |
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| 674067      | 201            | OBNEKO      | 1 Q8K1F1   |             |            |            | Q9UL81      |            |            | Q8NEK1 | Q9UL77 | Q96SA9      | Q9UL70 | Q9UL78 | 1 Q9JL80   | 1 Q920E9   | Ħ           |
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| sapien      | , southern     |             |            |             |            |            | sapien      |            |            | Bapien | sapien | sapien      | sapien | sapien | musculu    | musculu    |             |

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| 444                                                            | 40                                   | 335 44                                                                                                            | 32 30 32 32 32 32 32 32 32 32 32 32 32 32 32   | 2265422                                                  | 17<br>18<br>19<br>20<br>21                                                                                                       |
|----------------------------------------------------------------|--------------------------------------|-------------------------------------------------------------------------------------------------------------------|------------------------------------------------|----------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------|
| 289<br>284                                                     | 302<br>302<br>298                    | 310<br>310<br>308.5<br>308.5                                                                                      | 322<br>320.5<br>315.5                          | 329.5<br>329.5<br>326.5<br>326.5                         | 339.5<br>337.5<br>336.5<br>334.5                                                                                                 |
| 49.5<br>48.6                                                   | 51.7<br>51.7<br>51.5                 | 52.53.1                                                                                                           | 54.9                                           | 55.99                                                    | 58.1<br>57.6<br>57.3                                                                                                             |
| 109<br>107<br>127                                              | 109<br>97<br>218                     | 234<br>234<br>239<br>116                                                                                          | 107<br>107<br>104<br>235<br>233                | 106<br>114<br>234<br>112<br>134                          | 239<br>109<br>239<br>109<br>214                                                                                                  |
| 11 6                                                           | ====                                 |                                                                                                                   | :::::::                                        | 222245                                                   | 44141                                                                                                                            |
| Q9NOW5<br>Q9JL84<br>Q925S9                                     | Q9JL74<br>Q920E6<br>Q9JL76<br>Q9JL76 | Q8VIJO Q8RO28 Q8KOF8 Q96PF6                                                                                       | Q9JL78<br>Q9ERZ9<br>Q9JL82<br>Q9JW12<br>Q91W12 | Q9U410<br>Q9UL80<br>Q91WF8<br>Q8X1F0<br>Q8XDD0<br>Q8XDD0 | QBTCDO<br>Q9ULBS<br>QBVC55<br>Q9ULB6<br>Q9R1A5                                                                                   |
| Q9n0w5 oryctolagus<br>Q9j184 mus musculu<br>Q925s9 mus musculu | mus<br>mus<br>mus                    | OBvopo mus musculu OBvijo mus musculu OBvijo mus musculu OBvojo mus musculu OBvojo mus musculu OBvojo mus musculu | mus<br>mus<br>mus<br>mus                       | mus<br>mus<br>mus<br>mus                                 | Q8tcd0 homo sapien<br>Q9u185 homo sapien<br>Q8u255 mus masculu<br>Q9u186 homo sapien<br>Q9u186 homo sapien<br>Q9u185 mus musculu |

#### ALIGNMENTS

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RESULT 1
Q920E9
ID Q920
 Owery Match 78.3%; Score 457; DB 11; Length 111; Best Local Similarity 80.7%; Pred No. 1.70-44; Matches 88; Conservative 8; Mismatches 13; Indels (
 Arkin JD., Japa A., Jennings I.G., Horaitis O., Cotton R.G.H.;

"Definition of the idiotope of Ferin Mimicking Antibodies Expressed
in Mammalian Cells."

Submitted (SEP-2000) to the EMEL/GenBank/DDBJ databases.

BRBL; ARSO733; ALUS919;1;1.

InterPool, IRRO0150; 3-1ide.

InterPool, IRRO0150; 3-1ide.

InterPool, IRRO0150; 3-1ide.

InterPool, IRRO0150; 3-1ide.
 092089 PRELIMINARY; PRT; 111 AA.
092089,
01-DEC-2001 (TrEMELrel. 19, Created)
01-DEC-2001 (TrEMELrel. 19, Last sequence update)
01-DEC-2001 (TrEMELrel. 19, Last sequence update)
01-DEC-2001 (TrEMELrel. 19, Last sequence representation update)
Presin-minicking anti-idiotope kappa chain variable region
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 SEQUENCE FROM N.A.
 NCBI_TaxID+10090;
 Mus musculus (Mouse).
 (Fragment)
63 PARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 3 VLTQSPASIAVSLGQRATISCRASESVDSYGYNFMHWYQQIFGQPFKLLIYRASNLESGI 62
 VLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGV
 12046 MW; 1E46988AA6858526 CRC64;
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 Gaps
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QSUL78

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 RESULT
Q9JL80
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 Query Match
Best Local S
Matches 79
 OPULTS: FRET, 109 AA.

OPULTS: Created
01-MAY-2000 (TERMILTE: 1.3 Leat sequence update)
01-MAY-2000 (TERMILTE: 2.3 Leat sequence update)
01-MAY-2000 (TERMILTE: 2.3 Leat annotation update)
MOSIN-reactive immunoglobulin light chain variable region
(Fragment).
 (1)
SEQUENCE FROM N.A.
MEDILINE-98277119; PubMed=9614934;
Fin B., Van der Merwe P.L.,
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PSS0835; IG_LIKE; 1.
 ""-Cell-dependent antibody response to the dominant
streptococcal polyacoharide, N-acetyl-glucosamine,
with cardiac myosin, "pose (2000).
Infect. Immun 68:5803-5808 (2000).
BMBL, Ar206026; ANTE 9924.1; ".
 "Myosin-reactive autoantibodies in
 Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 Homo sapiens (Human).
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 Bukaryota; Metazoa;
Mammalia; Eutheria;
 01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
Anti-myosin immunoglobulin
 Q9JL80;
01-OCT-2000
 NCBI_TaxID=9606;
 SEQUENCE
 HSSP; P80362; 1WTL.
 Malkiel S., Liao L.,
 MEDLINE=20448942; PubMed=10992488;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Mus musculus (Mouse)
 Q9JL80
 ы
Immunol. Immunopathol. 87:184-192(1998)
AF035036; AAD56272.1; -.
 62
 69
 ь
 79;
 9 ASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIPARESG
 Similarity
 SGSGTDFSLNIHPVEEDDIAMYFCQQSRKVPWTFGGGTKLEIK 103
 SGSRTDFTLTINPVBADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 ASLAVSLGQRATISCRASESVEYYGTSLMQWYQQKPGQPPKLLIYAASNVESGVPARFSG
 103
103 AA;
 Conservative
 PRELIMINARY;
 103
 11224 NW;
 Rodentia;
 Chordata;
 70.5%; Score 412; DB 11; 76.7%; Pred. No. 2.2e-39;
 Cunningham M.W.,
 10;
 , Last sequence update)
, Last annotation update)
light chain variable region
 Created)
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
 EC87D653DB3AAB21 CRC64;
 PRT;
 Mismatches
 rheumatic
 Kalis N.N., Berney S.M.,
 103
 Diamond B.;
 8
 carditis and normal
 14;
 Length
 Indels
 epitope of
is cross-reactive
 103;
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 Gaps
 60
 83
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 Matches
 Query Match
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 Query Match
 Q9UL70;
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 01-MAY-2000 (TYEMBLYE1. 13, Created)
01-MAY-2000 (TYEMBLYE1. 13, Last sequence update)
01-MAR-2003 (TYEMBLYE1. 23, Last samotation update)
01-MAR-2003 (TYEMBLYE1. 23, Last samotation update)
Myosin-reactive immunoglobulin light chain variable
 MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Young D.C.;
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
NON_TER 109 109
 SEQUENCE
 Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
 InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 EMBL; AF035044; AAD56280.1;
HSSP; P01607; 1REI.
 fetus."
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 NCBI_TaxID=9606;
 Homo sapiens (Human)
 SEQUENCE
 HSSP; P80362; NTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_v.
 ROSITE; PS50835;
 SEQUENCE FROM N.A.
 (Fragment).
 60
 64 ARFSGSGSKTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLBIKR
 Immunol. Immunopathol. 87:184-192(1998)
 88
 61 GIPARESGSGSRTDFTLTINFVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 4
 4 LTQSPASLAVSLGQRATISCRASESVDSYGYNEMHWYQQIPGQPPKLLIYRASNLESGIP
 1 Similarity
67; Conser-
 71;
 1 ENVLTOSPASIAVSIGORATISCRASESVDSYGYNFMHWYQQIPGOPPKILIYRASNLES
 MTQSPSSLSASVGDRVTITCRASQGIS----NYLAWYQQKPGKVPKSLIYAASTLQSGVP
SRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIKR
 ĠĬPDŔŔŚĠŚĠŚĠŦĎŔŦĹŦĬSRLEPEĎĊĂVŶŶĊQQYGSSPĹŦŔĠĠĠŤKVEĬKŔ
 BIVITQSPGTLSLSPGERATISCRASQSVSS---SYLAWYQQKPGQAPRLLIYGASSRAT
 108 AA;
 109 AA;
 108
 Conservative
 Conservative
 PRELIMINARY;
 IG_LIKE;
 61.3%;
 11633 MW; B7BEDC3E41FCCA37 CRC64;
 11646 MW;
 61.4%;
 19,
 17;
 Score 358;
Pred. No. 3
 Score 358.5; DB 4
Pred. No. 3.1e-33;
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 5F675C52EC7EE197 CRC64;
 Mismatches
 Mismatches
 Kalis N.N., Berney
 chain variable
 108
 DB 4;
3.5e-33;
 ₹
 DB 4;
 21;
 Length 108;
 Indels
 Indels
 Length
 region
 109;
 112
 3,
 4,
 Gaps
 Gaps
 59
 57
```

RESULT 5 Q96SA9 ID Q96S

Q96SA9

PRELIMINARY;

PRT

107

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SEQUENCE

108 AA;

11738 MW;

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RESULT 6
Q9UL77
 S
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 Query Match
Best Local S
Matches 69
 EMBL; U96396; AAB60785.1; ...
Interpro; IPR007110; Ig-like.
Interpro; IPR003906; Ig MRC.
Interpro; IPR003596; Ig-v.
Pfam; PF00047; ig 1.
SMART; SM00466; IGv; 1.
Pfam; PF00047; ig; 1. ~~
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 108 108
 Q96SA9;
01-DEC-2001
01-DEC-2001
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 01-MAY-2000 (TERMELrel. 13, Created)
01-MAY-2000 (TERMELrel. 13, Last sequence update)
01-MAR-2003 (TERMELrel. 23, Last ampotation update)
Myosin-reactive immunoglobulin light chain variable
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 EMBL; AF035037; AAI
HSSP; P01607; 1REI.
 Wu X., Liu B., Van der Merwe P.L.,
 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
 Q9UL77
 01-DEC-2001 (TREMBLZel. 19, Created)
01-DEC-2001 (TREMBLZel.) J. Last sequence update)
01-MAR-2003 (TREMBLZel. 23, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa
variable, region [Fragment)
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 Young D
 NCBI_TaxID=9606;
 Homo sapiens (Human)
 (Fragment).
 SEQUENCE
 SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
 antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
 Adderson B.B., Shikhman A.R., Ward K.B., Cunningham M.W., Wolecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamins/anti-myosin
 SEQUENCE FROM N.A.
MEDLINE=98375893; PubMed=9712075;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 ON TER
 NCBI_TaxID=9606;
 Homo sapiens (Human).
 Immunol. Immunopathol. 8
AF035037; AAD56273.1; -.
 60
 4
 4
 Similarity
 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLBIKR 112
 WTQSPSSLSASVGDRVTITCRASQSISSY----LNWYQQKPGKAPKLLIYAASSLQSGVP
 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIFGQPPKLLIYRASNLESGIP
 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQS-YSTLTFGGGTKVBIKK
 107
107 AA;
 PRELIMINARY;
 Conservative
 Primates;
 Chordata;
 11520 MW; 4BB43E9C5B577F16 CRC64;
 61.2%;
 20;
 87:184-192(1998)
 Score 357.5;
Pred. No. 3.9
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Mismatches
 Kalis N.N.,
 108 AA.
 .9e-33;
 DB 4;
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 Berney S.M.,
 Indels
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 107;
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 Gaps
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RESULT 8
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 RESULT 7
Q8NEK1
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 Query Match
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 Submitted (UTN-2002) to the EMB
EMBL; BCO30813; AM330813; 1; -...
InterPro; IPR007110; Ig-like
InterPro; IPR003597; Ig. c1.
InterPro; IPR003597; Ig. MC.
InterPro; IPR003595; Ig. MC.
 QBVCI6;
 Q8NEK1;
01-OCT-2002
01-OCT-2002
 01-MAR-2002 (TIEMBLIFEL 20, Cr. 01-MAR-2002 (TIEMBLIFEL 20, La. 01-MAR-2003 (TIEMBLIFEL 23, La. 101-MAR-2003 (TIEMBLIFEL 23, La. Hypothetical 26.2 kDa protein. Mus musculus (Mouse)
 Bukaryota; Metazoa;
Mammalia; Butheria;
TISSUE=Colon;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Hypothetical
SEQUENCE 2:
 PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; 1.
 Pfam; PF00047; ig; 2.
SMART; SM00407; IGcl; 1.
SMART; SM00406; IGV; 1.
 Strausberg
 TISSUE=Lung;
 NCBI_TaxID=9606;
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 Hypothetical protein.
Homo sapiens (Human).
 01-MAR-2003
 Q8NEK3
 SEQUENCE FROM N.A.
 Local Similarity
 77
 61
 21
 60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIKR
 64 ARFSGSGSRIDFILTINEVEADDVATYYCQQSNEDELIFGTGTRLEIKR
 67;
 1 ENVLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLES
 70;
 4
 4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP
 Similarity
 GVPARFSGSGSGTEFTLTÍSSLQSEDFÁVÝÝCQQYNKWPHTFGQGTKLDIKR
 GIPARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDPLTFGTGTRLSIKR
 EIVMTQSPATLSVSPGERATLSCRASQSVTSN----LAWYQQTPGQSERLVIYGASSRAS
 MTQSPSSLSASVGDRVTITCRASQSISSY----LNWYQQKPGKAPNLLIYAASSLQSGVP
 234 AA;
 (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
 Conservative
 PRELIMINARY;
 protein
 PRELIMINARY;
 Conservative
 Chordata; Craniata; Vertebrata;
Rodentia; Sciurognathi; Muridae,
 Chordata; (
Primates;
 25530 MW;
 61.0%;
 to the EMBL/GenBank/DDBJ
 61.1%;
 22,
 20;
 20;
 Last sequence update)
Last annotation update
 Score 356;
Pred. No. 1
 Last sequence update)
Last annotation update)
 Created)
 Score
Pred.
 Sciurognathi; Muridae; Murinae;
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 PRT;
 6316E8DEF8D132F8 CRC64;
 C06681716C4D16F3 CRC64
 Mismatches
 Mismatches
 357; DB 4;
No. 4.5e-33;
 234
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 Length 234;
 Length 108;
 Indels
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Best Local Similarity
 Matches
 InterPro; IPB00359; Jg.
InterPro; IPB00310; Jg.1ike
InterPro; IPB003106; Jg.MMC.
InterPro; IPB003506; Jg.WC.
InterPro; IPB003506; Jg.Y.
Ffam; PR0047; Jg; J.
SMART; SM00406; IGV; J.
FM03ITE; PR05063; IGV; J.
FM03ITE; PR05063; IGV; J.
 Submitted (DEC-2011) to the EMBL. BC019760.1; --
InterPro. JPR000306; Ig_WBC.
InterPro. JPR000306; Ig_V.
Feam. PF00047; Ig; 2
SMART, SM0006; IG; 17
BP00147; Ig; 2
SMART, SM00106; IG; 17
BP00147; IG; 18
BP00147; IG; 18
BP00147; IG; 18
BP00147; IG; 18
BP00147; IG; 18
BP00147; IG; 18
BP00147; IG; 18
BP00147; IG; 18
BP00147; IG; 18
BP00147; IG; IG; 18
BP00148CB 23B A; 2624 WW;
Q9UL81;
 0.1-001-2002 (TrBHBLrel. 22, Created)
0.1-001-2002 (TrBHBLrel. 22, Last mequance update)
0.1-002-2002 (TrBHBLrel. 23, Last mediation update)
0.1-002-2002 (TrBHBLrel. 23, Last mediation update)
0.1-002-2002 (TrBHBLrel. 23, Last mediation update)
0.1-002-2002 (TrBHBLrel. 23, Last mediation update)
0.1-002-2002 (TrBHBLrel. 22, Created)
0.1-002-2002 (TrBHBLrel. 22, Last mediated)
0.1-0
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Q8K1F2;
01-OCT-2002
 NCBI_TaxID=10090;
 Q8K1F2
 Strausberg R.;
Submitted (DEC
 Local
 58
 63
 82
 22
 ω
 3 VLTQSPASLAVSLGQRATISCRASESYDSYGYNFWHWYQQIPGQPPKLLIYRASNLESGI
 67; Conserv
 3 VLTQSPASLAVSLGQRATISCRASES-VDSYGYNFMHWYQQIPGQPPKLLIYRASNLESG
 70;
 PARFSGSGSGTSYSLTISRMEAEDAATYYCOORSSYPLTFGAGTKLELKR
 PARFSGSGSRTDFTLTINFVEADDVATYYCQQSNBDPLTFGTGTRLEIKR 112
 VPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPTFGGGTKLEIKR 132
 IPARFSGSGSRTDETLTINPVEADDVATYYCQQSNEDPLTFGTGTRLBIKR 112
 VMTQTELSLEVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKEGQSEKLLIYKVSNRFSG
 112 AA; 11953 MW; 4716B87FADB543ED CRC64;
 Conservative
 PRELIMINARY
 Conservative
 PRELIMINARY;
 60.0%;
 26224 MW;
 60.4%;
 15;
 Score 350.5; In Pred. No. 2.6e-
 EMBL/GenBank/DDBJ databases.
 Score 352.5;
Pred. No. 4.1
 PRT;
 35EC08E3DE5414AD CRC64
 Mismatches
 107
 112
 4.1e-32
 6e-32;
 ž
 DB 11; Length 112;
 DB 11; Length
 21;
 Indels
 Indels
 5
 1;
 Mus
 Gaps
 62
 57
 61
 81
```

Query Match
Best Local Similarity
Matches 69; Conserv

Conservative

59.5%;

Score 347.5; DB Pred, No. 1.5e-31 L6; Mismatches 2

DB 11; Length

238; 1,

Gaps

**#** 

Pfam; PF00047; 1g; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG\_LIKE; 2.
PROSITE; PS00290; IG\_MHC; 1.

Hypothetical protein. SEQUENCE 238 AA; 2

26344 MW;

FB2B06A0B801330A CRC64;

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RESULT 11
Q99M37
 S
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 PT DE RETERMENT
 Query Match
Best Local S
Matches 66
 InterPro; IPRO07110; Ig-1ike.
InterPro; IPRO07006; Ig MHC.
InterPro; IPRO07006; Ig_W.
InterPro; IPRO0706; Ig_V.
Ffam; PF00047; ig; 1.
SMART; SM0406; IGV; 1.
PRO0717B; PS50835; IG_LIKE; 1.
 Q99M37;
01-JUN-2001
01-JUN-2001
 Hypothetical 26.3 kDa protein.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Czaniata; Vertebrata; I
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae;
 NON TER
NON TER
SEQUENCE
 EMBL; BC002035; AAH02035.
HSSP; P01679; 2FBJ.
 Submitted (JAN
 01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
 Q99M37
 01-MAY-2000 (TERMELRel. 13, Created)
01-MAY-2000 (TERMELRel. 13, Last sequence update)
01-MAY-2003 (TERMELRel. 23, Last amnotation update)
Myosin-reactive immunoglobulin light chain variable
(Fragment).
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 NCBI_TaxID=10090;
 EMBL; AF035033; AF
HSSP; P01607; 1REI
 Young D.C.;
"Myosin-reactive autoantibodies in rheumatic
 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 Homo sapiens (Human).
 NCBI_TaxID=9606;
 EQUENCE FROM N.A.
 60
 64
 4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP 63
 Similarity
 SRESGSGSGTDFTLTISGLQAEDFATYYCQQS-YSALTFGPGTKVDIRR 107
 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR
 MTQSPSSLSASVGDRVTITCRASQSIS----NYLNWYQQKPGKAPNLLIYAASSLQSGVP
 (JAN-2001) to the
 107 AA;
 107
 PRELIMINARY;
 Conservative
 Immunopathol. 87:184-192(1998)
; AAD56269.1; -.
 11501 MW;
 Chordata;
Primates;
 59.8%; Score 349.5;
60.6%; Pred. No. 3.20
tive 23; Mismatches
 EMBL/GenBank/DDBJ databases
 Last
 Created)
 Last
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 070549FDE0754748 CRC64;
 annotation update
 sequence update)
 Kalis N.N.,
 3.2e-32;
 A
 DB 4; Length 107;
 carditis
 Berney
 Euteleostomi;
; Murinae; Mus
 region
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 59
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22

81

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RESULT 12

0841F3

10 0841F3

10 0841F3

10 0841F3

10 0941F3

10
 RESULT 13
Q9UL83
 RRA RP OCC OCC DE TOTO
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 8
 Ś
 밁
 Query Match
Best Local &
Matches 68
Wu X., L.,
 Q8K1F3;
01-OCT-2002
01-OCT-2002
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
 Q9UL83;
01-MAY-2000
 NON TER
 STRAIN-BAIB/C; TISSUB-Hyperimminized spleen;
Zhou X. -X. TSQUCHH H. Flanque S., Karle S., Nishiyama Y., Raul S.;
Thomat proteolytic artibodies; Failed D-VIPase response to the D-
entantioner of UT and identification of L-VIPase Response to the D-
submitted (MY-2002) to the EMEL/GenBank/DDBJ databases.

EMBL, AFSIZES, AAM64200.1 :-MIC.
INTERPRO, IPRO10369; JS.
INTERPRO, IPRO10366; JS.—Nike.
INTERPRO, IPRO10366; JS.—MC.
 01-007-2002 (TERMINE). 22, Created)
01-007-2002 (TERMINE). 22, Last sequence update)
01-007-2002 (TERMINE). 23, Last samovation update)
Auti-117Base light chain variable region (Fregment).
Mus muscollus (Mouse).
 MEDLINE=98277139;
 Homo sapiens (Human).
 Q9UL83
 SEQUENCE FROM N.A.
 SMART; SM00409; IG; 1.
SMART; SM00406; IGV; 1.
 (Fragment)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Q8K1F3
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 58
 83
 82
 62
 Liu B.,
 ω
 68;
 Similarity
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 PARFSGSGSGTSYSLTISSMEAEDAATYYCQQYHSYPYTFGGGTKLEIKR
 PARTSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 VLTQSPAIMSASPGEKVTISCSASSSV----SYMYWYQQKPGSSPKPWIYRTSNLASGV
 VPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGTKLBIKR 132
 IPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR
 112 AA;
 Conservative
 PRELIMINARY;
 PRELIMINARY;
 Van
 PubMed=9614934;
 der
 Chordata;
Primates;
 59.2%;
61.8%;
 12017 MW;
 Merwe
 15;
 P.L.,
 Score 345.5;
Pred. No. 9.
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 PRT;
 PRT;
 22DD75B5414CDB18 CRC64;
 Mismatches
 Kalis
 108
 112
 9.8e-32;
 N.N.
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 DB 11;
 22;
 Berney
 Indels
 Length
 region
 S.M.
 5.
 112
 Gaps
 57
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문

60

PARFSGSGSGTSYSLTISSMEAEDAATYYCQQYHSYPRTFGGGTKLEIKR

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RESULT 14
Q8K1F1
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 STIRREDERENT
 Query Match
Best Local S
Matches 69
 Query Match
Best Local Similarity
Matches 67; Conserv
 Q8K1F1;
01-OCT-2002
01-OCT-2002
 NON TER
 NON TER
 Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae,
 PEam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE;
 Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGV; 1.
 STRAIN-BALB/c; TISSUE-Hyperimmunized spleen
 01-00T-2002 (TERMBLFel. 22, Created)
01-00T-2003 (TERMBLFel. 22, Last sequence update)
01-00R-2003 (TERMBLFel. 22, Last sequence update)
01-00R-2003 (TERMBLFel. 23, Last sanotation update)
Anti-VIPase light chain variable region (Fragment).
 Q8K1F1
 EMBL; AF035031; AAD!
HSSP; P80362; 1WTL.
 SEQUENCE
 PROSITE;
 NCBI_TaxID=10090;
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 "Myosin-reactive autoantibodies
fetus.";
 EQUENCE FROM N.A.
 63
 w
 ω
 57 GIPARFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNNWPFTFGPGTKVDIKR
 61
 Immunol. Immunopathol. 87:184-192(1998)
 μ
 ,_
 69;
 Similarity
PARESGSGSRTDFTLTINEVEADDVATYYCQQSNBDPLTFGTGTRLBIKR
 VITQSPAIMSASPGEKVINTCRASSSVSS---SYLHMYQQKSGASPKLMIYSTSNLASGV
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIPGQPPKLLIYRASNLESGI 62
 PSS0835;
 GIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR
 EIVMTQSPATLSVSPGERATLSCRASQSVSSN----LAWYQQXPGQAPRLLIYCASTRAT
 ENVLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLES
 108
 114 AA,
 Conservative
 108
 Conservative
 AA,
 AAD56267.1;
 12162 MW; 8BD9833DBF3EEFD1 CRC64;
 11834 MW;
 59.0%;
 59.1%; Score 345; DB 4; 61.6%; Pred. No. 1.1e-31;
 17;
 17;
 Score 344.5; DB 11; Length Pred. No. 1.3e-31;
 9F9C5A92EBA96EEA CRC64;
 Mismatches
 Mismatches
 in rheumatic carditis and normal
 114
 DB 4; Length 108
 ż
 Indels
 Indels
 Euteleostomi;
; Murinae; Mus
 <u>υ</u>
 4;
 Gaps
 Gaps
 59
 86
```

RESULT 15 Q8NEKO

```
DORREO PREJIGIANAY, PRT, 239 AA.

AC GANEKO, PREJIGIANAY, PRT, 239 AA.

AC GANEKO, PREJIGIANAY, PRT, 239 AA.

AC GANEKO, 2002 (TERMELTEL, 22, Last sequence update)

DT 01-OCT_2002 (TERMELTEL, 23, Last annotation update)

DT 01-OCT_2002 (TERMELTEL, 23, Last annotation update)

DT 01-OCT_2002 (TERMELTEL, 23, Last annotation update)

DE HOWERS (2002 (TERMELT), L
```

p64-k4 protein pro Light chain of MuM Synthetic antibody Antibody scrv8 lig Synthetic antibody Monoclonal antibod

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OM protein -
protein search, using sw model
 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
```

Title: Perfect score: 1 ENVLTQSPASLAVSLGQRAT.....QQSNEDPLTFGTGTRLEIKR 112 November 7, 2003, 07:21:17; Search time 48.2991 Seconds ("vithout alignments) 368.069 Million cell updates/sec US-09-661-992B-86\_COPY\_138\_249

Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62

sequence:

Run on:

1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 9                  | 00                 | 7                  | o.                 | υı                 | 4                  | w                  | N                  | -                  | Result<br>No.               |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-----------------------------|
| 528                | 531                | 542                | 542                | 543                | 569                | 573                | 573                | 584                | Score                       |
| 90.4               | 90.9               | 92.8               | 92.8               | 93.0               | 97.4               | 98.1               | 98.1               | 100.0              | Query                       |
| 131                | 111                | 112                | 112                | 249                | 325                | 732                | 294                | 249                | Query<br>Match Length DB ID |
| 17                 | 15                 | 23                 | 12                 | 22                 | 22                 | 22                 | 22                 | 22                 | 8                           |
| AAW01143           | AAR47494           | ABB77332           | AAR13089           | AAB20436           | AAB20438           | AAB20437           | AAB20442           | AAB20435           | Ħ                           |
| MAD 1.4 light chai | Murine anti-CD18 A | Mouse 184 light ch | Murine 184 light c | Anti-FIX/FIXa anti | Anti-FIX/FIXa anti | Anti-FIX/FIXa anti | Anti-FIX/FIXa anti | Anti-FIX/FIXa anti | Description                 |

| 45       | 44    | 43           | 42    | 41   | 40   | 39     | 38    | 37   | 36           | 35           | 34   | 33   | 32   | 31   | 30           | 29  | 28  | 27 | 26  | 25  | 24  | 23   | 22   | 21     | 20   | 19    | 18    | 17   | 16   | 15   | 14 | 13   | 12     | 11   | 10 |
|----------|-------|--------------|-------|------|------|--------|-------|------|--------------|--------------|------|------|------|------|--------------|-----|-----|----|-----|-----|-----|------|------|--------|------|-------|-------|------|------|------|----|------|--------|------|----|
| 7        | 7     | œ            |       | 9    | 9    | w      | 9     | 9    | 9            | 9            | w    | S    | w    | 4    | LO           | 0   | 0   | 0  | 0   | 0   | 0   | 0    | 0    | 0      | -    | ۰     | -     | *    | -    | K3   | 14 | N    | 4.4    | 526  | K) |
| :-       | ٢     | Ψ            | ۳.    | ۳    | 4.   | 4.     |       |      | 4            |              | 4.   | 4    | 4.   | 4.   | 5            | ŗ   | ū   | 5  | 5   | 6   | 6.  | •    | 7    | ?      | 7.   | .7    | œ     |      | 8    | ۴    | 9  | 0    | 0      | 90.1 |    |
| o        | 0     | N            | w     | 0    | 9    | ~      | S     | 4    | $\mathbf{H}$ | $\mathbf{r}$ | -    | -    | g,   | w    | $\mathbf{L}$ | ,   | -   | N  | ₩.  | w   | W   | N    | 1    | 6.3    | N    | N     | -     | -    | 1    | w    | w  | tn   | 1      | 112  | w  |
| 22       | 22    | 22           | 14    | 18   | 22   | 17     | 17    | 17   | 16           | 16           | 18   | 23   | 16   | 12   | 15           | 18  | 17  | 15 | 16  | 23  | 14  | 15   | 16   | 15     | 17   | 17    | 24    | 24   | 12   | 18   | 13 | 22   | 22     | 22   | 19 |
| AAU07492 | U0749 | <b>B7084</b> | R3771 | 2735 | 7241 | AW0229 | W0229 | 0229 | 7915         | 20           | 2735 | 7733 | 7761 | 1092 | 6081         | 901 | 083 | 13 | 915 | 972 | 334 | 4862 | 6517 | AR4861 | 0927 | W0925 | P9677 | 9676 | 1053 | 3027 | Ō  | 0749 | .00751 | 0748 | 'n |
|          |       |              |       |      |      |        |       |      |              |              |      |      |      |      |              |     |     |    |     |     |     |      |      |        |      |       |       |      |      |      |    |      |        |      |    |
|          |       |              |       |      |      |        |       |      |              |              |      |      |      |      |              |     |     |    |     |     |     |      |      |        |      |       |       |      |      |      |    |      |        |      |    |
|          |       |              |       |      |      |        |       |      |              |              |      |      |      |      |              |     |     |    |     |     |     |      |      |        |      |       |       |      |      |      |    |      |        |      |    |

chinetic Mab 9.2.2
TSH receptor antib
TSH receptor antib
Moncolonal antibod
Monborolonal antibod
Mab MM-01 light ch
Sequence of the mo
Murine NM-01 variab
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#### ALIGNMENTS

Yeast-FvKC-II VL region.
Yeast-FvKC-II-KEX2
FvKC-II-KEX2. Chi
Double-head antibo
Light chain variab
Mouse 4C10 anti-id

FvKC-II VL region. Monoclonal antibod

Synthetic antibody Synthetic antibody SNV-env leader/hum

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|---|---|---|
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|   | S | μ |
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|   |   |   |

AAB20435 standard; Protein; 249 AA.

AAB20435;

21-JUN-2001 (first entry)

Anti-FIX/FIXa antibody 198/AB2 scFv.

Factor IX; FIX; Factor IXa; FIXa; scPv; antihody; procosquilant; Factor VIII cofactor; blood cosquiation disorder; haemophilia h; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

Chimeric -Chimeric -Mus musculus. Synthetic.

Key Protein 22-MAR-2001. WO200119992-A2 Region Region Protein Peptide /label= VH 98..102 /label= CDR3 230..238 'label= VL 137..249 23..136 /label= Linker Location/Qualifiers abel= CDR3

```
RESULT 2
AAB20442
멍
 몆
 Ś
 S
 or The present sequence is that of a single chain PV (scPV) derivative of antiboly 199/AB2, comprising the heavy (PH) and inject (PU) chain variable regions of 199/AB2 joined by an artificial, flexible linker peptide. The scPV was obtained by PCR amplification of cDNAs for 199/AB2 WH and VL regions and cloning in vector pDnP2. 199/AB2 is an transple of PH1. Immanis actors IX FDY)/AB2 is contracted accors IX (FDXA) (PH2) and CONTRACT (FDXA) (PH2) and CONTRACT (FDXA) (PH2) and CONTRACT (FDXA) (PH2) and CONTRACT (PH2) and C
 Query Match
Best Local S
Matches 112
 Chimeric
Chimeric
Protein
 Peptide
 Factor IX, FIX, Factor IXa, FIXa, scby, antibody, procequilant, Factor VIII cofactor, blood cogulation discorder, haemophilia h, haemorrhagic diathesis; haemostatic; amidolytic; cherapy; mouse;
 New factor IX/factor IXa antibodies and their derivatives useful for
increasing amidolytic activity of factor IXa, and for treating blood
coagulation disorders such as haemophilia A and baemorrhagic diathesis
 Chimeric
 myc-tag
 Anti-FIX/FIXa antibody 198/B1-myc-tag fusion
 21-JUN-2001
 AAB20442 standard; Protein;
 Sequence
 Claim 12; Fig 16; 138pp; English.
 Scheiflinger F, Kerschbaumer
 13-SEP-2000; 2000WO-EP08936
 (BAXT) BAXTER
 Local Similarity
 138
 2001-290358/30
 61
 112;
 GIPARTSGSGSRTDFTLTINFVEADDVATYYCQQSNEDPLTFGTGTRLEIKR
 GIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLBIKR 112
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 AAF30725
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 Mus musculus.
Synthetic.
 249 AA;
 Conservative
 (first entry)
 AG
 99AT-0001576
/label= Signal_peptide
23..294
 Location/Qualifiers
 100.0%;
 0;
 Score 584; DB 22;
Pred. No. 2.2e-42;
; Mismatches 0;
 ×
 Falkner
 Dorner
 Indels
 Length
 'n
 249;
 0
 Gaps
 197
 60
```

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63

PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112

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 2222222222222
 3333
 Comparising the heavy (WH) and light (WL) derivative of antibody 198/BL comprising the heavy (WH) and light (WL) chain variable regions of comprising the heavy (WH) and light (WL) chain variable regions of comprising the heavy (WH) and light (WL) chain variable regions of comprising the heavy (WH) and light (WL) chain variable regions of comparison of the comparison of the second of the comparison of the second of the comparison of the second of the comparison of the second
 Query Match
Best Local Similarity
Matches 110; Conserv
 Sequence
 New factor IX/factor IXa antibodies and their derivatives useful for
increasing amidolytic activity of factor IXa, and for treating blood
coagulation disorders such as haemophilia A and haemorrhagic distincts.
 Protein
 Example 18; Fig 34; 138pp; English.
 WPI; 2001-290358/30.
N-PSDB; AAF30732.
 Scheiflinger F,
 14-SEP-1999;
 13-SEP-2000; 2000WO-EP08936
 WO200119992-A2.
 Peptide
 Peptide
 Protein
 Peptide
 Region
 Peptide
 Misc-difference
 (BAXT) BAXTER AG
 162
 ω
VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIPGQPPKLLIYRASNLESGI
 294 AA;
 Conservative
 99AT-0001576
 287.
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 /label= His_tag
 /label= Spacer
 160.
 145..159
 /label= VH
 /label= scFv
23..144
 /label= Mature_protein
23..271
 'label= Spacer
 /label= VL
 'label= Linker
 note= "encoded by GGN"
 labe1=Myc_tag
 98.1%; Score 573; DB 22;
100.0%; Pred. No. 2.3e-41;
 . 288
 .286
 271
 0
 Mismatches
 Falkner F,
 0,
 Dorner F;
 Length 294;
 Indels
 0
 Gaps
 223
 62
```

```
RESULT 3
AAB20437
 The present sequence is that of a fusion procein comprising, a Pell Beader; a single chain Py (serv) derivative of antibody 198/81 comprising the heavy (WH) and light (WL) chain variable regions of 198/B1 joined by an artificial flexible linker pedid; a spacer; Becherichia coli alkaline phosphataes; and a C-peminal dr; a spacer; affinity tail. 198/B1 is an example of anti-human Ractor IX (PIX) /Activated Pactor IX (PIX) antibodies of the invention. Anti-FXX/FIXa antibodies and their derivatives, including scrytagenits, have FVIIIa cofactory activity or FIXa activating tragments, have FVIIIa cofactory activity or FIXa activating.
 New factor IX/factor IXa antibodies and their derivatives useful for
increasing amidolytic activity of factor IXa, and for treating blood
coagulation disorders such as haemophilia A and haemorrhagic diathesis
 Example 16; Fig 26; 138pp; English.
 N-PSDB; AAB30727
 Scheiflinger F, Kerschbaumer
 14-SEP-1999;
 13-SEP-2000; 2000WO-EP08936
 22-MAR-2001.
 Peptide
 Misc-difference
 (BAXT) BAXTER
 WO200119992-A2
 Protein
 Peptide
 Region
 Peptide
 Protein
 Protein
 Peptide
 Chimeric
 Chimeric
 Chimeric
 alkaline
 haemorrhagic diathesis;
 Anti-FIX/FIXa antibody 198/81-alkaline phosphatase
 21-JUN-2001
 AAB20437 standard; Protein; 732
 factor
 factor
 2001-290358/30.
 IX, FIX; Factor IXa; FIXa; scPv; antibody; procespilant;
VIII cofactor; blood cospilation disorder; heemophilia A;
rhagic diathesis; haemostatic; amidolytic; therapy; mouse;
 phosphatase.
 Administration leads
 Escherichia coli.
 Synthetic
 Mus musculus.
 (first entry)
 AG
 99AT-0001576
 /label= Signal_peptide
23..732
 'label= His_tag
 /label= Alkaline_phosphatase
726..732
 276..725
 272..275
 Location/Qualifiers
 note= "encoded by GGN"
 'label= scrv
 'label= Mature_protein
 60..271
 label= VH
 label= Spacer
 Label
 label= Linker
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to an increase in the procoagulant
 3
 Falkner F,
 Dorner F,
 fusion
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 Matches 110;
 Best
 Query Match
 activity of fria, even in the presence of FVIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or TVIIIa, and in the case of FVIII inhibitor patients. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially hasmophilia A and hasmorrhagic distribusis. The scrivalization pharmaceutical transportation for the pharmaceutical composition of the co
WO200119992-A2
 Peptide
 Protein
 Protein
 Peptide
 Misc-difference
 Misc-difference
 Region
 Peptide
 Misc-difference
 Region
 bivalent antibody; plasmid pzip-198AB2#102
 Protein
 Protein
 Peptide
 Chimeric
 Chimeric
 Chimeric -
 Factor IX; FIX; Fax; blood cognitation disorder; proceepilant; Factor VIII coffactor; blood cognitation disorder; hemophilia A; Factor VIII coffactor; blood cognitation disorder; hemophilia A; haemorrhagic disthesis; hemopratic; anidolytic; therapy; mouse; htvoler partybad. e314 discretains and only the companion.
 Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody
 21-JUN-2001
 AAB20438
 AAB20438 standard; Protein; 325
 Sequence
 Local Similarity
 222
 162
 63
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 VLTQSPASLAVSLCQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 Mus musculus.
 Escherichia coli.
 Synchecic
 732 AA;
 Conservative
 (first entry)
 166
 285..319
 /label= Signal peptide
/note= "PelB leader"
 /label= His_tag
 /label= Helix
 /label= Hinge
 'label= Spacer
 /note= "encoded by
 /label= VL
 'label= Linker
 145..159
 note= "encoded
 'label= VH
 'label= Mature_protein
 Location/Qualifiers
 note=
 label= scrv
 98.1%;
 "encoded
 Score 573; DE
; Pred. No. 5.5
0; Mismatches
 0
 ķ
 ý
 ⋧
 TNT
 TCN.
 GON
 5.5e-41;
 DB 22;
 0
 Length 732;
 Indels
 ٥,
 Gaps
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RESULT 5
AAB20436
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 cantibody 199/bi (subblone abg); an amphipathic holical muture and a C-terminal fifst sig. The protein use expressed in tructure Escherichia soli from plasmid psipisyabgilito (see Apr30728).

Mantibody 199/bi is an example of anti-husan factor IX (FIX) /activated Factor IX (FIXa) antibodies of the invention.

Canti-PIX/FIXa antibodies and thoir derivatives have FVIII cofactor activity of FIXa activating activity. Administration leads to an cincrease in the processpallant activity of FIXa, even in the presence of FVIII or FVIIIa, and in the case of FVIII this allows for rapid blood coagulation even in the abstract of FVIII or FVIIIa, and in the case of FVIII calined plantaceutical composition for treating patients with blood obscillation disorders, especially hasmophilia A and hasmorthagic additions in both the state of the case of FVIII is a fire in the state of the case of FVIII in the state of FVIII is an interest of the case of FVIII in the state of FVIII is an interest of the state of the case of FVIII in the state of FVIII is an interest of FVIII in the state of FVIII in the sta
 Query Match
Best Local :
 Matches 109;
 Key
Protein
 Factor IX; FXX; Factor IXa; FXXa; scPv; antibody; procegulant, Factor VIII coffactor; blood coagulation disorder; haemophilia e, haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
 Chimeric
 Chimeric
 Anti-FIX/FIXa antibody 198/A1 scFv.
 21-JUN-2001
 AAB20436;
 AAB20436 standard; Protein; 249 AA.
 Sequence
 The present sequence is that of a bivalent miniantibody comprising a PelB leader peptide, the single chain FV (scFV) fragment of
 New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood
 a PelB leader peptide,
antibody 198/B1 (subclo
 Example 16; Fig 28; 138pp; English.
 coagulation disorders such as haemophilia A and haemorrhagic diathesis
 N-PSDB; AAF30728.
 Scheiflinger F,
 14-SEP-1999;
 13-SEP-2000; 2000WO-EP08936
 22-MAR-2001
 (BAXT) BAXTER AG
 Local Similarity
 222
 162
 2001-290358/30.
 63
 ω
 VLTQXPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 Mus musculus.
Synthetic.
 325 AA,
 Conservative
 (first entry
 99AT-0001576
 Location/Qualifiers
 Kerschbaumer R,
 97.4%;
99.1%;
 0
 Score 569; DB 22;
Pred. No. 5.5e-41;
 Mismatches
 Falkner F,
 1;
 Dorner F;
 Length 325;
 Indels
 0
 Gaps
 221
 0
```

RESULT 6
AAR13089
ID AAR1
XX
AC AAR1
XX
DT 25-M

AAR13089

standard;

Protein; 112

25-MAR-2003 AAR13089;

(updated

밁 δ 밁

141 201

64 ARESGSGSRTDFTLTINEVSADDVATYYCQQSNEDFLTFGTGTRLEIKR 112

ARFSGSGSRTDFTLTINEVEADDVATYYCOOSNEDPLTFGAGTRLEIKR

249

200 S

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FFFFXEXEXEXEXEXEXERXEFFEXEXSOOOOOOOOO
 it the present sequence is that of a single chain by (scFy) darystive of antiboly 190/Al, computising the heavy (VI) and light (VI) chain or variable regions of 190/Al joined by an artificial, floxible linker occupied. The scFy was obtained by PCR emplification of cDNAs for 190/Al VI and VI, regions and cloning in vector pDAP2. 199/Al is can example of anti-human Factor IX (FIX)/activated Factor IX (FIXa) of antibodies of the invention. Anti-FIX/FIXa and their derivatives, calcivity or FIXa activating activity. Administration leads to an increase in the procession and the case of FVIII and the fixed control of
 Matches
 Query Match
 Sequence
 New factor IX/factor IXa antibodise and their derivatives useful for increasing andolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorthagic disthesis
 Example 10; Fig 17; 138pp; English.
 Misc-difference
 N-PSDB;
 Scheiflinger F, Kerschbaumer
 13-SEP-2000; 2000WO-EP08936.
 WO200119992-A2
 Misc-difference
 Protein
 Peptide
 Region
 (BAXT) BAXTER AG.
 22-MAR-2001
 Local Similarity
 2001-290358/30.
DB; AAF30726.
 105;
 4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP
ITQSPASIAVSIGQRATISCRASESVDSYGKSFMHWYQQKPGQPPKLLIYRASNLESGIP
 249 AA;
 Conservative
 99AT-0001576
 /note= "encoded by GCN"
 /note= "encoded
 /label= CDR3
 /label= VL
 137..249
 123..136
/label= Linker
 /label= CDR3
 93.0%;
 .238
 ζ,
 Score 543; DB 2
Pred. No. 7e-39;
 ×
 Mismatches
 by ACN"
 Falkner
 DB 22;
 'n
 Dorner
 Length 249;
 Indels
 0
 Gaps
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RESULT 7
ABB77332
ID ABB7
XX
AC ABB7
XX
AC ABB7
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AC ABB7
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 Matches
 Query Match
Best Local 9
 Mouse 1B4 light chain variable region
 17-JUN-2002
 ABB77332 standard; Protein; 112 AA
 near the CDRs), a human light chain framework and murine CDRs. It has a mean IC50 nearly equal to that of the murine monoclonal antibody from which the CDRs were derived. It is designated mutated 6al/Rei. The human Ig is capable of binding to a human
 New recombinant immunoglobulin(s) reactive with leukocyte CD18 antigen - comprise human heavy chain framework and murine complementarity regions useful in treatment of inflammation
 See also
 (ATCC HB 10164). The light chain fram human myeloma protein REI (EP-239400).
 A recombinant human Ig comprises a human heavy chain framework and murine CDRs (with the heavy chain framework mutated at sit
 Disclosure; Fig 25; 77pp; English.
 (MERI)
 WPI; 1991-216985/30
 Law MF,
 EP438312-A.
EP440351-A.
 09-JAN-2003
01-OCT-1991
 20-DEC-1990;
19-JAN-1990;
 17-JAN-1991;
 24-JUL-1991
 Monoclonal antibody; complementarity determining region; CDR; integrin; hybridoma 1B4; protein REI; Gal/Rei; Ig.
 Murine 1B4 light chain-2 variable region
 murine CDRs are obtd. from murine hybridoma 1B4
CC HB 10164). The light chain framework is derived
 integrin.
 104;
 63
 63
 ω
 ω
 LAW M
 Similarity
 AAQ12684.
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLBIK 112
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 on 09-JAN-2003 to add missing OS field.) on 25-MAR-2003 to correct PA field.)
 AAQ12682-84
 PARPSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGAGTKLELKR 112
 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQXPGQPPXLLIYRASNLESGI
 Mark GE,
 112 AA;
 Conservative
 (first entry)
 C & CO INC.
 (updated)
(first entry)
 90US-0627421.
90US-0467692.
 91EP-0300367
 Schmidt JA,
 92.8%;
 Score 542; DB 12;
Pred. No. 3.9e-39;
3; Mismatches 3
 Singer II;
 SEQ
 Ä
 No
 37.
 Length 112;
 Indels
 sites
 0
 Gaps
 62
 62
 0
```

```
RESULT 8
ARRA7494
ID ARRA
ID ARRA
XX
XX
AC ARRA
DT 25-W
DT 06-1
XX
XX
XX
MONT
KW MONT
KW COMI
KW JPOLL
XX
XX
Immu
XX
XX
Immu
XX
 Matches 104;
 Query Match
Best Local
 The invention relates to identifying differences (I) in mammalian species specific surface amino acid residues on an immunojohbili which converts the antigenicity of a first menalish species to a second menalish species. The new method is used for identifying the second menalish species. The new method is used for identifying the second menalish species while and replacing immunojohbilin surface amino acid residues while and to second menalish species. The method simultaneously reduces the immunogenicity acterior species. The method simultaneously reduces the immunogenicity acterior method simultaneously reduces the immunogenicity and second menalish structly preserves identifying the present sequence in the case of the primer used in the construction of the "weneversity laters to be present sequences in the case of a real primer used in the construction of the "weneversity laters have yet all the construction of the "weneversity laters have yet in the construction of the "weneversity laters have yet in the construction of the "weneversity laters have yet in the construction of the "weneversity laters have yet in the construction of the "weneversity laters have yet in the construction of the "weneversity laters have yet in the construction of the "weneversity laters have yet in the construction of the present sequence is a bar of a real property of the present sequence is a bar of the present sequence in the present sequence is a bar of the present sequence in the present sequence is a bar of the present sequence in the present sequence is a bar of the present sequence in the present sequence is a bar of the present sequence in the present sequence in the present sequence is a bar of the present sequence in the present sequence in the present sequence is a present sequence in the present sequence in the present sequence in the present sequence in the present sequence in the present sequence in the present sequence in the present sequence in the present sequence in the present sequence in the present sequence in
 Monoclonal antibody; Mab; heavy chain; light chain; constant region; variable region; amplification; priner; polymerase chain reaction; PCR; chimera; Jg; immunoglobulin; humanised antibody; leucocyte; integrin.
 25-MAR-2003
06-JUL-1994
 AAR47494;
 Murine anti-CD18 Ab 60.3 light chain.
 AAR47494 standard; Protein; 111
 Sequence
 Identifying and replacing ; useful for converting the a second mammalian species
 01-MAR-1996;
01-AUG-1997;
 Example 1; Fig 12; 36pp; English
 WPI; 2002-338924/37.
 Daugherty BL,
 (MERI) MERCK & CO INC.
 19-AUG-1993;
 16-MAR-2001; 2001US-0810502
 21-MAR-2002
 US2002034765-A1
 Mouse; human; immunoglobulin; antigenicity; immunogenicity
 63
 63 PARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 Similarity
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGAGTKLELKR
 VLTQSPASLAVSLGORATISCRASESVDSYGNSPMHWYQQKPGQPPKLLIYRASNLESGI
 112 AA;
 Conservative
 mouse 1B4 light chain variable region.
 (updated)
(first entry)
 Mark GE,
 91US-0702217
 96US-0609218.
97US-0905280.
 9308-0109187
 92.8%;
 immunoglobulin surface amino acid residues antigenicity of a first mammalian species to
 Padlan
 3
 Score 542; DB 23;
Pred. No. 3.9e-39;
 Š
 Mismatches
 Ę
 Length 112;
 Indels
 0,
 Gaps
 62
 0
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RESULT 9
AAW01143
ID AAW0
XX
AC AAW0
AC AAW0
DT 10-F
XX
DE MAD
XX
MONC
 Continued memoral antibody corresponding to the murine anti-CD18 antibody (0.3 was prepared. The variable (V) region expunces from both the heavy (H) and light (U) chains were determined from continued to the previous p
 Matches 103;
 Query Match
Best Local :
Monoclonal antibody; phospholipase; myocardial infarction;
 MAb 1.4 light chain, directed against type II phospholipase
 10-FEB-1997
 AAW01143 standard; Protein; 131 AA
 Humanised monoclonal antibodies prepn. - building, by computer database searching
 Sequence
 Disclosure; Page 21; 68pp; English.
 N-PSDB; AAQ55002.
 WPI; 1994-010334/02
 Bajorath J,
 26-MAY-1992;
 24-MAY-1993;
 12-JAN-1994.
 EP578515-A2
 Mus sp
 (Updated
 (BRIM) BRISTOL-MYERS SQUIBB CO.
 Local Similarity
 63
 63
 ω
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 on 25-MAR-2003 to correct PN field.)
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPRTFGGGTKLEIK 111
 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGI
 111 AA;
 Conservative
 Harris LJ,
 (first
 92US-0888233
 93EP-0401328
 entry)
 90.98;
 HSiao K,
 Score 531; DB 15; Length 111;
Pred. No. 3.4e-38;
2; Mismatches 4; Indels
 Ku-Chuan H;

 using comparative model

 FACS analyses
 0
 Gaps
 62
 0
```

```
Matches 101;
 Query Match
 infarction, acute kidney failure, chronic rhemmatism, cardiac short, pancreatitis, adult respiratory distress syndrome and collitis. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2. Spleen cells from the nice were obtained were screened for phospholipase A3 inhibitory activity. Active Clones were isolated Finchiding 1285, 1.4 and 10.1. These were subtracted and the antibody isolated from the culture supernatant by precipitation with ammonium sulphate and purification on a column of protein A sephacose CHB. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is particularly sultable for precipitation testing.
 Sequence
 pancreatitis, cerebral infarction, acute kidney failure; colitis, chronic rheumatism; adult respiratory distress syndrome; cardiac shock; treatment; preclinical testing; disease; hybridoma
 Monoclonal antibodies which inhibit type II phospholipase A2 useful in the treatment of myocardial infarction, cerebral
 Claim 6; Figure 10; 69pp; Japanese.
 Monoclonal antibody inhibiting type II phospholipase A2 activity for treatment of myocardial and cerebral infarction
 WPI; 1996-333946/33.
 Kawauchi Y, Masuho Y,
 (YAMA) YAMANOUCHI PHARM CO LTD
 29-DEC-1994;
 27-DEC-1995;
 11-JUL-1996
 WO9620959-A1
 Binding-site
 Binding-site
 Binding-site
 Mus musculus.
 Local Similarity
 23
VLTQSPASLAVSLGQRATISCRASESVDSYG1SFMHWYQQKPGQPPKLL1YRASNLESG1
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGX
 131 AA;
 Conservative
 94JP-0340006
 95WO-JP02714
 /label= CDR 3
 /label= CDR 2
 /label= CDR 1
 Location/Qualifiers
 ..121
 90.4%;
 Takasaki J,
 5,
 Score 528; DB 17;
Pred. No. 7.2e-38;
 Mismatches
 Yasunaga T;
 3,
 Length 131;
 Indels
 0
 are
 Gaps
 82
 62
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RESULT 10
AAW44168
ID AAW44
16-JUN-1998 (first entry)
 AAW44168 standard; Protein; 131
 83
 63
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 PARESGSGSRTBFTLTINPVEADDVATYHCQQSNEDPFTFGSGTKLEIK 131
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Monoclonal

antibody 1.4 light chain against type II phospholipase A2

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В

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RESULT 11
AAU07480
ID AAU07
XX
AC AAU07
XX
AC AAU07
XX
AC Synth
DE Synth
 8
 8
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 Comment sequence represents the monoclonal antibody 1.4 light chain cagainst type II phospholipase A2 from the present invention. The carbon describes a novel method for the ameliocation of caldiny discorders (such as acute ranal failure) associated with the administration of cisplatin for the treatment of cancer. The method comprises treatment with a monoclonal antibody which inhibits the activity of type II phospholipase A2 (particularly of type II I companies the antibody activity and containing a part of the apparatus of the antibody agreemers. Preferably the antibody again shibits the activity of type II phospholipase A2, and has the ability to cape and/or mouse type II phospholipase A2, and has the ability to cape and/or mouse type II phospholipase A2, and has the ability to cape and the complete antibody against the activity of the same antibody against the apparatus of the cape used its used close antibody against the activity of the same and the same and the same properties which can be used its used close antibody against the same antibody against the same and therefore a laurence and the same activity of the same and the
 Matches
 Query Match
Best Local
 Synthetic antibody scFv(F8) light chain variable region, VL-F8.
 24-0CT-2001
 AAU07480 standard; Protein; 112
 Amelioration of kidney disorders caused by by treatment with an antibody inhibiting
 to be used
 Disclosure; Page 35-36; 74pp; Japanese
 WPI; 1998-076914/07
 Hayashi K, Kawauchi Y,
 19-SEP-1996;
 27-JUN-1997;
 31-DEC-1997
 Unidentified
 Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin amelioration; kidney disorder; nephrotoxicity; anticancer.
 (YAMA) YAMANOUCHI PHARM CO LTD
 27-JUN-1996;
 W09749427-A1
 63
 83
 23
 Similarity
 PARFSGSGSRTDFTLTINFVEADDVATYYCQQSNBDPLTFGTGTRLEIX 111
 VLTQSPASLAVSLGQRATISCRASESVDSYGISFMHWYQQXFGQPPXLLIYRASNLESGI
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLL1YRASNLESGI
 PARFSGSGSRTEFTLTINPVEADDVATYHCQQSNEDPFTFGSGTKLEIK 131
 131
 Conservative
 (first entry)
 96JP-0247635.
96JP-0167286.
 97WO-JP02241
 90.4%;
 Masuho Y,
 Score 528; DB 19;
Pred. No. 7.2e-38;
 Mismatches
 Takasaki
 cisplatin administration
type II phospholipase A2
 ç
 Length 131;
 Indels
 0
 Gaps
 62
 82
 0
```

AAU07516 ID AAU XX AC AAU XX

AAU07516 standard; Peptide; 112

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AAU07516

В

Matches 102; Query Match Best Local:

Similarity

90.1%;

Conservative

2 Score 526; Pred. No. 9.

Mismatches B

1e-38 22;

Length 112; Indels

٥, Gaps

밁 문 8

64

64 ARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDELTFGTGTRLBIKR

ARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDPWTFGGGTKLBIKR

4 LTQSPASLAVSLGQRATISCRASESVDSYGXNEWHWYQQIPGQPPKLLIYRASNLESGIP

LTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKFGQPPKLLIYRALNLESGIP

```
Goldhilli, wo an antibody recurrisaming the many control with the peptides are especially Hermi, Herm 2 Hermi at Braya, Braya, Ches The peptides and control within a variable region of an antibody which makes the antibody of soluble and stable in cytoplasm, peptides inviting the sequences of HPRI to HFRA; HFRA are present within the variable region of the heavy chain of an antibody, covalently linked to the H-CRR; H-CRRA; H-CRRA; in the order (H-RRA)-(H-CRRA
Sequence
 The invention relates to peptides which are able to confer stability and
 Septides which are able to confer stability and solubility to an antibody comprising these peptides, useful for tracking tablelogies (e.g. tumour) associated with accumulation of a molecule inside or outside a human, or animal cell.
 Claim 8; Page 69; 109pp; English
 N-PSDB; AAS11886
 WPI; 2001-502555/55
 Synthetic
 VI-78; seFv(F8); antimicrobial; antiviral; cytostatic; immunomodulatory; antibody; gene therapy; HIV; light chain; human immunodeficiency virus; tumour; metabolic disorder; immune disorder; auto-immune disorder.
 Benvenuto E,
 (CNEN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA. (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL
 30-DEC-1999;
 29-DEC-2000; 2000WO-IT00554
 WO200149713-A2
112 AA;
 Franconi R,
 99IT-RM00803
 Desiderio A,
 Tavladoraki P;
 antibody
 ö
```

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AAU07497
ID AAU
XX
 RESULT 13
 ce solubility to an antibody comprising those periods. The representations of are especially H-FRI,
 Query Match
Best Local Similarity
Matches 102; Conserv
 AAU07497 standard; Protein; 252 AA
 Disclosure; Fig 4; 109pp; English.
 outside a human, or animal cell -
 Poptides which are able to confer stability and solubility to an antibody comprising these poptides, useful for treating pathologies (e.g. rumour) associated with accumulation of a molecule inside or
 Antinicrobial, antivital, cycestatic; immunomodulatory, antibody, gene therapy, HW; human immunodeficiancy virus; tumour; metabolic disorder; immune disorder, auto-immune disorder; lysozyme;
 WPI; 2001-502555/55
 Benvenuto
 30-DEC-1999;
 29-DEC-2000; 2000WO-IT00554.
 WO200149713-A2
 Antibody scFv8 light chain variable region.
 24-OCT-2001
 (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.
 (CNEN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA
 antibody light chain variable region; scFv8.
 invention relates to peptides which are able to confer stability and
 64
 64 ARFSGSGSRTDFTLTINFVBADDVATYYCQQSNEDPLTFGTGTRLBIKR 112
 4
 4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP
 ARPSGSGSRTDPTLTINPVEADDVATYYCÓQSNEDPWTFGGGTKLEIKR 112
 112
 Conservative
 (first entry)
 Franconi R,
 AA,
 99IT-RM00803.
 90.1%;
 Desiderio A,
 Score 526; DB 22;
Pred. No. 9.1e-38;
2; Mismatches 5
 Tavladoraki
 Length 112;
 Indels
 0
 Gaps
 63
 0,
```

뭐 Ś 밁 8

Query Match Sequence

90.1%; Score 526;

DB 22;

252

AA;

```
Peptidgs which are able to confer stability and solubility to an antibody comprising these peptides, useful for treating pathologies (e.g. tumour) associated with accumulation of a molecule inside or
 Example 1; Page 81; 109pp; English.
 outside a human, or animal cell -
 29-DEC-2000; 2000WO-IT00554
 Antimiczobial, antiviral; cytostatic;
immunomodulatory; antibody; gene therapy; HIV; light chain;
human immunodeficiency wiws; twony; metabolic disorder;
immune disorder; auto-immune disorder; scfv(F8);
 WO200149713-A2.
 Protein
 Peptide
 Protein
 Synthetic
 cucumber mosaic virus.
 Synthetic antibody scFv(F8).
 24-OCT-2001 (first entry)
 AAU07497;
 CNEN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA
 CONSORTILE METAPONTUM AGROBIOS SRL.
 Franconi
 /label= Linker_peptide
/note= "This peptide i
 126..140
 /label= VH
 Location/Qualifiers
 'note= "Light chain variable region
 note= "Heavy chain variable region'
 æ
 Desiderio A, Tavladoraki P,
 is specifically claimed in claim 17"
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S
 AAR29008
ID AAR
 밁
 δ
 밁
 S
 Query Match
Best Local S
Matches 101
 Matches
 Best Local Similarity
 The sequences given in AMR22008-09 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interded the feet of the recognises human interded to the recognises human antibody produced the regions which computies 1906 (10) chain and heavy (II) chain variable regions which whorlden allowed from a mouse monoclonal antibody produced from the hybriddens allowed from a mouse monoclonal antibody produced from the whorlden allowed from the plasmids p64-84 and p64-H2.
 Sequence
 Reconstituted human antibody to human interleukin-6 receptor - has low antigenicity and contains mouse V-region complementarity determining regions
 Disclosure; Page 124-125; 207pp; Japanese
 N-PSDB; AAQ30757
 Bendig MM,
 25-APR-1991;
19-FEB-1992;
 24-APR-1992;
 12-NOV-1992.
 25-MAR-2003
 WPI, 1992-398882/48.
 (CHUS) CHUGAI SEIYAKU KK.
 W09219759-A1
 Protein
 Peptide
 Synthetic.
 plasmid; p64-k4; p64-h2
 Human; antibody; interleukin-6; receptor; II-6R; light chain; L; H; heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
 p64-k4 protein product.
 30-MAR-1993
 AAR29008 standard;
 204 ARFSGSGSRIDFTLTINFVEADDVATYYCQQSNEDPWTFGGGTKLEIKR 252
 144
 101;
 64
 102;
 4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP
 Similarity
VLTQSPASLAVSLGQRATISCSASESVDSYGYNFMHWYQQIFQQPPKLLIYRASNLESGI
 LTQSPASLAVSLGQRATISCRASESVDSYGNSFMHMYQQXPGQPPKLLIYRALNLESGIP
 ARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDPLTFGTGTRLBIKR 112
 131 AA;
 Conservative
 Jones ST,
 Conservative
 (updated)
(first entry)
 91JP-0095476
92JP-0032084
 92WO-JP00544
 /note= "Signal peptide"
 Location/Qualifiers
 Protein; 131 AA.
 92.7%;
 93.6%;
 "Mature peptide
 Saldanha
 ω
 2
 Score 524; DB 13;
Pred. No. 1.6e-37;
3; Mismatches 5;
 Pred. No. 2e-37;
 Ĭ,
 Mismatches
 Sato K,
 Tsuchiya
 5
 Length 131;
 Indels
 Indels
 0;
 ç,
 Gaps
 Gaps
 62
 203
 63
 0
```

S

3 VLTQSFASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIFGQPFKLLIYRASNLESGI 62

Query Match Best Local Sim Matches 101;

Similarity

92.7%;

Score 521; DB 18; Pred. No. 2.8e-37; 2; Mismatches 6;

Length 131; Indels

0 Gaps

0,

Conservative

Seguence

131 AA;

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RESULT 15
AAW30278
ID AAW30
XXX
 ΣX
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 밁
 This is the amino acid sequence for the light chain of muMATS.11, a novel antibody which specifically binds to the platelet derived growth beta receptor (FDGF-R beta), but not within the fifth extracellular 3g-like domain, where the antibody inhibits PDGF beta receptor. Be induced proliferation of a cell expressing the PDGF beta receptor. The antibody can be used in a method of inhibiting intumal hyperplasia in the vasculature of a mammal. The antibodies can be used for the treatment of disorders related to PDGF activity such as disorders involving poliferation of smooth muscle cells, and including receptors.
 Antibodies to platelet derived growth factor beta receptor - inhibit
PDGF BB-induced proliferation of cells expressing the receptor, used
particularly for inhibiting intimal hyperplasia
 WPI; 1997-503114/46.
N-PSDB; AAT90985.
 Claim 11; Fig 7B; 87pp; English.
 Chang CN,
 (BOSF) BOEHRINGER MANNHEIM (PROT-) PROTEIN DESIGN LABS
 22-MAR-1996;
 19-MAR-1997;
 09-OCT-1997
 W09737029-A1
 Binding-site
 Binding-site
 Binding-site
 Mus sp.
 MuM4TS.11; antibody; platelet; beta receptor; PDGF-R beta; inhibition; intimal hyperplasia; vasculature; restenosis; angioplasty; light chain.
 Light chain
 07-JUL-1998
 AAW30278;
 AAW30278 standard; Protein; 131 AA
 Protein
 83
 63
 23 VLIQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGI
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPPTFGAGTKLELK 131
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 Landolfi NF,
 of MuM4TS.11
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 96US-0621751.
 97WO-US04198.
 Location/Qualifiers
20..131
 /note= "Complementarity determining region 3"
 112..120
 /note= "Complementarity determining region
 /note= "Complementarity determining region
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 /note=
 "Mature protein"
 Martin U;
 GMBH
 82
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 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 Total number of hits satisfying chosen parameters:
 Searched
 Scoring table:
 sequence:
 Perfect score:
 Title:
 kun on:
 OM protein
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
 ı
 Published Applications Ans.

1 (Sqn2 & forcidate // Dibpas/USO7 PUBCOMB, pep. 8

2 (Sqn2 & forcidate // Dibpas/USO7 MRW PUB pep. 8

3 (Sqn2 & forcidate // Dibpas/USO8 (MRW PUB pep. 8

4 (Sqn2 & forcidate // Dibpas/USO8 (PUBCOMB, pep. 8

6 (Sqn2 & forcidate // Dibpas/USO8 (PUBCOMB, pep. 8

6 (Sqn2 & forcidate // Dibpas/USO8 (PUBCOMB, pep. 9

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18 (Sqn2 & forcidate // Dibpas/USO8 (PUBCOMB, pep. 9

18 (Sqn2 & forcidate // Dibpas/U
 protein search, using sw model
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 U8-09-661-992B-86_COPY_138_249
18-09-661-992B-86_COPY_138_249
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 Gapop 10.0 , Gapext 0.5
 BLOSUM62
 November 7, 2003, 07:30:19; Search time 98.23 Seconds (Without alignments) 195.799 Willion cell updates/sec
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Listing first 45 summaries
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 12
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10 US-09-144-886-81

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2 US-10-166-351-32

2 US-10-166-351-32

2 US-01-44-886-87

10 US-09-144-886-87

10 US-09-144-886-98

10 US-09-144-88-98

10 US-09-144-88-98

10 US-09-144-88-98

10 US-09-144-88-98

10 US-09-144-88-98

10 US-09-144-88

10 US-
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 SUMMARIES
 644079
Sequence 37, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 31, Appl
 Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | SULT 1 -09-810-5 Sequence : Patent No GENERAL API TI                                                                                | 44444444444444444444444444444444444444                                                                                                                                                                                                                                          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| COMPU<br>COMPU<br>CURRE<br>CURRE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 0-502-<br>ce 37,<br>NO. U<br>RAL IN<br>APPLI                                                                                        | 4<br>40<br>40<br>40<br>40<br>40<br>40<br>40<br>40<br>40<br>40<br>40<br>40<br>40                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| CORRESPO<br>STR.<br>STR.<br>STR.<br>STR.<br>STR.<br>STR.<br>STR.<br>STR.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | -502-3: NO. US: NO. US: AL INFO APPLIC TITLE (                                                                                      | 44440044444444444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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COUNTRY: COUNTRY: COUNTRY: COUNTRY: COUNTRY: COUNTRY:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Appl<br>Appl<br>2002<br>ORMA<br>DANT:                                                                                               | 81<br>81<br>81<br>81<br>81<br>81<br>81<br>81<br>81<br>81<br>81<br>81<br>81<br>8                                                                                                                                                                                          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| CORRESPONDENCE A DDRESSEE; P.O. STREET; P.O. CITY; RAMA STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ STATE: NJ 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 0-502-37 ce 37, Applicati No. US200200347 RAL INCORNATION: RALICANT: Padl APPLICANT: Padl Daug Mark TITLE OF INVENT NUMBER OF SEQUE | 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                         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| SEPONDENCE ADDRESS' ADDRESSEE MATCK & STREET: P.O. 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| MERSERS MERCA CO., IL<br>SEET: P.O. BOX 2000, 12:<br>SEET: P.O. BOX 2000, 12:<br>YIE. MU<br>MITEL U.A.<br>WITEL U. |                                                                                                                                     | 1112<br>112<br>113<br>113<br>114<br>115<br>115<br>115<br>115<br>115<br>115<br>115<br>115<br>115                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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| Lincoln<br>Version                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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| Lincoln Ave. Version 2.0b                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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sequence 32, Application US/10169351
Publication No. US20030157090A1
GENERAL INFORMATION
APPLICANT: BENVENUTO, BUGBNIO
APPLICANT: PRANCONI, ROSELLA
 RESULT 3
US-10-169-351-32
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 US-09-144-886-81
 US-09-144-886-81
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 US-09-810-502-37
 Sequence 81, Application US/09144886 Patent No. US20020155114A1 GENERAL INFORMATION:
 Matches 102;
 Query Match
Best Local Similarity
 SOFTWARE: P
 Matches 104;
 Query Match
Best Local Similarity
 NPPLICANT: Marks, James D
APPLICANT: Markedorfex, Feete Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Socialization Memoria
FILL REFERENCE: 2500.117950
CUREENT APPLICATION MOMESTE: 185/09/144,886
CUREENT APPLICATION MOMESTE: 1859-08-31
NUMBER OF 5801 ID NOS: 38
NUMBER OF 5801 ID NOS: 38
 OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: 109 region VL epitope 1
 TYPE: PRT
ORGANISM: Artificial Sequence
 FEATURE:
 LENGTH: 112
 TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
 REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 732-594-3905
 63
 63
 4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIFGQPFKLLIYRASNLESGIP 63
 w
 PatentIn Ver. 2.0
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIFGQPFKLLIYRASNLESGI
 LTQSPASLAVSLGQRAIISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGIP
 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGI
 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGAGTKLELKR 112
 LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
 TOPOLOGY: linear
 TELEFAX: 732-594-4720
 Conservative
 Conservative
 90.2%;
 92.8%;
 2
 Mismatches
 Score 527; DB 10;
Pred. No. 1.9e-42;
 Score 542; DB 9;
Pred. No. 7.2e-44;
 Mismatches
 18410CC
 3; Indels
 Length 112;
 Length 112;
 Indels
 ٥,
 o,
 Gaps
 63
 62
 0
 0,
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APPLICANT:

ANGIOLA

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 US-10-169-351-49
 RESULT 4
US-10-169-351-49
 S
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 OTHER INFORMATION: Description of Artificial Sequence: VL-F8 amino
; OTHER INFORMATION: acid sequenne
US-10-169-351-32
 SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 252
 Matches
 GENERAL INFORMATION:
 Sequence 49, Application US/10169351
Publication No. US20030157090A1
 NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIA VET. 2.1
SEQ ID NO 32
LENGTH: 112
TYPE: PRT
 Query Match
 Matches
 Query Match
Best Local Similarity
 PRIOR APPLICATION NUMBER: IT RM99A000803
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 118
 PRIOR APPLICATION NUMBER: PCT/IT00/00554
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: IT RM99A000803
 FILE REFERENCE: 4161-4
CURRENT APPLICATION NUMBER: US/10/169,351
CURRENT FILING DATE: 2002-10-29
 APPLICANT: DESIDERIÓ, ANGICIA
APPLICANT: TAVLADORAKI, PARASKEVI
TITLE OF INVENTION: STRBELICING PEPTIDES,
TITLE OF INVENTION: WHICH INCLUDE THEM
 APPLICANT: BENVENUTO, EUGENIO APPLICANT: FRANCONI, ROSELLA
 FILE REPERINCE: 4161-4
CURRENT APPLICATION NUMBER: US/10/159,351
CURRENT FILING DATE: 2002-10-29
PRICE REPLICATION UNMERS: PCT/TTO/00554
PRICE FILING DATE: 2000-12-29
PRICE FILING DATE: 2000-12-20
PRICE REPLICATION NUMBER: IT RM99A000803
PRICE FILING DATE: 2000-12-2-30
 OTHER INFORMATION: Description of Artificial Sequence: scFv(F8)
OTHER INFORMATION: amino acid sequence
 ORGANISM: Artificial Sequence FEATURE:
 TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
 APPLICANT: TAVLADORAKI, PARASKEVI
 TYPE: PRT
 ORGANISM: Artificial Sequence FEATURE:
 Local Similarity
nes 102; Conserv
 144 LTQSPASLAVSLGQRATISCRASESVDSYGNSFWHWYQQKFGQPFKLLIYRALNLESGIP 203
64 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 102;
 64
 64 ARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDFLTFGTGTRLEIKR 112
 4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP 63
 4
 4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP 63
 ARFSGSGSRTDFTLTINPYEADDVATYYCQQSNEDPWTFGGGTKLBIKR 112
 LTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRALNLESGIP
 Conservative
 Conservative
 93.6%;
 90.1%;
 2
 Score 526; DB 12
Pred. No. 5.6e-42
 Score 526; DB 12;
Pred. No. 2.3e-42;
 Mismatches
 Mismatches
 POLYPEPTIDES AND ANTIBODIES
 Length 252
 Length 112
 Indels
 Indels
 °.
 0
 Gaps
 Gaps
 63
 0
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 APPLICANT MARCHATION.

APPLICANT MARKS JONES D

APPLICANT AMERICANCE P

TITLE OF INVESTION. HORIZONAL MONOCIONAL AN

TITLE OF INVESTION. HORIZONAL MONOCIONAL AN

CHERRY APPLICANTON NUMBER: US/09/144,886

CHERRY TILING DATE: 198-08-31

NUMBER OF SEG IN NOS: 98
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 ; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone; OTHER INFORMATION: 186 region VL epitope 1 US-09-144-885-80
 US-09-144-886-87
 묽
 US-09-144-886-80
 Matches
 Query Match
Best Local Similarity
 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 87
LENGTH: 112
 Sequence 87, Application US/09144886 Patent No. US20020155114A1 GENERAL INFORMATION:
 OTHER IMPORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: C25 region VL epitope 2 -09-144-885-87
 Matches 101;
 Query Match
Best Local Similarity
 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
 APPLICANT: Ameradorfer; Peter
TITHE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITHE OF INVENTION: Betuliama Neurotoxins
FILE REFERENCE: 2500 111908
CURRENT APPLICATION NOMBER: US/09/144,886
CURRENT FILMIC DATE: 1596-08-31
NUMBER OF SERI ID NOS: 98
NUMBER OF SERI ID NOS: 98
 Sequence 80,
 APPLICANT: Marks, James D
 Patent No.
 TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
 ORGANISM: Artificial Sequence FEATURE:
 TYPE: PRT
 LENGTH: 112
 204 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPWTFGGGTKLEIKR 252
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 64
 100;
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 64 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTTRLEIKR 112
 4
 4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP
 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLBIKR 112
 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP 63
 0, Application US/09144886
US20020155114A1
ARFSGSGSGTDFTLTINEVEADDVATYYCQQSNEDPFTFGSGTKLBIKR 112
 LTQSPASLAVSLGQRATISCRASESVDSYGHSFMQWYQQKPGQPPKLLIYRASNLEPGIP
 LTQSPASLAVSLGQRAIISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGIP
 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPPTFGAGTKLELKR 112
 Conservative
 Conservative
 91.7%;
 92.7%;
 Score 521; DB
Pred. No. 6.9e
4; Mismatches
 ω
 Score 525; DB 10;
Pred. No. 2.9e-42;
 Mismatches
 6.9e-42;
 Antibodies That Neutralize
 Length 112;
 Length 112;
 Indels
 Indels
 ٥,
 0;
 Gaps
 63
 63
 63
 0
 0
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RESULT 8
US-09-144-886-84
 US-09-144-886-84
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 뭥
 US-10-169-351-103
 SEQ ID NO 84
LENGTH: 112
TYPE: PRT
 US-10-169-351-103
 Sequence 84, Application US/09144886
Patent No. US/090201551144
REPLICANT: AMARYA, James D
APPLICANT: Ameradorfer, Peter
TITLE OF INVENTION: Botulinum Neurocoxins
FILE REFERENCE: 2500,1170S
CURRENT APPLICATION NOMBER: US/09/144,886
CURRENT APPLICATION NOMBER: US/09/144,886
CURRENT APPLICATION NOMBER: US/09/144,886
CURRENT APPLICATION NOMBER: US/09/144,886
CURRENT APPLICATION NOMBER: US/09/144,886
CURRENT PILING DATE: 1989-88-31
NOMBER OF SEX ID NOS: 98
ROSPITARS: 3 SECRETAIN 04: 2.0
 Matches
 Query Match
 Sequence 103, Applic
Publication No. US20
GENERAL INFORMATION:
 Best Local Similarity
 Best Local :
 Matches
 SEQ ID NO 103
LENGTH: 112
 APPLICANT: BENVENUTO, EUGENIO
APPLICANT: FRANCONI, ROSELLA
APPLICANT: DESIDERIO, ANGIOLI
 PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 118
 CURRENT APPLICATION NUMBER: US/10/169,351
CURRENT FILING DATE: 0002-10-29
PRIOR APPLICATION NUMBER: PCT/IT00/00554
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: IT RN99A000803
 APPLICANT: TAVIADORAGI, PARASERYI
TITLE OF INVENTION: STABLIZING PERTIDES, POLYPERTIDES AND ANTIBODIES
TITLE OF INVENTION: WHICH INCLUDE THEM
 OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION; IA1 region VL epitope 2
 ORGANISM: Artificial Sequence
 SOFTWARE: PatentIn Ver. 2.1
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: VL-F8 amino OTHER INFORMATION: acid sequence
 ORGANISM: Artificial Sequence
 TYPE: PRT
 FEATURE:
 Match 88.0%;
Local Similarity 92.7%;
 101;
 64
 64 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 103, Application US/10169351
 ,86
 4 LTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKDGQPPKLLIYRALNLESGIP 63
 4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIPGQPPKLLIYRASNLESGIP 63
 ARFSGSGSRIDFILIINPVEADDVATYYGQQSNEDPWIFGGGTKLEIKR 112
 DESIDERIO, ANGIOLA
 Conservative
 Conservative
 US20030157090A1
 87.8%;
 Score 513; DB 10;
Pred. No. 3.9e-41;
5; Mismatches 6;
 Score 514; DB 12;
Pred. No. 3.1e-41;
 Mismatches
 DB 12;
 Length 112;
 Indels
 Indels
 0
 ٥,
Gaps
 Gaps
 0,
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4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP 63

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 US-09-144-886-85
 US-09-144-886-85
 RESULT 9
US-09-144-886-86
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 US-09-144-886-86
 APPLICANT: Marks. James D
APPLICANT: Marks. James D
APPLICANT: ABSTRACTER, Peter
TITLE OF INVENTICA: Therapautic Monoclonal Antibodies That Neutralize
TITLE OF INVENTICA: Therapautic Monoclonal
TILE REFERENCE: 2500.117860
CURRENT APPLICATION NOWBER: US/09/144,886
UNDERNY DELING DATE: 1990-08-31
NOWBERT DELING DATE: 1990-08-31
SEQ.ID.08.85
SEQ.ID.08.85
SEQ.ID.08.85
SEQ.ID.08.85
 Sequence 85, Application US/09144886 Patent No. US20020155114A1 GENERAL INFORMATION:
 APPLICANT: Marks Jumes D
APPLICANT: Marks Jumes D
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Devolinm Neurotoxins
FILE REPERSIVE: 2500, 1178: US/09/144,886
CURRENT APPLICATION MUNBER: US/09/144,886
CURRENT PERSICATION MUNBER: US/09/144,886
CURRENT PERSICATION MATE: 1398-08-31
MUNBER OF SEQ ID NOS: 98
SOPTMARE: PERSENTIN VET. 2.0
SOPTMARE: PERSENTIN VET. 2.0
 Matches
 Best Local Similarity
 Query Match
 Matches
 Query Match
Best Local
 GENERAL INFORMATION:
 Sequence 86, Application US/09144886
Patent No. US20020155114A1
 OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: 1F1 region VL epitope 2
 FEATURE:
 ORGANISM: Artificial Sequence
 LENGTH: 112
 OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: C39 region VL epitope 2
 FEATURE:
 ORGANISM: Artificial Sequence
 Local Similarity
les 97; Conserv
 64
 64 ARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDFLTFGTGTRLEIKR 112
 64
 64
 4 LTQSPASLAVSLGQRATISCRASESVDSYGXNEMHWYQQIPGQPPKLLIYRASNLESGIP 63
 44
ARFSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPYTFGGGTKLEIKR
 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP
 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNBDPLTFGTGTRLEIKR 112
 LTQSPASLAVSLGRRATISCRASESVDSYGHSFMHWYQQKFGQPPKLLIYLASNLESGVP
 ARFSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPYTFGGGTKLEIKR 112
 LTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYLASNLESGVP
 Conservative
 Conservative
 87.8%;
 87.2%;
89.0%;
 5; Mismatches
 7; Mismatches
 Score 509; DB 10;
Pred. No. 9.3e-41;
 Score 513; DB 10;
Pred. No. 3.9e-41;
 Length 112,
 Length 112;
 Indels
 0
 0
 Gaps
 63
 0
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; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 286 region VL epitope 3
US-09-144-886-94
 RESULT 12
US-09-144-886-94
 Ś
 밁
 RESULT 11
US-09-881-823-2
 무
 8
 ; ORGANISM: Murine
US-09-881-823-2
 CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE, 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIAN VET. 2.0
SEQ ID NO 94
SEQ ID NO 94
 Sequence 94, Application US/09144886
Patent No. US/00/00155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
 Matches
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
 SOFTWARE: PatentIn version 3.0 SEQ ID NO 2
 GENERAL INFORMATION:
 TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize TITLE OF INVENTION: Botulinum Neurotoxins FILE REFERENCE: 4500.117080
 Matches
 Sequence
 TITIE OF INVENTION: Method for the Treatment and Prevention of Dental Caries Fils REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT PILING DATE: 2001-06-15
FRIOR FILING DATE: 2007-078,577
FRIOR FILING DATE: 1999-08-20
 APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MAXWELI
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
 Sequence 2, Application US/09881823
Patent No. US20020068066A1
 LENGTH: 1:
TYPE: PRT
 APPLICANT: WIMS, LETITIA APPLICANT: CHEN, LI
 NUMBER OF SEQ ID NOS: 32
 ORGANISM: Artificial Sequence
 LENGTH: 134
TYPE: PRT
 FEATURE:
 63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 23 VITQSPVSLAVŠIGORĀTĪSCRASESVDSYGNSFWNWYQQKPGQPPQILIYRASNLEYGI
 64
 83 PARFSGSGSRTDFTLTINEVEADDVATYYCQQNNADPPTFGGGTKLEIKR 132
 64 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR
 112
 98;
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
 ARFSGSGSRTDFTLTIDEVEADDAATYYCQQNNEDEYTFGGGTKLEIKR
 TRINH, RYAN
85.4%;
ilarity 88.0%;
Conservative
 Conservative
 86.5%;
 MAXWELL
Score 499; DB 10;
Pred. No. 8.1e-40;
6; Mismatches 7;
 Score 505; DB 9; Length 134; Pred. No. 2.7e-40;
 Mismatches
Indels
0,
 0
Gaps
 82
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4 LTQSPASLAVSLGQRATISCRASESVDSYGYNEMHWYQQIPGQPPKLLIYRASNLESGIP 63

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LTQSPASLAVSLGQRATTSCRASESVDSYGNSFWHWYQQKPGQPPKLLIYLASNLESGVP 63

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 US-09-810-502-36
 RESULT 13
US-09-810-502-36
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 Matches
 Query Match
 Sequence 36, Application US/09810502
Patent No. US20020034765A1
GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 36:
 Local Similarity
 ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
NEGISTRATION NUMBER: 16,545
REGISTRATION NUMBER: 16,141
REFERENCE/DOCKST NUMBER: 18410CC
TELECHONEN: 732-594-3905
 CURRENT APPLICATION DATA.

APPLICATION WINMER: US/09/810,502
FILING DATE: 16-Mar-2001
CLASSIFICATION: CURRINGN
PRIOR APPLICATION DATA.
 MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 TOPOLOGY: linear
MOLECULE TYPE: peptid
 COMPUTER READABLE FORM,
MEDIUM TYPE: Diskettle
COMPUTER: 1BM Compatible
OREATING SYSTEM: Windows
SOFTWARE: EssCSQ for Windows Version 2.0b
 SEQUENCE CHARACTERISTICS:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY OF ANTIBODY VARIABLE DOMAINS
 APPLICANT: Padlan, Eduardo A.
 63
 63 PARESGSGSRIDETLTINEVEADDVATYYCQQSNEDELTEGTGTRLEIKR 112
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 APPLICATION NUMBER: 08/905,280
FILING DATE: 01-ANG-1995
APPLICATION NUMBER: 08/609,218
FILING DATE: 0.0-Fax-1996
APPLICATION NUMBER: 08/109,187
FILING DATE: 19-ANG-1993
APPLICATION NUMBER: 08/109,187
FILING DATE: 19-ANG-1993
APPLICATION NUMBER: 07/702,217
FILING DATE: 17-May-1991
PDRFSGSGSGTDFTLTISSVEAEDVATYYCQQSNEDPLTFGQGTKLEIKR 112
 VMTQSSNSLAVŠLGERATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGI
 STRANDEDNESS: single
 TYPE: amino acids
 ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave
CITY: Rahway
 ZIP: 07065-0907
 COUNTRY: USA
 STATE: NJ
 ARFSGSGSRTDFTLTIDPVEAEDAATYYCQQNNEDPYTFGGGTKLBIK 111
 ARESGSGSRTDETLTINEVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 TELEFAX: 732-594-4720
 Conservative
 Mark, George E.
 84.6%;
 George E.
 6; Mismatches
 Score 494; DB 9;
Pred. No. 2.4e-39;
 8,
 Length 112;
 Indels
 0;
 Gaps
 62
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 0
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PRIOR APPLICATION NUMBER: 60/362/612
PRIOR FILLING DATE: 300/20-00-08
NUMBER OF SSQ ID NOS: 128
SOCTMARE: FRASESQ for Windows Version 4.0
SSQ ID NO 81
LENGTH: 115
LENGTH: 115
OCCEST: DET Mus musculus
 US-10-169-351-48
 8
 B
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 US-10-169-351-48
 RESULT 15
 US-10-160-506-81
 RESULT 14
US-10-160-506-81
 Matches
 Query Match
Best Local Similarity
 SEQ ID NO 48
 GENERAL INFORMATION:
 Sequence 48, Application US/10169351
Publication No. US20030157090A1
 Sequence 81, Application US/10160506
FUBLICATION NO. US20030161832A1
GENERAL INFORMATION: US20030161832A1
INFORMATION: WEIGHT OF THE SECURITY
 FILE REFERENCE: 4161-4
CURRENT APPLICATION NUMBER: US/10/169,351
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: PCT/IT00/00554
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2000-12-29
 Matches
 Query Match
 PRIOR APPLICATION NUMBER: IT RM99A000803
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.1
 APPLICANT: DESIDERIO, ANGICIA
APPLICANT: TRYNADORAKI, PRASSEYI
TITLE OF INVENTION: STRAILIZING PETTIDES, POLYPEPTIDES AND ANTIBODIES
TITLE OF INVENTION: WHICH INCLUDE THEM
 APPLICANT: BENVENUTO, EUGENIO APPLICANT: FRANCONI, ROSELLA
 CURRENT APPLICATION NUMBER: US/10/160,506
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/324,100
PRIOR FILING DATE: 2001-09-20
 OTHER INFORMATION: Description of Artificial Sequence: VL-CMY/2G OTHER INFORMATION: amino acid sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 ENGTH: 108
 Local
 95;
 63 PARFSGSGSGTDFTLNIHPVEEDDAATYYCQQSNEDPPWTFGGGTKLEIK 112
 63 PARFSGSGSRTDFTLTINEVEADDVATYYCQQSNED-PLTFGTGTRLEIK 111
 96;
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 Similarity
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 Conservative
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 82.0%;
 4; Mismatches
 Pred. No.
 Pred. No. 9.9e-39;
 ed. No. 6e-38;
Mismatches
 DB 12;
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 7;
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Gaps
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4 LTQSPASLAVSLGQBATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP 63

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Db 60 ARPSGSGSSTDFTLTINPVEADDVATYYCQGSNEDPLTFGTGTRLEIKR 110

B 60 ARPSGSGSSTDFTLTINPVEADDVATYYCQGSNEPWTFGGTKLEIKR 108

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Jbb time : 99,243 secs

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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 Total number of hits satisfying chosen parameters:
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 Perfect score:
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 OM protein -
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
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11 /cgpZ_6/ptcodate/l/isa/5A_COMB_pap;*
22 /cgpZ_6/ptcodate/l/isa/5B_COMB_pap;*
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24 /cgpZ_6/ptcodate/l/isa/6B_COMB_pap;*
25 /cgpZ_6/ptcodate/l/isa/6B_COMB_pap;*
26 /cgpZ_6/ptcodate/l/isa/backfliesl_pap;*
26 /cgpZ_6/ptcodate/l/isa/backfliesl_pap;*
 328717 seqs, 42310858 residues
 Gapop 10.0 , Gapext 0.5
 BLOSUM62
 1 ENVLTQSPASLAVSLGQRAT.....QQSNEDPLTFGTGTRLEIKR 112
 US-09-661-992B-86_COPY_138_249
584
 November 7, 2003, 07:21:18; Search time 15.4486 Seconds (without alignments) 288.098 Million cell updates/sec
 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
 Length DB
112
215
215
252
252
271
106
132
132
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133
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133
 US-08-137-1170-33
US-08-217-717-33
US-08-217-718-10
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US-08-217-718-10
US-08-217-718-10
US-08-217-718-10
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 summaries
 SUMMARIES
 328717
 Sequence 33 Appl
Sequence 10 Appl
Sequence 10 Appl
Sequence 12 Appl
Sequence 12 Appl
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Sequence 13 Appl
Sequence 14 Appl
Sequence 16 Appl
Sequence 17 Appl
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Sequence 12 Appl
Sequence 12 Appl
Sequence 13 Appl
Sequence 14 Appl
Sequence 14 Appl
Sequence 15 Appl
Sequence 16 Appl
Sequence 17 Appl
Sequence 17 Appl
Sequence 18 Appl
Sequence 19 Appl
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Sequence 13 Appl
Sequence 14 Appl
Sequence 14 Appl
Sequence 15 Appl
Sequence 16 Appl
Sequence 16 Appl
Sequence 17 Appl
Sequence 18 Appl
Sequence 18 Appl
Sequen
 Description
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Result No.

| Sequence 2, sequence 5, sequence 6, sequen |
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; MOLECULE TYPE: protein US-08-436-717-33
 US-08-436-717-33
 밁
 B
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-33
 Sequence 33,
 Patent No.
 FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WIGNIER, Harvold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 34,0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)72-5300
 Matches 101; Conservative
 Query Match
 GENERAL INFORMATION:
 TELEX: 904136
NFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
'TOPOLOGY: linear
 PRIOR APPLICATION DATA:
APPLICATION WHORE: US/08/137,117
FILING DATE: D0-DEC-1993
APPLICATION WHOREE: W0-DECT/JP92/00544
FILING DATE: A-PPL-1992
RELOW APPLICATION WOMBER: W0-4-32084
APPLICATION WOMBER: UP 4-32084
 COMPUTER READABLE FOOM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC Compatible
COMPATER: FLOOPYM-DOS
OPENATIOS SYSTEM: PC-DOS/MS-DOS
SOPTMARE: PSECHITIN BARIS
CURRENT APPLICATION DAYA:
 FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INVENTEURING RECEPTOR
NUMBER OF SEQUENCES: 158
 APPLICANT: JONES, SEE
APPLICANT: SALDANHA,
 APPLICANT:
 APPLICANT:
 TELEFAX:
 FILING DATE:
CLASSIFICATION: 536
 APPLICATION NUMBER: JP 3-95476
 APPLICATION NUMBER:
 STREET:
 ADDRESSEE:
 Local Similarity
 83 PARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDEPTFGAGTKLELK 131
 63 PARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 23 VLIQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGI
 20007-5109
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
 Washington
 3, Application US/08436717
5817790
 D.C
 B: Foley & Lardner
3000 K Street, N.W., Suite 500
 (202) 672-5399
 JONES, Steven
 USA
 SATO, Koh
 TSUCHIYA, Masayuki
 89.7%;
 US/08/436,717
 53466/126/AAOK
 Score 524; DB 1; Length 131;
Pred. No. 6.5e-51;
3; Mismatches 5; Indels
 o;
 Gaps
 82
 62
 0
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RESULT 4
US-08-111-080-18
; Sequence 18, Application 08/111080
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 皮
 ; MOLECULE TYPE: protein US-08-621-751A-10
 g
 밁
 US-08-621-751A-10
 RESULT 3
 Matches
 Query Match
 Patent No.
 Sequence 10, Application US/08621751A Patent No. 5882644
 Query Match 89.7%;
Best Local Similarity 92.7%;
Matches 101; Conservative
 TELEPHONE: (650) 813-5600
TELEPAK: (650) 494-0792
TELEY: 706141 MRN FOERS SFO
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
 ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDILM TYPE: Floopy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batenil Release #1.0, V
CURRENT APPLICATION DATA:
 GENERAL INFORMATION:
 ATTORNEY/AGENT INFORMATION:
NAME: Lehthardt, Susan K.
RECISTRATION UNMER: 33,943
REFERENCE/DOCKET NUMER: 321152000100
TELECOMUNICATION LIPPORMATION:
TELEPHONE: (550) 813-5500
 CORRESPONDENCE ADDRESS:
ADDRESSES: MORRISON & FOERSTER LLP
STREET: 755 PAGE MILL ROAD
 NUMBER OF SEQUENCES:
 TÎTLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE
TÎTLE OF INVENTION: PLATEIET-DERIVED GROWH FACTOR RECEPTOR BETA RECEPTOR AND
TÎTLE OF INVENTION: METHODS OF USE THERROF
 APPLICANT: Chang, Chung N.
APPLICANT: Landolfi, Nicholas F.
 APPLICANT:
 Local Similarity
 TOPOLOGY:
 APPLICATION NUMBER: US/0
PILING DATE: 22-MAR-1996
CLASSIFICATION:
 COUNTRY:
 101;
 83 PARFSGGGSRTDFTLTINPVEADDVATYYCQQSNEDPPTFGGGTKLEIK 131
 63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTKLEIK 111
 23 VLTQSPBSLAVSLGQRATISCRASESVDSYGNSFMHWYQQKBGQPFKLLIYRASNLSSGI
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGVNFMHWYQQIPGQPPKLLIYRASNLESGI 62
 83 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPPTFGAGTKLELK 131
 63 PARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
 23 VLIQSPASLAVSLOQRATISCRASESVDSYGNSFMHWYQQRPGQPPKLLIYRASNLESGI
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPQQPPKLLIYRASNLESGI
 : 131 amino acids
amino acid
 PALO ALTO
 ç
 USA
 Martin, Ulrich
 Conservative
 linear
 89.2%;
 17
 US/08/621,751A
 Score 521; DB 2;
Pred. No. 1.4e-50;
2; Mismatches 6
 Pred. No. 6.5e-51;
 Mismatches
 Version #1.30
 Length 131;
 Length 131;
 Indels
 Indels
 0
 0
 Gaps
 Gaps
 82
 82
 52
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밁
 Db
 Ś
 US-08-111-080-22
 RESULT 5
 US-08-111-080-18
 Sequence 23, Application 08/111080
Parent No. 5556965
Parent No. 5556965
GENERAL IMPORMATION: TRAINGLY
TITLE OF INVENTION: HIV Immunotherapeutics
NAMERS OF SAURECES 38
CORRESPONDENCE ADDRESS:
 Matches
 Best Local Similarity
 Query Match
 Patent No. 5558865
 GENERAL
 INFORMATION FOR SEQ ID NO: 18:
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNUBER: US 07/748,562
PILING DATE: 22-AUG-1991
PRIOR APPLICATION DATA:
 STREET: Chicago
CITY: Chicago
TATE: Illinois
 TOPOLOGY: linear
MOLECULE TYPE: protein
 SEQUENCE CHARACTERISTICS
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
 APPLICATION NUMBER: US 01
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
 FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marehall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
 APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
 TELEFAX: (312)
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
 TYPE: amino acid
 REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31
 STREET:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
 LENGIH:
 APPLICATION NUMBER:
 FILING DATE
 APPLICATION NUMBER:
 MEDIUM TYPS: Floppy disk
 INFORMATION:
 63 PARFSGSGSRTDFTLTIDFVEADDAATYYCQQNNEDPLAFGTGTKLELKR 112
 63 PARPSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 98; Conservative
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQSPKLLIYVASNLESGV 62
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIPGQPPKLLIYRASNLESGI 62
 60606
Chicago
 Borun, Michael F.
 E: Borun
6300 Sears Tower, 233 S. Wacker Drive
 6300 Sears Tower, 233 S. Wacker Drive
 121 amino acids
 (312) 474-0448
 87.8%;
 US 08/039,457
 PCT/US92/07111
 08/111,080
 6; Mismatches
 31629
 Score 513; DB 1; Length 121;
Pred. No. 9.9e-50;
 Indels
 0,
 Gaps
```

0,

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밁
 Ś
 US-08-211-980-18
 RESULT 6
 US-08-111-080-22
 PAtent No. 565569 general investigations. Particiant, Normal Seneya APPLICANT, Otho, Fauncya TITLE OF INVESTIGAT, HIV Immunotherapeutics NUMBER OF SEQUENCES: 38
 Sequence 18, Application US/08211980 Patent No. 5665569
 Matches
 Query Match
 TRIEX: 25-3856
INFORMATION FOR SEC ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TYPE: innino acid
TOPOLOGY: linear
 ZIP: 60606

ZIP: 60606

COMPUTER REALDALE FORM:
MEDITM TYPE: Floopy disk
COMPUTER: LAW CO-compatible
COMPUTER: LAW CO-compatible
COMPUTER: LAW CO-compatible
COMPANIE: SECRETI RELEASE #1.0, Version #1.25

COMPRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
CORRESPONDENCE AMERICAN, O'Toole, Gerstein, Murray
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
 REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: 08/111,080
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
 MOLECULE TYPE: protein
 PRIOR APPLICATION DATA:
 TELEPHONE: (312) 474-0448
APPLICATION NUMBER:
 COUNTRY:
 STREET: 6300 g
CITY: Chicago
STATE: Illino:
 ADDRESSEE: Marsh
ADDRESSEE: Borun
 CLASSIFICATION:
 PILING DATE:
 ZIP: 60606
 COUNTRY:
 STATE: Illinois
 Local Similarity
 63 PARFSGSGSRTDFTLTIDPVEADDAATYYCQQWNEDPLTFGAGTKLELKR 112
 63 PARESGSGSRTDETLTINEVEADDVATYYCQQSNEDPLTEGTGTRLBIKK 112
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
 98;
 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQSPKLLIYVASNLESGV
 Illinois
 6300 Sears Tower, 233 S. Wacker Drive
 USA
 Conservative
 USA
 87.8%;
US/08/211,980
 31629
 6; Mismatches
 Score 513; DB 1; F
Pred. No. 9.9e-50;
6; Mismatches 6;
 Length 121;
 Indels
 0; Gaps
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0

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US-08-211-980-22
 US-08-211-980-18
 Patent No.
 Sequence 22, Application US/08211980 Patent No. 5665569
 Matches
 Query Match
 APPLICATION NVHSER: PCI/VS92/07111

PILING DNE: 24-MG-1992

PRIOR APPLICATION DNTA:

APPLICATION NUMBER: US 08/039,457

PILING DNTE: 22-APF-1993

ATTOSNEY/ASTOT INFORMATION:

BANE: PRIOR VNFCHSER'S 14/20

PRIOR PRIOR VNFCHSER'S 14/20
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 18:
 APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF EXCENSIONS
CORESSONDENCE ADDRESS:
ADDRESSES: Born
ADPRESSES: Born
 APPLICATION NUMBER. US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
HAME: BOTUM, MICHAEL F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
 COMPUTER READNAGE FORM:
MEDIUM TYPE: #loppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS(MS-DOS
SOFTWARE: Fatentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
 STREET: STREET: Chicago CITY: Chicago Illinois
 MOLECULE TYPE: protein
 SEQUENCE CHARACTERISTICS
 REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION
 FILING DATE:
CLASSIFICATION:
 TYPE: amino acid
 APPLICATION NUMBER:
 TOPOLOGY:
 CLASSIFICATION:
 ZIP: 60606
 FILING DATE:
 Local Similarity
 63 PARPSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPLAFGTGTKLELKR 112
 63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
 98;
 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQSPKLLIYVASNLESGV 62
 25-3856
 6300 Sears Tower, 233 S. Wacker Drive
 Conservative
 DATA:
 87.8%;
 US/08/211,980
 6; Mismatches
 Score 513; DB 1; Length 121;
Pred. No. 9.9e-50;
 6; Indels
 0;
 Gaps
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 PCT-US92-07111-17
 PCT-US92-07111-17
 US-08-211-980-22
 Query Match
 Sequence 17, Application PC/TUS9207111
GENERAL INFORMATION:
APPLICANT: Ohno, Tauneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
 Matches
 Query Match
 TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
 PRIOR APPLICATION DATA,
REPLICATION MOMERS, US 07/140
FILING DATE: 22-MUG-1991
APPODEEZ/AGENT TROPOMENTION
NAME: NO-LEAR CORE & S. 302
REGISTRATION NOMBER: 33, 302
REGISTRATION INFORMATION: 1782ACOMENTICATION INFORMATION: 1782ACOMENTICATION INFORMATION: 1312) 346-2550
 TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPB: amino acid
TOPOLOGY: linear
 MOLECULE TYPE: protein
 MOLECULE TYPE: protein
 CURRENT APPLICATION DATA:
 MEDIUM TYPE: Floppy
 STREET: Two Fi
STREET: Street
CITY: Chicago
 TOPOLOGY:
 LENGTH: 121 amino acids
 CLASSIFICATION:
 APPLICATION NUMBER: PO
FILING DATE: 19920824
 SOFTWARE:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ZIP: 60603
 COUNTRY:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
 Local Similarity 89.
 TELEFAX:
 TELEPHONE:
 63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 63 PARFSGSGSRTDFTLTIDFVEADDAATYYCQQNNEDPLTFGAGTKLELKR 112
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQSPKLLIYVASNLESGV 62
 3 VITQSPASLAVSIGQRATISCRASBSVDSYGYNFMHWYQQIPGQPPKILIYRASNIESGI 62
 Illinois
 Street
 Two First National Plaza, 20 South Clark
 USA
 (312) 474-0448
 PatentIn Release #1.0, Version #1.25
 linear
 (312) 474-6300
 UMBER: US 07/748,562
22-AUG-1991
 Floppy disk
 87.8%;
 87.8%;
 PCT/US92/07111
 31016
Score 513; DB 5; Le
Pred. No. 9.9e-50;
 6; Mismatches
 Score 513; DB 1; Length 121;
Pred. No. 9.9e-50;
 Length 121;
 0;
 Gaps
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Matches

Local Similarity

98; Conservative

6; Mismatches

Indels

0

Gaps

0,

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 RESULT 10
PCT-US93-07967-22
 밁
 PCT-US93-07967-18
 PCT-US93-07967-18
 Sequence 22, Application PC/TU89307967
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunother.
 Sequence 18, Application PC/TUS9307967 GENERAL INFORMATION:
 Matches
 Best
 Query Match
 INFORMATION FOR SEQ ID NO: 18:
 COMPUTER READNALE FORM:
MEDITA TYPE: Plopy disk
COMPUTER: IBM DC COMPACTIAL
COMPUTER: IBM CC COMPACTIAL
COMPUTER: PLOPY MINISTRA PLOPE MINISTRA PLOPE
SOPTMARE: PatentIn Release #1.0, Version #1.25
 MOLECULE TYPE: protein
 SEQUENCE CHARACTERISTICS:
 REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
 FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
 PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
 NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: HIV Immunotherapeutics
 TOPOLOGY:
 TELEPHONE: (312) 474-0448
 CLASSIFICATION:
 COUNTRY:
 STREET:
 ADDRESSEE:
 tocal Similarity
 FILING DATE: 24-AUG-1992
 APPLICATION NUMBER: PCT/US92/07111
 FILING DATE
 APPLICATION NUMBER: PCT/US93/07967
 CITY: Chicago
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 LENGIH:
 63 PARESGSGSRIDFILTIDPVEADDAATYYCQQNNEDPLAFGTGTKLELKR 112
 63
 63 PARFSGSGSRIDETLITINEVEADDVATYYCQQSNEDPLITSGIGTRLEIKR 112
 63 PARFSGSGSETDFTLTINFVEADDVATYYCQQSNBDFLTFGTGTRLBIKR 112
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
 98;
 60606
 amino acid
 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQSPKLLIYVASNLESGV 62
 PARFSGSGSRTDFTLTIDFVEADDAATYYCQQNNBDPLAFGTGTKLBLKR 112
 Illinois
 121 amino acids
 6300 Sears Tower, 233 S. Wacker Drive
 USA
 Conservative
 Ohno, Tsuneya
 Tinear
 Borun
 87.8%;
 HIV Immunotherapeutics
 US 08/039,457
 31629
 6; Mismatches
 Score $13; DB 5; Length 121;
Pred. No. 9.9e-50;
 6; Indels
 0; Gaps
 0,
 뭉
 US-08-111-080-26
 RESULT 11
 PCT-US93-07967-22
 Sequence 26, Application 08/111080
Patent No. 5558865
 Matches
 Query Match
 GENERAL INFORMATION:
 TELEFAX: (312) 474-044
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
COUNTAIN COUNTAIN COUNTAIN COUNTAIN READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PC-DOS/NS-DOS
 STREET: Chicago
CITY: Chicago
CTATE: Illinois
 APELICATION NUMBER: PCT/US92/0711:
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA: 08/039,457
APPLICATION WINDER: US 08/039,457
FILING DATE: 22-ARF.1993
ATTORNEY/AGENT IMPORMATION:
 COUNTRY: USA
ZIP: 66606
COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/M9-DOS
SOFTWARDE DESCRIPTIONS
 STREET: 0...
STREET: Chicago
CITY: Chicago
TATE: 111inois
 TOPOLOGY: linear
MOLECULE TYPE: protein
 SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
 NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31.
TELECOMMUNICATION INFORMATION:
 CORRESPONDENCE ADDRESS:
 PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES:
 TELEPHONE: (312) 474-0448
 ADDRESSEE: Marsh
 Local Similarity
 TYPE: amino acid
 CLASSIFICATION:
 FILING DATE
 98; Conservative
 (312) 474-6300
 87.8%;
 38
 PCT/US92/07111
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APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
ADDRESSEE: Borun
 63 PARFSGSGSRTDFTLTTDPVEADDAATYYCOONNEDPLTFGAGTKLELKR 112
 63 PARFSGSGSRIDETLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQSPKLLIYVASNLESGV 62
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
6300 Sears Tower, 233 S. Wacker Drive
 6300 Sears Tower, 233 S. Wacker Drive
 Marshall, O'Toole, Gerstein, Murray &
 6; Mismatches
 Score 513; DB 5; Length 121;
Pred. No. 9.9e-50;
 Indels
 0; Gaps
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US-08-211-980-26
 US-08-111-080-26
 Matches
 Sequence 26, Application US/09211980 Patent No. 5665569
 Query Match
 FILING DATE:
CLASSIFICATION 424
PRIOR APPLICATION UNMER: PCT/US
FILING DATE: 24-NG-1992
FRIOR APPLICATION DATA:
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
 OCOMPUTER READMELS FORM:
MEDIUM TYPES: Ploppy disk
COMPUTER: IEW FO COMPATÈNE
ORESHTIN SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BatentIn Ralease #1.0, Version #1.25
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
 NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS:
 MOLECULE TYPE: protein
 REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
 APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/748,562 FILING DATE: 22-AUG-1991 PRIOR APPLICATION DATA:
 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
 TELEPAX: 25-3856
 PRIOR APPLICATION DATA:
 y Match (27.3%; Score 510, DB 1; Length 120; Local Similarity 89.1%; Pred. No. 2.1e-49; hes 98; Conservative 5; Mismatches 7; Indels
 TELEPHONE: (312) 474-0448
 STREET:
 TYPE: amino acid
 APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
 APPLICATION NUMBER:
APPLICATION NUMBER:
 ZIP: 60606
 COUNTRY:
 CITY: Chicago
 ADDRESSEE:
 TOPOLOGY:
 LENGTH:
 NAME:
 CLASSIFICATION:
 ADDRESSEE:
 63 PARPSGSGSGTEFTLTINPVETDDVATYYCQQSNKDPLTFGAGTKLELKR 112
 63 PARPSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFNHWYQQIPGQPPKLLIYRASNLESGI 62
 Borun,
 VLTQSPASLAVSLGQRATISCRASESVDDYGISFMHWYQQKLGQPPKLLIYRASNLESGI
 Illinois
 120 amino acids
 6300 Sears Tower, 233 S. Wacker Drive
 USA
 linear
 Marshall, O'Toole, Gerstein, Murray &
 Borun
 Michael F.
 PCT/US92/07111
US 08/039,457
 08/111,080
 0
 Gaps
 62
 0
```

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RESULT 13
PCT-US93-07967-26
 Ś
 g
 Ś
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-980-26
 Sequence 26, Application PC/TUS9307967
SEQUENCE INFORMATION:
APPLICANT: Ohno, Teuneya
TITLE OF INVENTION: HIV Immunotherapeutics
 Matches
 Query Match
 INFORMATION FOR SEQ ID NO: 26:
 APPLICATION NUMBER: US 08/
FILING DATE: 22-ARR-193
ATTORNEY/AGENT INFORMATION:
NAME: BOTUM, Michael F.
REGISTRATION NUMBER: 25/
REFERENCE/DOCKET NUMBER: 3
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
 ZIF: 60606
COMPUTER READABLE FORM:
WEDITM TYPE: Floppy disk
COMPUTER: LIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-1-00
UNERSM APPLICATION DATA:
APPLICATION MOMBER: PC-VISS3/07967
 REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
 STREET: Chicago
CITY: Chicago
TITE: Illinois
 FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, WICHAELF.
REGISTRATION NUMBER: 25,447
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
 FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES:
 SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
 CLASSIFICATION:
PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 TELEFAX: 25-3856
 TELEFAX:
 APPLICATION NUMBER: PCT/US92/07111
 FILING DATE
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
 Local Similarity
 TYPE: amino acid
 63 PARFSGSGSGTEFTLTINEVETDDVATYYCQQSNKDPLTFGAGTKLELKR 112
 63 PARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDFLTFGTGTRLEIKR 112
 98;
 3 VLTQSPASLAVSLGQRATISCRASESVDDYGISFMHWYQQKLGQPPKLLIYRASNLESGI
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
 6300 Sears Tower, 233 S. Wacker Drive
 (312) 474-0448
 Conservative
 87.3%;
89.1%;
 38
 US 08/039,457
 25,447
 31629
 5; Mismatches
 Score 510; DB 1; Length 120;
Pred. No. 2.1e-49;
5; Mismatches 7; Indels
 0;
```

TOPOLOGY:

MOLECULE TYPE: protein

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RESULT 15
US-09-065-059-13
 8
 WOLECULE TYPE: protein US-08-275-053-11
 RESULT 14
US-08-275-053-11
 밁
 á
 밁
 8
 PCT-US93-07967-26
 Query Match
Best Local S
Matches 97
 NPPLICATION NUMBER: PCT/GB93
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: maino acids
TYPE: maino acids
STRANDEDNESS: single
 Sequence 11, Application US/08275053
Patent No. 5607847
 Sequence 13, Application US/09065059
Patent No. 6068841
 Matches
 Query Match
 GENERAL INFORMATION:
 GENERAL INFORMATION:
 APPLICANT: SEINO, Ken-ichizo
APPLICANT: KAYAGAKI No. 6068841uhiko
APPLICANT: KWATKI, Hideo
APPLICANT: KWATKI, Hideo
APPLICANT: KWATKI, Hideo
APPLICANT: MAKATI, Motomi
TITLE OF INFESTION: THEAPPLITIC AGENT FOR HEPATITIS
TITLE OF INFESTION: THEAPPLITIC AGENT FOR HEPATITIS
CORLESFONDENCE: 18
CORLESFONDENCE: 19
 CONGTURE READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: ISM CC compatible
OPERATING STETM: PC-DOS/MS-DOS
SOFTWARE: Patcentin Release #1.0, Version #1.25 (EPO)
UDERSY APPLICATION DATA: DS/08/275,083
PRIOR INCREMENTATION STATEMENT DS/08/275,083
PRIOR INCREMENTATION DATA: JAN 104 08
 TITIE OF INVENTION: Recombinant human anti-human immunodeficiency
TITLE OF INVENTION: VIRUS antibody.
NUMBER OF SEQUENCES: 16
 APPLICANT:
 AUDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
 / Match 87.0%;
Local Similarity 89.0%;
hes 97; Conservative
 TOPOLOGY:
 госат
 63 PARESGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPLTFGAGTKLELK 111
 63 PARFSGSGSRTDFTLTINEVEADDVATYXCQQSNEDPLTFGTGTRLEIK 111
 63 PARFSGSGSGTEFTLTINPVETDDVATYYCQQSNKDPLTFGAGTKLELKR 112
 63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
 98;
 3 VLTQSPASLAVSLGQRATISCRASESVDDYGISFMHWYQQKLGQPPKLLIYRASNLESGI
 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
 Similarity
Virginia
 Conservative
 linear
 87.3%; Score 510; DB 5; Length 120;
89.1%; Pred. No. 2.1e-49;
ative 5; Mismatches 7; Indels
 PCT/GB93/01798
 Score 508; DB 1; Length 111;
Pred. No. 3.2e-49;
6; Mismatches 6; Indels
 0; Gaps
 0
 62
 0
```

```
Search completed: November 7, 2003, 07:30:11 Job time: 17.4486 secs
 S
 ğ
 // MOLECULE TYPE: peptide
US-09-065-059-13
 Matches
 Query Match
 TELEPAX: 703-694-1124
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
 OMPUTER READMALE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM FO Compathla
COMPUTER: IBM FO Compathla
OPERATING SYSTEM: FO-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURERRY APPLICATION DAYA:
 ATTORNEY/AGENT INFORMATION:
NAME: BUCCA Ph.D., Daniel
REGISTRATION UNDER: 9-42.368
REFERENCE/DOCKET NUMBER: 50356-151
 TELEPHONE: 703-518-5100
 STRANDEDNESS: sir
TOPOLOGY: linear
 Local Similarity
 TELEPHONE:
 CLASSIFICATION:
 APPLICATION NUMBER: US/09/065,059 FILING DATE:
 COUNTRY:
 63 PARESGSGETDETTIDEVEADDAATYYCQQNNEDEWTEGGGTKLEIKR 112
 63 PARESGSGSRTDETLTINEVEADDVATYYCQQSNEDELTEGTGTRLEIKR 112
 3 VLTQSPASIAVSIGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
 96; Conservative
 VITQSFASLAVSLRQRATISCRASEGVDSYGISFMHYYQQKPGQPPKLLIYRASXLKSGV 62
 single
 85.6%;
 6; Mismatches
 Score 500; DB 3; Length 112;
Pred. No. 2.5e-48;
 8; Indels
 0; Gaps
```

0,

! FINDPATTERNS on geneseqp: \* allowing 0 mismatches 1 CXXYGNSPKGFAYXXC

AAB20444 ck: 623 len: 16

November 7, 2003 07:46 ..

! Aab20444 Anti-FIX/FIXa antibody CDR3. 6/200

Databases searched: Genessq-AA, Release 13.0, Released on 19Jun2003, Formatted on 15Jul2003 CXXYGNSPKGFAYXXC CXXYGNSPKGFAYXXC

Total finds:
Total length:
Total sequences:
CPU time: 1 158,726,570 1,107,863 02:53.22

```
IISEOURNCE_LIST_1.0

I PINDATTERNS on generogp:* allowing 0 mismatches

I CXXYGNSPKGFAYXXC

I CXXYGNSPKGFAYXXC

GZEMESGD2001S:AAB20444 ck: 623 len: 16 finds: 1 | Aab20444 Anti-FIX/FIXa antih
\land of list

Databases searched:
Geneseq.AA, Release 13.0, Released on 19Jun2003, Formatted on 15Jul2003

Total leggth: 158,726,570

Total sequences: 11.07,863

Total sequences: 159,726,570

Total sequences: 1107,863

Total sequences: 159,726,570

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XFFFXXX88888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID AAB20444 standard; Peptide; 16 AA.
                                                    AAB20444 Length: 16 November 7, 2003 08:14
                                                                                                                                                            The present sequence is that of complementarity determining regions (CDMs) of an artibody having anti-factor IX (FIX) artification IX (FIX) and the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementarity of the complementar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood congulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pactor YX; FXX; Ractor YXa; FXXa; antibody; procoagulant; pactor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic dathesis, haemostatic; anidolytic; therapy; mouse; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 74; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2000; 2000WO-EP08936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-290358/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WOZ00119992-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB20444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BAXT ) BAXTER MG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-FIX/FIXa antibody CDR3
CXXYGNSPKG FAYXXC
                                                                                                                 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99AT-0001576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kerschbaumer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Falkner F, Dorner F;
                                                    Type: P Check: 623
```

```
v 0 0
0 0 0
0 0 0
1 match found in sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Selected search type is key against sequence data banks or files. Selected scope is Sequence. Selected sequence key from "new.key": seq105 (AM) ID seq105 AM preliminary pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Format Options:
Nucleic acid code matching
Find non-matching hits only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Selected data banks and files:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quest -
                                                                                                                                                                                                                                      FILE REFERENCE:
CURRENT NOPLICATION NUMBER: US/09/661,992
CURRENT FILLING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 106
SOFFMARE: PRENCHIN VET: 2.1
SEQ ID NO 105
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 match found in sequence:

US-09-661-992-105; Sequence 105, Application US/09661992

(from "/grch/paa/VS096_COMB.pep")

Sequence 105, Application US/09661992

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release
                                                                                                                                                                                                                                                                                                                                                                        NepiiCANT: Scheiflinger, Friedrich
NePiiCANT: Kerschbaumer, FandOlf
NePIICANT: Daner, Falko-Guenter
NepiICANT: Daner, Friedrich
TITIB OF INVENTION: Foctor IX/Factor IXA Activating Amtibodies and Antibody Derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run mode
Time to start comparison
Notify at end of run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Report key used
Note position of hit
Display full annotations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence context
                                                                                                                                                                                          TYPE: PRY ORGANISM: Artificial Sequence
                                                                                                                                        OTHER INFORMATION: Description of the artificial sequence:CDR3 region pund using 'seq105' (new.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Data bank : Pending_AA , all entries
                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quick User-directed Expression Search Tool
                                                                               CXXYGNSPKGFAYXXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       any character
ygnspkgfay
any character
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    any character
c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                any character
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- Outline of search "seq105-pen" --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- Output Parameters --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- Run Parameters --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exact
No
Yes
Yes
Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Batch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            File Options:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hit display
Name and annotations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indirect file
Sequence or key file
List of hits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yes
Yes
```

```
Number of sequences searched:
Number of sequence hits:
Number of separate matches:
Number of sequence hits saved:
                                                 Times:
                                                                                                                    Found using 'seq105'
                                                                                                                            OTHER INFORMATION:
                                                                                                                                           FEATURE:
NAME/KEY: MOD RES
                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: CDR3 peptide
                                                                                                CXXYGNSPKGFAYXXC
                                                                                                                                     (16)
                                         00:26:02.11
                                                                                                                     (new.key
                                                                                                                              Xaa = any amino acid
                                                                -- Search Statistics --
                                         00:26:31.00
                                               Total Elapsed
                         5811017
```

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Page
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```
Pormat Options:

Nucleic acid code matching Epind roomatcading hits only Republic and the Roomatcading hits only Robe position of hit Disply full amotations Sequence context
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>00</u>0
  Number of
Number of
Number of
Number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Selected search type is key against sequence data banks or files. Selected scope is Sequence. Selected sequence key from "new key"; seq105 (A) ID seq105 (A) December 1 Followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selected data banks and files:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quest - Quick User-directed Expression Search Tool Release 5.4
                                                                                       Times:
                                                                                                                                                       No hits found.
                                                                                                                                                                                              Run mode
Time to start comparison
Notify at end of run
                                                                                                                                                                                                                                                                                                                                                                                                                                  Data bank : Issued_AA , all entries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IntelliGenetics
f sequences searched:
f sequence hits:
f separate matches:
f sequence hits saved:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           any character
any character
ygnspkgfay
any character
any character
c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outline of search "seq105-iss" --
                                                                      CPU
00:01:34.06
                                                                                                                                                                                                                                                                                                                                                                                                            -- Output Parameters --
                                                                                                                                                                                                                                                       -- Run Parameters --
                                                                                                                  Search Statistics --
                                                                                                                                                                                                                                                                                               Bxact
No
Yes
Yes
Yes
                                                                                                                                                                                                   Batch
now
No
                                                                                                                                                                                                                                                                                                            File Options:
Indirect file
Sequence or key file
List of hits
Hit display
Name and annotations
                                                                        Total Elapsed
00:01:37.00
                                              328807
    000
                                                                                                                                                                                                                                                                                                              Yes No
```

! FINDPATTERNS on pir: * allowing 0 mismatches

1 CXXYGNSPKGFAYXXC

November 7, 2003 07:41 ..

Databases searched: NBKF, Release 76.1, Released on 12May2003, Formatted on 10Jun2003

Total finds: Total length: Total sequences: CPU time:

0 96,168,682 283,308 54.01

! FINDPATTERNS on swp:* allowing 0 mismatches

1 CXXYGNSPKGFAYXXC

November 7, 2003 07:42 ..

Total finds:
Total length:
Total sequences:
CPU time: Datahases searched: SWISS-EROT, Release 41.1, Released on 6Jun2003, Formatted on 9Jun2003 SPIREMBL, Release 23.0, Released on 4Mar2003, Formatted on 7Mar2003

305,079,309 958,388 03:26.62

```
Run on:
                                                                                    OM protein -
                                                                                protein search, using sw model
                                             November
                                                                                                                                              Copyright
7, 2003, 07:21:18; Search time 2.0721 Seconds (without alignments)
742.581 Million cell updates/sec
                                                                                                                                              GenCore version 5.1.6
(c) 1993 - 2003 Compug
                                                                                                                                              Compugen Ltd.
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Scoring table: Sequence: Perfect score: US-09-661-992B-105 80 CXXYGNSPKGFAYXXC 16

283308 seqs, 96168682 residues Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283308

Minimum DB Maximum DB seg length: 0 seg length: 2000000000

Database Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR_76:* pir1:*
pir2:*
pir3:*
pir4:*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	တ	7	6	IJ	4	u	2	۲	Result No.
	38	39	39	39	39	39.5	39.5	40	40	40	40	40	40	40	40	40	40	40	41	41	41	41	41	42	42	42	42	44	44	Score
:		48.8	48.8		48.8	49.4	49.4	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	51.2	51.2	51.2	51.2	51.2	52.5	52.5	52.5	52.5	55.0	0	Query Match
;	92	503	401	318	218	1800	1787	404	404	395	395	395	384	382	382	359	109	107	2515	1866	453	429	389	626	568	166	109	306	205	Length
	v	μ	N	2	N	N	N	И	N	N	N	μ	N	N	N	N		N	N	۳,	N	N	N	N	μ.	N	N	ь	N	B
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a recurse addess for	To kanna chain V	arginyltransferase		hypothetical prote	hypothetical prote	serine/threonine	serine/threonine k	hypothetical pro	hypothetical prote						methionine adenosy	methionine adenosy	Ig kappa chain V-	hypothetical expor	posterior-group pr	genome polyprotein	hypothetical prote	threonine ammonia-	polyadenylate-bind	probable Acyl-Co	CPE-binding protei	rna binding prote	Ig kappa chain V-J	polyA binding prot	hypothetical prote	

		13														
		38														
46.2	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5		47.5			
92	588	583	488	488	488	402	352	351	128	118	110	109	109	96	92	
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	
S37514	JC7206	B87204	B96521	AG0621	AD0735	D90034	A49146	C36470	S20636	T03036	S20635	D30601	G30601	T07138	837517	
Ig kappa chain	phosphoprotein	probable acyl-CoA	protein F21D18.20	probable bacterior	conserved hypothe	hypothetical	developmental	Wnt-4 protein	Ig kappa chain	Ig light chair	Ig kappa chai	Ig kappa chair	Ig kappa chair	O.	Ig kappa chain	

ALIGNMENTS

hypothetical protein 01784.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19356
R;Percy, C.
R;Percy, C.

October 1996

submitted to the EMBL Data Library, A;Reference number: Z19113
A;Accession: T19356

A; Molecule type: DNA A; Residues: 1-205 < WIL> A; Status: preliminary; translated from GB/EMBL/DDBJ

A.Cross-references: RMB1:281037; PIDN:CAB02750.1; GSPDB:GN00019; CESP:C17E4.5 A.Experimental source: clone C17E4 C.Genatios:

A; Introns: 22/3; 120/2 A;Gene: CESP:C17E4.5 A;Map position: 1

Matches Query Match Local l Similarity 7; Conserv Conservative 55.0%; Score 44; DB 2; Length 205; Pred. No. 2.9; Mismatches 5

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Gaps

111 CDRFSGHPKGFAY 123 CXXYGNSPKGFAY 13

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polyA binding protein II - bowine Cipter: 0.5ep-1999 #text_change 05-Nov-1999 Cipter: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Nov-1999 Cipteresion: 0.5ep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Nov-1999 Cipteresion: 0.5ep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Nov-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1

A. Statuts: preliminary; nucleic acid sequence not shown; translation not shown A. Modecule type; mEWA A. Residues: 1-306 (NEM)

A;Cross-references: EMBL:189969; NID:91056777; PIDN:CAA62006.1.P EDR:91051125 A;Fote: the nucleocitide sequence was submitted to the EMBL Data Library. 1995 C;Super:Emally: bovine polyA binding protein II; ribonucleoprotein repeat homology F;I71-239/Domain: ribonucleoprotein repeat homology KRM20:

Matches Local Similarity hes 7; Conserv Conservative 53.8%; Score 44; DB 1; Length 306; Pred. No. 4.2; Mismatches 5; Indels

Gaps

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Holroyd, Gordon

genom

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CPP-binding protein - African clawed frog

N,Alternate names: cytoplasmic polyadenylation element-binding protein

C;Specides: Menopus laevis (African clawed frog)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C;Accession. A55377

R;Hake, L.E.; Richter, J.D.

Cell 79, 617-627, 1994

A;Telle: CPEB is a specificity factor that mediates cytoplasmic polyadenylation during

A;Telle: CPEB is a specificity factor that mediates cytoplasmic polyadenylation during

A;Reference number: A55377; MIID:95042759; PMID:7954828
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A55377
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A; Molecule type: DNA
A; Meseidues: 1-166 < OOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Volckaert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rma binding protein - fission yeast (Schizosaccharomyces pombe)
Cispecies: Solizosaccharomyces pombe
Cispecies: 03.Dec-1999 #sequence_revision 03-Dec-1999 #text_change
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C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Immunol. 142, 3158-315, 7998.
A.Title: Structural and idiotypic characterization of the L chains of human IgM autoanth. A.Reference number: A30601; MUID:89215279; PMID:2496160
A.Reference number: A30601; MUID:89215279; PMID:2496160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V-III region (Bor) - human (fragment)
C:Specios: Homo eapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: SPDB:SPBC16E9.12c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: strain C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: Z99759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z21865
A; Accession: T39586
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A; Residues: 1-109 <GON>
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2h-; cosmid c16E9
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Pred. No. 5.2;
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                                                            A;Map position: 1
A;Genome: nucleomorph
C;Keywords: nucleomor
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H90083
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                                                            Keywords: nucleomorph
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probable Acyl-CoA Synthetase - Mycobacterium tuberculosis (strain 1978V)
C.Spacias: Mycobacterium tuberculosis
C.Spacias: Mycobacterium tuberculosis
C.Jaces 17-Jul-1998 Hesquence_revision 17-Jul-1998 Hesq. Change 20-Jun-2000
C.Accession: B70749, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go
R.Gole, S.T.; Brooch, R.; Devilin, K.; Belbeell, T.; Gentles, S.; Hamlin, N.; Holl
Mandor, R.; Davies, R.; Devilin, K.; Belbeell, T.; Gentles, S.; Hamlin, N.; Holl
Manue 333, 517-544, 2988
Manue 333, 517-544, 2988
Manue 333, 517-544, 2988
Manue 335, Mycles, R.; Bulscon, J.B.; Taylor, K.; Mhicehead, S.; Barrell, B.G.
M.Fille: Deciphering the biology of Mycobacterium tuberculosis from the complete
M.Reference number: A70500, WID: 98235987, PMID: 9814210
M.Roccession: B70749
M.Status: preliminary; mucleic acid sequence not shown translation not shown
M.Rocceule type: DMA
M. Reference number: A70500, MID: 98235987, PMID: 9814210
                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 < LOUD
A;Cross-references: GB:AF165818;
                                                                                                                                                          polyademylate-binding protein (imported) - Guillardia theta mucleomorph CySpecies: mucleomorph Guillardia their Buckless of a eukaryotic endosymbiont CyDate: 10-may-2001 #sequence_revision 10-may-2001 #text_change 24-may-2001 CyDates: 10-may-2001 #sequence_revision 10-may-2001 #text_change 24-may-2001 R.Pouglas, S.; Frauncer, S.; Fraunchlz, M.; Penton, M.; Penny, S.; Deng, L.T. Mature 410, 1091-1096, 2001
A.; Mille: The highly reduced genome of an enslaved algal nucleus.
A.; Reference number: A99082; MIID:11323671; PMID:11333671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: fadD26
C;Superfamily: 4-coumarate-CoA ligase;
F;103-610/Domain: acetate-CoA ligase h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.|Crose-references: GB.274697; GB:AL123456; NID:g3261602; PIDN:CNA98985.1; PID:g140596
A.|Experimental source: strain H37Rv
C.|Genetigs:
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A/Statuts; preliminary, not compared with conceptual translation
A/Statuts; 1-550 ABAN.
A/Residutes; 1-550 ABAN.
A/Crose-references; GB:UV.169; NID:9987224; PINN:AAA80483.1; FID:9624634
A/Crose-references; GB:UV.169; NID:9987224; PINN:AAA80483.1; FID:9624634
C/Superfamily: African clawed frog CEF-binding process, ribonicleoprotein repeat homology ARM1.
FJ14-189/Domain: ribonucleoprotein repeat homology ARM1.
A;Cross-references:
C;Genetics:
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7; Conserv
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                                    NID:g13794428;
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Pred. No.
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Pred. No. 19;
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17;
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                                    PIDN: AAK39803.1; GSPDB:GN00150
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51.2%;

Score 41; Pred. No.

DB 18;

2,

Length 389;

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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connoc, R.; Davies, R.; Devin, K.; Feltwell, T.; Gentles, S.; Hanlin, N.; Helroyd, S.; Rajandream, M.A.; Rogers, U.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Sharris, S.; Seeger, K.; Skelton, S.; Squares, S.; Sharris, S.; Seeger, K.; Skelton, S.; Squares, S.; Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris, Sharris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequenc
C;Accession: S75579
R;Kaneko, T.; Sato, S.; Kota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: G8:274020; G8:A1123456; NID:93261584; PIDN:CAA98332.1; PID:91403483
A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          threonine ammonia-lyase (BC 4.3.1.19) ilvA (similarity) - Mycobacterium tuberculosis (st
C.Species: Mycobacterium tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jun-2002
C.Accession: D20763
                                                                                                                                                                                                                                                                  A:Cross-references: RMBL:D09011; GB:AB001139; NID:gl65083; FINLMANI410.1; PID:gl65322
A:Note: the nucleoride sequence was submitted to the EMBL hat Nibrary. June 1996
C:Superfamily: hypothetical protein al1084; Iranslation elongation factor Tu homology
C:Keywords: GTP binding; nucleoride binding; P-loop
F:62-716/Domain: translation elongation factor Tu homology <8TU>
F:63-75/Region: nucleoride-binding motif A (P-loop)
F:63-75/Region: nucleoride-binding McDi motif;
F:63-75/Region: nucleoride-binding McDi motif;
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A;Molecule type: DNA
A;Residues: 1-453 <KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: 874322; MUID: 97061201; PMID: 8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Kanako, T., Sato, S.; Kotani, H., Tanaka, A., Asamizu, E., Nakamiz, Y., Miyajima, N.
o, K., Okumiza, S.; Shingo, S., Takacahih, C., Wada, T., Matanabo, A., Yamada, M., Yasan
UNA Res. 3, 109-116, 1996
A,Title: Sequence analysis of the genome of the unicellular cyanobacterium Symechocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein sll0804 - Synechocystis sp.
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Best Local
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                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                       367-369/Region: GTP-binding SAK/L motif
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7; Conserv
YGNSPKG 10
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                                                                                                                                      Score 41;
; Pred. No.
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Pred. No. 21;
Mismatches
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A; Residues: 1-2515 < GOL>
                                                                                                                                                                                                                                                                        RESULT 12
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Matches 7
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7; Conserv
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Conservative

58.3%; 51.2%; 1;

Pred. No. 84; Score 41; Mismatches

DB 1; Length 1866

Gaps

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Indels
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N;Contchins: 24K viral proteinase (EC 1.4.22.-), 32K proteinase cofactor; 58K membrane-b
Ciphecias: compea abhid-borne mossic virus, CABMV
Ciphece: 18-Apr-1964 Hesquence_revision 18-Apr-1964 #text_change 31-Mar-2000
Ciphece: 18-Apr-1964 Hesquence_revision 18-Apr-1964 #text_change 31-Mar-2000
AlMore: the polyprotein is cleaved to give at least eight mature proteins; however, hallone: the authors translated the codon AMI for residue 50 as ABD, CAG for 844 as Cisuperfemily, coppes aphid-borne mosaic virus genome polyprotein; proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, proteins, p
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A;Title: The nucleotide sequence
A;Reference number: A04211
A;Accession: A04211
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A; Residues: 1-1866 < LOM>
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posiestior-group profesh tudor - fruit fly (Drosophila malanogaster)
C.Spaceise; Drosophila malanogaster
C.Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1999
C.Dacession AMISI9; S1901
C.Dacession AMISI9; S1901
R.E. Bardeley, A.; Tax, F.; Boswell, R.E.
Genes Dev. 5, 2660-2070, 1991 A.Fitle: tudor, a posterior-group gene of Drosophila melanogaster, A.Feterance number: A41519; MUID:92038995; PMID:1936993 A.A.Cosssion: A41519. encodes a novel

prot

A;Gene: tud A;Cross-references: FlyBase:FBgn0003891 C;Superfamily: posterior-group protein tudor

1 Similarity 7; Conserve YGNSPKGF 11 Conservative 51.2%; 87.5%; 0, Pred. No. 1.1); Mismatches 1.1e+02;

Score 41;

DB 2;

Length 2515;

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Gaps

0

ABJA499 hypothetical exported protein BMEI1982 (imported) - Brucella melitensis (strain CyBecies: Brucella melitensis (c.Paecies: Brucella melitensis (c.Paecies: O.Peb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 c.Accession: ABJA499

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 LOS, T.; Ivanova

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A;Molecule type: DNA
A;Residues: 1-359 <BAR>
A;Cross-references: EMBI
C;Genetics:
                                                                                                                                                                                           R.Barra, J.L.; Mautino, M.R.; Rosa, A.L.
submitted to the BMSL Data Library, September 1995
A;Description: Eth-Ir, a mutant allele of Neurospora crassa S-adenosylmethionine synthe
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G;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
fain disultide bonds. In some cases, such as 1gA and 1gM, the subunits associate into 1s
C;Superfamily: immunoglobulin v resjoin; immunoglobulin homology
G;Keywords: heterotetramer; immunoglobulin doming
C;Keywords: heterotetramer; immunoglobulin doming
C;Keywords: heterotetramer; immunoglobulin doming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Newkirk, M.; Chen, P.P.; Carson, D.; Posnett, D.; Capra, J.D. Mol. Imman. 23, 239-244, 1986 Mol. Imman. 23, 239-244, 1986 A;Title: Maino. 230d sequence of a light chain variable region of a human theumatoid fact A;Reference number: A01893; MUID:86230578; PMID:3086710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
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A;Experimental source: strain 16M
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A;Molecule type: DNA
A;Residues: 1-107 <KUR>
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A;Reference number: AD3252; PMID:11756688
                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                             A; Reference number: Z24392
A; Accession: T47208
                                                                                                                                                                                                                                                                        C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000 C;Accession: T47208
                                                                                                                                                                                                                                                                                                  C;Species: Neurospora crassa
C;Date: 20-Apr-2000 #sequence
                                                                                                                                                                                                                                                                                                                                                 methionine adenosyltransferase (BC 2.5.1.6) [imported] - Neurospora crassa (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;23-89/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 1-109 < NEW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A01893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V-III region (Gol) - human
N; Alternate names: rheumatoid factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: AH3499
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Matches
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Best Local
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   Intron positions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRSYGFKPKTDAFANC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                  EMBL: U36761; PIDN: AAA83756.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
not resolved (incomplete sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.5%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1;
Pred. No. 7.7;
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3.1721 secs

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2003, 07:36:21

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A./Map position: 12R
C:Function:
A.Description: transferase
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase
                                                                                                                                                                                                                                                                                                               A; Modacule type: DNA
A; Resdatues: 1-245, TY, 247-356, FF, 358-383 <THO>
A; Cross-references: RMSL:003477; NID:9173533; FIDN:AAA66932.1; FID:9172534
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                      R;Thomas, D.; Surdin-Kerjan, Y.
Biol. Chem. 262, 16704-16709, 1987
A;Title: SAM1, the structural gene for one
A;Reference number: A92621; MUID:88059059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; WOhldmann, P. submitted to the EMBL Data Library, November 1994 A; Description: The sequence of S. cerevisiae cosmid 9470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
SS1425
SS1425
Methionine adenosyltransferase (BC 2.5.1.6) 1 - yeast (Saccharomyces cerevisiae)
Methionine adenosylmethionine synthetase 1
N;Alternate names: protein 19470.9; protein YLR180w, S-adenosylmethionine synthetase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: methionine adenosyltransferase C;Keywords: S-adenosylmethionine; transferase
                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A28480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: S51414
A;Accession: S51425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Wohldmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S51425; A28480
                                                                                                                                                                                                                                                                       A; Cross-references:
                                                                                                                                                                                                                                                                                           A; Gene: SGD: SAM1; ETH10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U17246; NID:g577192; PIDN:AAB67461.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-382 < WOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, MOLECULE type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Species: Saccharomyces cerevisiae
;Date: 23-Feb-1995 #sequence_revision 11-Aug-1995 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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hes 7; Conserv
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79
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                                    4 YGNSPKGPAYXXC 16
                                                                            Similarity
7; Conserv
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YDDSAKGFDYKTC
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                                                                               Conservative
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                                                                                                50.0%;
91

    Mismatches

                                                                                                   Score 40;
Pred. No.
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Pred. No. 25;
                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      of the S-adenosylmethionine synthetases in PMID:3316224
                                                                                                26;
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GenCore version 5.1.6
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1993
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OM protein - protein search, using sw model Run on: November 7, 2003, 07:21:18; Search time 1.15354 Seconds (without alignments)
652.278 Million cell updates/sec

Scoring table: Sequence: Perfect score: US-09-661-992B-105 80 BLOSUM62 CXXYGNSPKGFAYXXC 16

127863 seqs, 47026705 residues Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result heing printed, and is derived by analysis of the total score distribution.

SUMMARIES

32 32	29 30	26	224	21 22	19 20	17 18	16	14	13	;=	10	0 00	7	o 1	ла	. u	N	۲,	Result
37 37 37	37 37	37	ມ ມ ມ ສ ສ ສ	38	39 39	39	40	4 0	440	40	4 4	4 4	40	41	4 4 12 F	*	43	43	Score
46.2 46.2	46.2 46.2		47.5	47.5	48.8	48.8	50.0	50.0	50.0	50.0	50.0	50.0	50.0		51.2	3 0	53.8	53.8	Query Match
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VTDB_MOUSE VTDB_RAT V233_FOWPV	PHHY PSEAR PHHY PSEAR	KV3B_HUMAN	WNT4_RAT WNT4_XENLA WN4A_BRARE	WNT4_HUMAN	ATE1_YEAST CH60_LEIMA	WNT4_CHICK	METL CAEEL	METK RAT	METK_NEUCR	METK_ASCIM	METL YEAST	METK SCHPO	KV3G_HUMAN	TUD DROME	VGNB CPMV	THIN MYCTH	S21C_RAT	SZIC_MOUSE	ID
P21614 mus musculu P04276 rattus norv Q9j502 fowlpox vir	P20586 pseudomonas P00438 pseudomonas		Q9qxq5 rattus norv P49338 xenopus lae P47793 brachydanio		P16639 saccharomyc Q94596 leishmania	7 2		-	P48466 neurospora			P10659 saccharomyc			_	010766 mycobacteri			Description

v	44	43	42	41	40	39	38	37	36	35	4
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45.0	45.0	45.0	45.0	45.0	45.0	45.0	45.0	45.0	45.0	46.2	46.2
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YK69_YEAST	S21C_HUMAN	LYP1_YEAST	RPSD_BUCBP	HOS2_YEAST	METK DROME	METL RAT	METL HUMAN	P2A5_TOBAC	KV3D HUMAN	RNT1_DROME	LAC3_THACU
P36165	Q96bd0	P32487	OTGERO	253096	P40320	P13444	000266	004860	P01622	FBAAGO	002079

ALIGNMENTS

888888888	88888888888		RESULT 1 S21C_MOU S21
Note-No experimental confirmation available notering. 1. SINILARITY: BELONGS TO THE SLC21 FAMILY OF TRANSPERS. 1. SINILARITY: BELONGS TO THE SLC21 FAMILY OF TRANSPERS. This SMISS-PROT entry is copyright. It is produced through a collabble through the same of the collaboration and the smiss Institute of Bioinformatics and the SMEJ outset the European Bioinformatics Institute. There are no restrictions the European Bioinformatics Institute, There are no restrictions by non-profit institutions as long as its content is in removed and this statement is not removed. Usage by and for commodified and this statement is not removed.	Schwarch A., Schwin J.B., Jones S.J.M., Marra W.A.; "Generation and mouse cDNA sequences"; human and mouse cDNA sequences"; proc. Marl. Acad. Sci. U.S.A. 99:16899-18903 (2002). - FUNCTION: Mediates the Na(+)-independent transport of organic - anions such as the thyroid hormone T3 (trilodo-y-thyronine) and tawrocholate (By similarity). - INTERMENTION BROUNCES: integral membrane protein. - MATERMENTION BROUNCES: integral membrane protein.	DURNCH FROM N.A. (18090RMS 1 AND 2) ALIM-G75H/6, TSUSHB-RELIAR LIMB-B2388257, PhiMed-12477992; munner R.D. Gollins P.S., Wagner L., schill S.P. Gollins P.S., Wagner L., schill S.P. Zeeberg B., Buccow K.H., schill S.P. Zeeberg B., Wagner L., schill S.P. Zeeberg B., Wagner L., schill S.P. Zeeberg B., Wagner M., placton M., Soundal M. D., Street B.G. Juliation D.K., Mazzy D.M., Koderman K.J., harda S. Mottley K.C., Hale S., Gatz- Mask S.H., Medsan P.J., McKerman M., Madan Lidadon D.K., Mazzy D.M., Sodergren S. hey J., Helton S., Ketteman M., Madan Lidadon D.K., Mazzy D.M., Green E., talyauz K.G., Grimwood J., Schmutz J., tterffield Y.S.M., Krzywinski M.T., SS	MOISE STANDARD; PRT; 723 AA. 1821 MOUSE STANDARD; PRT; 723 AA. 1826-FEE-2003 (Rel. 41, Created) 28-FEE-2003 (Rel. 42, Last amnotation update) 15-SEP-2003 (Rel. 42, Last amnotation update) 15-SEP-2003 (Rel. 42) Last amnotation update) 16-SEP-2003 (Rel. 42) Last amnotation update) 17-SEP-2003 (Rel. 42) Last amnotation update) 18-SEP-2003 (Rel. 41) Created) 18-SEP-2003 (Rel. 42) Last amnotation update) 18-SEP-2003 (Rel. 41) Last amno

min's S.S. Loquelianon's N. Peters'G.J. Abramson R.D. Millsly S.J.

Ra Blobark S.A. Modram D.J. McKernam K.J. Malek J.A., Gay L.J. Hulyk S.W.,

Richards S. Worley K.C. Hale S. Garcia A.M., Gay L.J. Hulyk S.W.,

Ra Richards S. Worley K.C. Hale S. Garcia A.M., Gay L.J. Hulyk S.W.,

Ra Richards S. Worley K.C. Hale S. Garcia A.M., Gay L.J. Hulyk S.W.,

Ra Palley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Ra Halkesley R.W. Touchman J.W., Green E.D., Dickson M.C.,

Ra Balkesley R.W. Touchman J.W., Green E.D., Dickson M.C.,

Ra Balkesley R.W., Young A.C., Schevchenko Y., Boutfard G.G.,

Ra Balkesley R.W., Young A.C., Schevchenko Y., Boutfard G.G.,

Ra Balkesley R.W., Young A.C., Schevchenko Y., Boutfard G.G.,

Ra Balkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ra Balkesley R.W., Schein J.S., Jones S.J.W., Marra M.A.;

Ra Balkesley R.W., Schein J.S., Jones S.J.W., Marra M.A.;

Ra Balkesley R.W., Schein J.S., Jones S.J.W., Marra M.A.;

Ra Balkesley R.W., Schein J.S., Jones S.J.W., Marra M.A.;

Ra Balkesley R.W., Schein J.S., Jones S.J.W., Marra M.A.;

Ra Balkesley R.W., Schein J.S., Jones S.J.W., Marra M.A.;

Ra Balkesley R.W., Schein J.S., Jones S.J.W., Marra M.A.;

Ra Balkesley R.W., Schein J.S., Jones S.J.W., Marra M.A.;

Ra Balkesley R.W., Schein J.S., Jones S.J.W., Marra M.A.;

Ra Balkesley R.W., Schein J.S., Jones S.J.W., Marra M.A.;

Ra Balkesley R.W., Schein J.S., Jones S.J.W., Marra M.A.;

Ra Balkesley R.W., Jones R.W., Marra M.A.;

Ra Balkesley R.W., Jones R.W., Marra M.A.;

Ra Balkesley R.W., Jones R.W., Jones R.W., Marra M.A.;

Ra Balkesley R.W., Jones R.W., Jones R.W., Jones R.W., Jones R.W., Jones R.W., Marra M.A.;

Ra Balkesley R.W., Jones R.W.

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(See http://www.isb-sib.ch/announce/

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Query Match
Best Local S
Matches
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Q99N01;
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EMBL; BC030720; AAH30720.1; -I.
EMBL; BC03062; AAH3620.1; ALT_INIT.
EMBL; BC03362; AAH3620.1; ALT_INIT.
MGD; MGI:1351866; Slc21a12.
IntexPro; IPR04156; OATP_Nterm.
                                            molecules are involved in a tissue-specific manner.";
Budocrinology 142:2005-2012(2001)
-1- PUNCTION: Declares the Na(+)-independent transport of organic
anions such as the thyroid hormone T3 (trilodo-L-thyronine) ar
                                                                                                                                                                                                                         28-FRB-2003 (Rel. 41, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Solute carrier family 21 member 12 (Sodium-independent
transporter B) (Organic anion transporting polypeptide
SLC21A12 08 OAPS
Battus norvegious (Rel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Alternative splicing.
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Pfam; PF03132; OATP_N; 2.
TIGRFAMs; TIGR00805; oat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an
                                                                                         Onogawa T., Szzuki T., Asano N., Tanemoto M., Seki
Suzuki M., Kondo Y., Nunoki K., Shimosegawa T., Ii
Matamo S., Abe T.,
"Identification of thyroid hormone transporters in
                                                                                                                         MEDLINE=21216537; PubMed=11316767;
Fujiwara K., Adachi H., Nishio T., Unno M.,
Onogawa T., Suzuki T., Asano N., Tanemoto M
                                                                                                                                                                                       NCBI_TaxID=10116;
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N-LINKED (GLCNAC...) (I
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Sciurognathi; Muridae; Murinae; Rattus
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Seki M., Shiiba K.,
T., Iinuma K., Ito S.
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                                                                                                                                                                                            cole S.T., Brosch R., Parkilll J., Garnier T., Churcher C., Harris Gordon S.V., Biglaeler K., Gas S., Barry C.E. III, Tekaia P., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Davier R., Deviln K., Feltvell T., Gentles S., Hanlin N., Bolroyd Hornsby T., Jagals K., Kroop A., McCam J., Moule S., Murph L., Oliver S., Gesper J., Guall M.A., Rajandream M.A., Rogers J., Sutter S., Gesper K., Stellon S., Squares S., Guaree R., Sulston J.E., Taylor K., Mitchead S., Barrell B.G.; Taylor K., Mitchead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPD5 (MYCTU STANDARD; PRT; 583 AA. Q10976; (61 - 14) Created) 01-0071-901 (Rel. 40, Last sequence update) 16-0071-2001 (Rel. 40, Last amoutation update) butaitive fatty-acid--0A ligase fablo26 (EC 6- 6)
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ŚEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae,
Corynebacterineae, Mycobacteriaceae, Mycoba
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                                                                                                                          Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence." Mycobacterium 239:537-544 (1998)."
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthetase).
FADD26 OR RV2930 OR MT2999 OR MTCY338.19.
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InterPro; IPR004156; OATP_Nterm
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Mycobacterium.
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THD1_MYCT
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Matches 7
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01-OCT-1996 (Rel. 3)
28-FEB-2003 (Rel. 4)
Probable threonine
Code S.T. Brosch R., Parkhill J., Garnier T., Churcher G., Har Gordon S.V. Bigjameirr K., Cas S., Barry C. B. III. Tekeis: Badcock K., Basham D., Brown D., Chillingworth T., Comor R., Davies R., Devilin K., Feltwell T., Genles S., Hamlin M., Holtow Hornsby T., Jagels K., Krogh A., McLeau J., Moule S., Murphy J., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Nogers J., Butter S., Seeger K., Keakton S., Squares S., Squares R., Sulscon J.E., Taylor K., Mahtehead S., marreil B.G., "Deciphering the blology of Mycobacterium tuberculosis from the complete genome sequence.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Q10766;
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                                                                                                                SEQUENCE FROM N.A.
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Tuberculst; R7230; ...
TutestPo; IPRO00873; AMP-bind.
FRam, PRO0051, MMP-binding; 1
FRam, PRO0051, MMP-binding; ALSE_MEG.
HROSTTE; PRO0455; AMP_BINDING; ALSE_MEG.
HYPOPhetLoal procean; Ligase; Fatry ācid metabolism;
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Submitted (APR-2001)
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Kolonay J.F., Nelson M.C., Umayam L.A., EmroLaeva M.D., Salibb
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikn
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Pred. No.
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n M.L., Haft
, Ermolaeva M
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., Mikula A.,
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RESULT 5
VGNB_CPMV
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Best Local s
Matches 7
                                                           SEQUENCE PROM N.A.

LOMONOSSOFÉ G.P., Shanks M.;

I'The nucleotide sequence of c

EMBO J. 2:2253-2258 (1983).

-i- CAPALYTIC ACTIVITY: N nucleotide sequence.
                                                                                                                                                                                POSCÓD:
21.-UL-1996 (Rel. Ol. Created)
21.-UL-1996 (Rel. Ol. Last sequence update)
28-FEB-2003 (Rel. Al. Last annobation update)
28-FEB-2003 (Rel. Al. Last annobation update)
genome polyprotein B (Contains: Processe cofactor; Membrane binding
protein; PGp Processe (CS 3.4.22.-); RNA polymerase (EC 2.7.7.48)].
Compse mosaid virus (CPMV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z74020; CAA98332.1; -.
EMBL; AB007027; AAX45877.1; -.
PIR; D70763; D70763.
HSSP; P04968; ITDJ.
TIGR; MT1510; -.
                                                                                                                                                   NCBI_TaxID=12264;
                                                                                                                                                                             Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00585; Thr dehydrat C; 1.
PROSITE; PS00165; DEHYDRATASE SER THR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00291; PALP;
Pfam; PF00585; Thr d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001926; B6 enzyme beta.
InterPro; IPR000634; S/T dehydrtse.
InterPro; IPR001721; ThrDh_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenses@sb-sib.ch/a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - PUNCTION: Catalyzes the formation of alpha-Recoburyrate from
threonine in a two-esp reaction. The first step is a debydration
of threonine, followed by rehydration and liberation of ammonia.
- CAPALYTE CATUTYTY: Letreonine - 2.000butanoace + NH(3).
- COPACTOR: Pyridoxal phosphate (By similarity.
- PATHMY: Isolaudine biosyminesis fitter step.
- PATHMY: Isolaudine biosyminesis fitter step.
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Bishai W.;
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                      {RNA}(N).
- PTM: SPECIFI
- SIMILARITY:
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429 AA;
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                        COMOVIRUSES GENOME POLYPROTEIN
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                                                               nucleoside triphosphate = N diphosphate
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                                     CLEAVAGES
                                                                                          cowpea mosaic virus
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                                                                                                                                                                           stage; Comoviridae;
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                                     PROTEINS
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copyright. It is produced through a collaboration

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RESULT 6
TUD_DROME
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMPL outstands on the EMPL outstands on the EMPL outstands on the EMPL outstands of the content is in no way use my non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                     NEDLINE-201995; PubMed-1916993;

GOLUMbeski G.S., Bardalay A., Tax F., Bonwell R.E.;

Trindor, a posterior-group gene of Drosphila melanogaster, encodes novel protein and an mRNA localized during mid-openesis.', Genes Dev. 5:2660-2070(1991)

-1- FUNCTION: REQUIRED UNITHO OCCENESIS FOR THE FORMATION OF PRIMORDIAL GROWN CELLS AND FOR NOMBOL ABOOMINAL SEGMENTATION.

-1- REGIOUNDE THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachbycera; Muscomorpha;
Biphydroidea; Drosophildae; Drosophila.
MCBI_TAXID=727;
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01-MAY-1992 (Rel. 22,
28-FEB-2003 (Rel. 41,
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Pfam; PF00910; RNA helicase; 1.
PRINTS; PR00918; CALICVIRUSNS.
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InterPro; IRR000605; RNA helicase.
InterPro; IRR007095; RNA pol DS PS.
InterPro; IPR001205; RNA pol P3D.
InterPro; IPR007094; RNA pol P8vir.
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    -!- SIMILARITY: Contains 9 Tudor domains.

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MEROPS; C03.003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41;
Pred. No.
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THIOL PROTEASE (POTENTIAL)
THIOL PROTEASE (POTENTIAL)
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PROTEASE COFACTOR (POTENTIAL)
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RNA-DIRECTED RNA POLYMERASE (POTENTIAL)
ATP (POTENTIAL).
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Query Match

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Best Local
                                                                                                                                                                                                         Nawkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
"Amino acid sequence of a light chain variable region of a human
reactivity with antispertide antibodies.",
Mol. Immunol. 23:239-244(1986).
PIR, And1893; KSUGOO.
BISSP, P80362; INTL.
GO; GO:0005525; Framtigen binding activity, NAS.
GO; GO:0005825; Framtigen binding activity, NAS.
GO; GO:0005825; Framtigen binding activity, NAS.
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                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINB=86230578; PubMed=3086710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutero
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAR-1987
20-MAR-1987
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SMART; SM00333; TUDOR; 10.
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60; GO:001999; P:mitochondrial rRNh, mitochondrial export; IMP.

60; GO:007315; P:pole plasm assembly; IMP.

InterPo; IPR001097; Maternal tudor.

InterPo; IPR001299; Tudor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X62420; CAA44286.1; -.
PIR; A41519; A41519.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
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   109 AA;
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(Rel. 04, Last sequence update)
(Rel. 38, Last annotation update)
                          109
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   11830 MW;
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87.5%;
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Pred. No.
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   9349A5B1D93588B6 CRC64;
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                                          SIMILARITY
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43;
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swiccid', "Gellisa's N. Tajandaras M. Jurge R. Scewart A.
RA Sgoures J. Peat N. Hayles J. Baker S. Basham D. Bownan S.
RA Brooks K., Bromn D. Brown S., Chillingworth T., Churcher C.R.
RA Cenlise M., Gonnor R., Cronin A., Davis P., Feltwell T., Fraser A.
RA Cenlise S., Gohle A., Hamiin N., Harris D., Hdalago J., Hodgen G.,
RA Gencles S., Gohle A., Hamiin N., Harris D., Hdalago J., Hodgen G.,
RA Holroyd S., Horneby T., Howarth S., Hoches LJ., Hunt S., Jagels K.,
RA Wooney E., Houle S., Mangall K., Marphy L., Mblett D., Goell C.,
RA Wooney E., Houle S., Mangall K., Marphy L., Mblett D., Goell C.,
RA Wooney E., Houle S., Mangall K., Marphy L., Mblett D., Goell C.,
RA Wooney E., Houle S., Mangall K., Marphy L., Mblett D., Goell C.,
RA Wooney E., Houle S., Mangall K., Marphy L., Mblett D., Goell C.,
RA Wooney E., Walter S. Samonder D., Seeger S., Stewens K.,
RA Taylor K., Taylor R.G., Tivey A., Walzh S.V., Warren T., Witchead S.,
RA Welljens I., Vonckser G., Apart R., Robber J., Gryonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mallar-Awer S.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mallar H.,
RA Welljens I., Wanstreels M., Lehrach H., Reinhardt R., Pohl T.M.,
RA Welljens I., Vanstreels M., Lehrach H., Reinhardt R., Pohl T.M.,
RA Welljens I., Wanstreels M., Lehrach H., Reinhardt R., Pohl T.M.,
RA Welljens I., Wanstreels M., Lehrach H., Reinhardt R., Pohl T.M.,
RA Welljens I., Wanstreels M., Lehrach H., Reinhardt R., Pohl T.M.,
RA Welljens I., Wanstreels M., Welder H., Wander K., Hurte S.,
RA Welljens I., Wanstreels M., Wanstreels M., Watter R.,
RA Welljens I., Wanstreels M., Wanstreels M., Watter R.,
RA Wander M., Ramermann M., Wedder H., Wander K., Puttall B.,
RA Watter M., Wanstreels M., Warren P., Strabourg S.L.,
RA Gallbert E., Nees S.J., Misser J., Marse P., Schabert M., Charles M., del Rey F., Benico J.,
RA Gallbert E., Wesser J., Barterla B.G., Warren P.,
RA Suphowski G., Wanstreels M., Warren P., Schabert M., Watter D., Horner J., Puttandruk P., Puttall M., Wanter P.,
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Matches
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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S-adenosylmethionine synthetase (EQ 2.5.1.6)
adenosyltransferase) (AdoMet synthetase).
SAMI OR SEPC1455.05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Gene saml encoding adenosylmethionine synthetase: effects of its expression in the fission yeast Schizosaccharomyces pombe.", Yeast 16:1-10(200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hilti N., Graub R., Jorg M., Arnold P., Schweingruber A.M. Schweingruber M.E.;
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15-DEC-1998
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MEDLINE=20089020; PubMed=10620770;
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Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces.
                                                                              diphosphate + S-adenosyl-I-methionine.
COPRCTOR: Binds 2 divident ions, such as magnesium c
1 potassium ion per subunit (By similarity).
PATHMAY: Activated methyl cycle.
SIMILARITY: BEDONGS TO THE ADONET SYNTHETASE FAMILY.
                                                                                                                                                                                             FUNCTION: Catalyzes the formation of S-adenosylmethionine from methionine and ATP.
CNTALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
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6; Conserv
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2; Mismatches
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Bioinformatics Institute.

There are no

restrictions on

CK STEALNS-SSSSG / MS972;
CK STEALNS-SSSSG / MS972;
CK STEALNS-SSSSG / MS972;
CK STEALNS-SSSSG / MS972;
CK STEALNS-SSSSG / MS972;
CK STEALNS-SSSG
SEQUENCE FROM N.A

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PROSITE, P800377, ADOMET_SYNTHETASE 2, 1.
Transferase; One-carbon mecabolism; ATP-binding, Magnesium;
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InterPro; IPR002133; S-AdoMet_synt.1.
Pfam; PF0438; S-AdoMet_syntD2; 1.
Pfam; PF02772; S-AdoMet_syntD2; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ001705; CAA04941.1; -. EMBL; AL023780; CAA19323.1; -. PIR; T39451; T39451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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MAGMESIUM (BY SIMILARITY).

POTASSIUM (BY SIMILARITY).

POTASSIUM (BY SIMILARITY).

MAGMESIUM (BY SIMILARITY).

ATP (POTENTIAL).
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synthetases in 
J. Biol. Chem.
                MEDLINE-88059059; PubMed=3316224;
Thomas D., Surdin-Kerjan Y.;
"SAMI, the structural gene for one of the
                                                  SEQUENCE FROM N.A.
Saccharomyces cerevisiae.
262:16704-16709(1987).
        Sequence
                  S-adenosylmethionine
        expression.";
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RESULT 10
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P19358;
01-NOV-1990
01-OCT-1994
28-FEB-2003
01-NOV-1990 (Rel. 16, Creeted)
01-077-1994 (Rel. 30, Last sequence update)
08-FEE-2003 (Rel. 41, Last amnotation update)
S-adenosylmethionine symthetase 2 (Rel 2.5.1.6)
adenosyltransferase 2) (Adoles symthetase 2).
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By non-profit institute. There are no restrictions on its motified and this statement is not removed. Usage by and for commercial or sented are quite a license spreement (see http://www.isb-sib.ch/announce/created are quite and are mail to licenses.sb-sib.ch).
                                                                                                                                                                                                                                                                                                                        SINDING
CONFLICT
CONFLICT
                                                                                                                 YEAST
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PROSITE: PS00377; ADOMET_SYMTHETASE 2; 1.
Transferase: One-carbon metabolism; Multigene family; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002133; S-AdoMet_synt.
Pfam; PF007438; S-AdoMet_synt. 1.
Pfam; PF00773; S-AdoMet_syntD2; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
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HSSP; P04/34; JMM,
SSD; S0004/70; SMI,
SSD; S0004/70; SMI,
CO; G0:0005/73; Cryrcplasm, IDA,
CO; G0:0005/73; Cryrcplasm, IDA,
CO; G0:00064/78; Franchionine adenosyltransferase activity; IGI.
                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  Magnesium; Potassium; Metal-binding.
NP_BIND 118 123 ATP (POTENTIAL)
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EMBL; U17246; AAB67461.1; -.
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[3]
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-!- FUNCTION: CATALYZES THE FORMATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Protein expression during exponential Saccharomyces cerevisiae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s WHISS-PROT entry is copyright. It is produced through
ween the Swiss Institute of Bloinformatics and the EN
Buropean Bioinformatics Institute. There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: Binds 2 divalent ions, such as mag:
1 potassium ion per subunit (By similarity).
PATHMAY: Activated methyl Cycle.
SUBUNIT: Heterotetramer.
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CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O diphosphate + S-adenosyl-L-methionine.
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7; Conserv
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                                                                                               STANDARD;
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POTASSIUM (BY SIMILARITY)
POTASSIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
                                                                                                                                                                                                                                                           Pred. No. 10;
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I -> F (IN REF. 1).
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                                                                                               PRT;
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                                                                                                                                                                                                                                          Mismatches
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EMBL outstation -
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use by non-productive institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or and an email to licenseesib-sib.ch).
                                                                                                                                                                                                                                                                   EMBL; M23368; AAA35017.1; -.
EMBL; U33057; AAB64944.1; -.
EMBL; U33057; AAB64944.1; -.
EIR; A31398; A31398
HSSP; P64384; 1NXB.
SSB; S00023010; SAW2.
SSB; S00023010; SAW2.
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PROSITE; P800377; ADOMET_SYNTHETASE_1; 1.

Transferase; One-carbon metabolism; Multigene fam:
Accerylation; Magnesium; Potassium; Metal-binding.
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Pfam, PF02772; S-AdoNet syntD2; 1.
Pfam, PF02773; S-AdoNet syntD3; 1.
TIGREAMs; TIGRO1034; metK; 1.
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between the Swiss Institute of Bioinformatics and the SW
the Buropean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHIONIME AND ATP.

- CAPALYTIC ACTIVITY: ATP + L-methionine + H(2)0 = pl diphosphate + 5-adenosyl-L-methionine.

- CoPACTOR: Binds 2 divalent ions, such as magnesium to per subunit (8y similarity).

- pathwar: Activated methyl cycle.

- SUBUNIT: Hectoroferramer.

- SUBUNIT: Hectoroferramer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garrels J.I., Futcher B., Kobayashi R., Latter G
Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SMISS-PROT data bank
-1- FUNCTION: CATALYZES THE FORMATION OF S-ADENO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bearno A., Carpenter J., Chen E., Cherry J.M., Chung E., Dunc
Bunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Li
Mosedale D., Nakahara K., Namath A., Osfnar P., Oh C., Petel
Roberts D., Schramm S., Schroeder M., Shogren T., Shrotf N.,
Winant A., Yelton M., Botstein D., Davis R. M.,
Summitted (100-1395) to the BMBJ/CenBark/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae: physiology and regulation of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N. A.
MEDLINE-89216973; PubWed-3072475;
MEDLINE-89216973; PubWed-3072475;
Thomas D., Rothsfetain R., Rosenberg N., Surdin-Kerjan Y.,
"SAW2 encodes the second methionine S-adenosyl transferase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevistae (Baker's yeast).
Bukaryota; Hungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Saccharomyces cerevisiae (Baker's y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNTHETASE.
SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. 8:5132-5139(1988).
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                                         MAGNESIUM (E
POTASSIUM (E
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ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THERE ARE TWO GENES CODING FOR
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Y SIMILARITY)
                                                                                                                                                          family; ATP-binding;
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Query Match Best Local Similarity

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Score 40; Pred. No.

DB 1;

Length 383; CRC64;

NP BIND BINDING

SEQUENCE METAL

MM;

466879A2797E80B1 (POTENTIAL).

ATP

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NP BIND 127

METAL 27

METAL 53

METAL 279
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                                                                                                               SEQUENCE
                                                                                                                              METAL
                                                                                                                                                                                                                       PROSITE; PS00377; ADOMET SYNTHETASE 1; 1.
PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.
                                                                                                                                                                                                                                                               InterPro, IPR002133; S-AdoMet synt.
Pfam; PF00438; S-AdoMet synt; 1.
Pfam; PF02772; S-AdoMet syntD3; 1.
Pfam; PF02773; S-AdoMet syntD3; 1.
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-- COPACTOR. Binds 2 divident ions, such as magnesium or cobalt,
1 potaesium ion per subunit (By similarity)
-- PATHRAY, ACTIVATE & MEN'AL OYAL &
-- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
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"Cloning and sequence of the Ascobolus immersus S-adenosyl-L-methiorine synthetase-encoding gene.";
Gene 170.155-156(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last annotation update) S-adenosylmethionine synthetase (BC 2.5.1.6) adenosyltransferase) (Adowet synthetase).
                                                                                                                                                                                                          Transferase; One-carbon metabolism; ATP-binding; Magnesium;
                                                                                                                                                                                                                                                       TIGRFAMs; TIGRO1034; metK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CATALYZES THE FORMATION OF S-ADENOSTIMETHIONINE EROM
METHIONINE AND ATP.
CATALYTIC ACTIVITY: ATP. + L-methionine + H(2)O = phosphate +
  88
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                                                         Similarity
7; Conser
YDDSAKGFDYKTC 100
                            YGNSPKGFAYXXC 16
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                                                                                                             393 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                  50.0%;
                                                                                                             43010 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
                                                                                                                        ATP (POTENTIAL).
MAGNESIUM (BY SI
POTASSIUM (BY SI
POTASSIUM (BY SI
MAGNESIUM (BY SI
                                                                  Score 40;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,
                                                                                                          88FB2F2F14B751C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                        4 (BY SIMILARITY).
4 (BY SIMILARITY).
4 (BY SIMILARITY).
9 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 AA
                                                                                  DB
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                                                                                Length 393;
                                                     Indels
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                                                     0;
                                                                                                                                                                                                            Potassium;
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                                                     Gape
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RESULT 12

EMBL; X68836; CAM48726.1; -EMBL; EC001686; AAH01686.1; -EMBL; EC001894; AAH01884.1; -PIR, S27257; S27257.
HSSP; P04384; IMXE
Genew; HGNC:6904; MAT2A.

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RM Kiraunderg E.L., Peirigold E.A., Grouse L.H., Decrge J.G.,
RM Altaunder E.D. Collins F.S. Wagner L. Shemmer C.M. Schwerg D. RM Altauch E. D. Collins F.S. Wagner L. Shemer C.P., Bhat N. X.
RM Albeichello E.P. Zeeberg B. Bastow K.H., Schwefer C.P., Bhat N. X.
RM Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsich R.
RM Hardhello L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RM Staplaton M., Soares M. B., Bonaldo M.F., Casavant T.L., Schwetz T.E.,
RM Stonestein M.J., Ugdin T.B., Toshiyuki S., Carnina H.P., Prange C.,
RM Hardha S.S., Loquellano N.A., Peters G.J., Abramon R.D., Mallahy S.J.,
RM Hopak S.A., McSwan P.J., Wakernan K.J., Malek J.A., Ghartane P.H.,
RM Hopak S.A., McSwan P.J., Wakernan K.J., Malek J.A., Ghartane P.H.,
RM Hilladon D.K., Manny D.M., Soderygen E.J., Lu X., Gabbs R.A.,
RM Halting M., Madan A., Young A.C., Shwochenko V., Souffard G.G.,
RM Halting M., Madan A., Young A.C., Shwochenko V., Souffard G.G.,
RM Halting M., Madan A., Wagner B.D., Dolkson M.C.,
RM Halting M., Madra M., Wagner B.M., McC.,
RM Halting M., Madra M., Hoper B.M., McC.,
RM Halting M., Madra M., Hoper B.M., McC.,
RM Halting M., Madra M., Wagner B.M., McC.,
RM Halting M., Madra M., Schein J. E., Jones S.J.M., Marza M., Smallus D.E.,
RM Halting M., Schein J. E., Jones S.J.M., Marza M., Smallus D.E.,
RM Halting M., Schein J.E., Jones S.J.M., Marza M., Smallus D.E.,
RM Halting M., Schein J.E., Jones S.J.M., Marza M., Smallus D.E.,
RM Halting M., Schein J.E., Jones S.J.M., Marza M., Smallus D.E.,
RM Halting M., Schein J.E., Jones S.J.M., Marza M., Smallus D.E.,
RM Halting M., McGalland H.M., McGalland M., Schein J.E.,
RM Halting M., Schein J.E., Jones S.J.M., Marza M., Smallus D.E.,
RM Halting M., McGalland M., Marza M., Smallus D.E.,
RM Halting M., McGalland M., Marza M., Smallus D.E.,
RM Halting M., McGalland M., McGalland M., Marza M., Smallus D.E.,
RM Halting M., McGalland M., McGalland M., McGalland M., McGalland M., McGalland M., McGalland M., McGalland M., McGalland M., McGalland M., McGalland M., McGalland M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     distribute of the address of the mechicinine of cobalt, of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the address of the add
                                                                                                                                                                                                                                    the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as Jong as its content is in oway modified and this statement is not removed. Usage by and for nonmerchall entitles requires a license agreement (See thip://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch/).
                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS PROT entry is copyright. It is produced through a collaboratio 
between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHIONINE AND ATP.
-i- CATALYTIC ACTIVITY: ATP + L-methionine +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-1- FUNCTION: CATALYZES THE FORMATION OF S-ADEMOSYLMETHIONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ol-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
$2-adenceyImethionine synthetase gamma form (EC 2.5.1.6) (Methionine adenceyItransferase) (Advet synthetase) (WAT-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAMOH
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"Molecular cloning and development
adenosylmethionine synthetase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATZA OR MATAZ OR AMSZ.
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15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 312:37-41(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE=93050159; PubMed=1426236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METK_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISTRIBUTED IN EXTRAHERATIC TISSUES.
SIMILARITY: BELONGS TO THE ADONET SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WHILE GAMMA IS WIDELY
                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration -
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STITITESSERER

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METK_NEUCI
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Best Local S
Matches 7
                                                                                                                                                                                This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SMBs outeration the Buropean Bioinformatics Institute. There are the contractions on its buropean Bioinformatics Institute. There are the contractions on the Buropean Bioinformatics institute. There are the contractions on the buropean Bioinformatics in the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contra
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P48466;
                                                    HSSP; P04384; 1MXB
                                                                       EMBL; U21547; AAC49260.1;
PIR; S65800; S65800.
                                                                                                                                       entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mautino M.R., Barra J.L., Rosa A.L.; reciding "eth-1, the Neurospora crassa locus encoding synthetase: molecular cloning, sequence analy overexpression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FBB-2003 (Rel. 41
S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996
28-FEB-2003
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                              InterPro; IPR002133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97002541; PubMed=8849888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Micelial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adenosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002133; S-AdoMet_synt
Pfam; PR00438; S-AdoMet_synt; 1.
Pfam; PR00772; S-AdoMet_syntD2; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
TIGRPAM6; TIGR01034; metX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metal-binding; Multigene family; ATP-binding.
NP_BIND 131 136 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.
PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.
Transferase; One-carbon metabolism; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
hes 7; Conser
                                                                                                                                                                                                                                                                                                                    METHICANINE AND APP
CATALATIC ACTUTITY. ATP + L-methicatine + H(2)0 = pho
disphosphate + S-adenosy1-L-methicatine.
COPACTOR: EMAGE 2 divalent ions, such as magnesium of
1 potessium ion per submit (By
PATHMAY). Activated methy1 cycle.
SIMILARITY: BELONGS TO THE MOONET SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUNCTION: CATALYZES THE FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0004478; F:methionine
Pro; IPR002133; S-AdoMet_synt
PF00438; S-AdoMet_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601468;
                                                                                                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDDSSKGFDYKTC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGNSPKGFAYXXC 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Last sequence update)
, Last annotation update)
synthetase (EC 2.5.1.6)
(AdoMet synthetase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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Pred. No.
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POTASSIUM (BY SIMILARITY)
POTASSIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
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Matches
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Best Local :
                                                                                                                                                                          METK RAT
                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                     Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
                                                                                              15-5EF-2003 (Rel. 42, Last annotation update)
S-ademosylmethionine synthetase gamma form (EC 2.5.1.6) (Methionine
ademosyltransferase) (AdoMet synthetase) (MAT-II).
                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last amoutation updat
S-adenosylmethionine synthetase gamma form
                                                                                                                                                                                                                                                                                                                                                                                                                                                NP BIND
SEQUENCE FROM N.A.
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                          NCBI_TaxID=10116
                                                                                     MAT2A OR AMS2
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                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
Transferase; One-carbon metabolism; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02772; S-AdoMet_syntD2; Pfam; PF02773; S-AdoMet_syntD3; TIGRFAMs; TIGR01034; metK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metal-binding.
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                                                                                                                                                                                                                                                                                   YGNSPKGFAYXXC 16
                                                                                                                                                                                                                                                           YDDSSKGFDYKTC 103
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395 AA;
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282
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282
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53.8%;
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Pred. No. 11;
1; Mismatches
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MAGNESIUM (BY S:
POTASSIUM (BY S:
POTASSIUM (BY S:
MAGNESIUM (BY S:
                                                                                                                                                                                                                                                                                                                                                                                    ATP
                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                     PRT;
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(BY SIMILARITY)
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SIMILARITY)
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"Structure of the rat methionine adenosyltransferase 2A
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                                                                                                                                                                                                                                                                                                                                                   promoter."
                                                                                                                                                                                                                                                                                                                                                                                   Hiroki T., Horikawa
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98121185; PubMed=9461287
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Wistar; TISSUE-Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90337979; PubMed=1696256;
                                                                    diphosphise - Sadonosyl-Lesthicatine.

CORRICTOR: Binder divident long south as magnesium or cobalt, and potessium ion per subunit. (By similarity).

PATHMAY: Activated methyl cycle.

SUBUNIT: Homodimar: IN MAMALIAN TISSUES, THERE ARE THREE DISTINCT TISSUE SPECIFICITY: IN MAMALIAN TISSUES, THERE ARE THREE DISTINCT SCHOOL FOR ADDRESS CHYPH. BESTANDED HER ARE REFRESSED ONLY IN ADDITION THE GAMMA, IS WIDELY AND DEETH ARE REFRESSED ONLY IN ADDITION THE GAMMA, TOWN PRECOMMENTED HER ALPHA, AND BETA POWER SETTION TO BE PROCESSED THE ALPHA, AND BETA POWER SETTION THE MAMALIAN TOWN REPLACED BY THE ALPHA, AND BETA POWER SETTION THE MAMALIAN TOWN REPLACED BY THE ALPHA, AND BETA POWER SETTION TO THE MAMALIAN SETTION THE MAMALIAN THE SAME TOWN REPLACED BY THE ALPHA, AND BETA POWER STATUSHERS.
                                                                                                                                                                                                                                                                            FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMSTHIONINE FROM METHIONINE AND AFF CATALYTIC ACTIVITY: AFF + L-methionine + H(2)O = phosphate +
                                                                                                                                                                                                                                                                                                                                   J. Biochem. 250:653-660(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsukada K.;
cDNA encoding the
                                                                                                                                                                                                                                                                                                                                                              gene and its
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rat

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RESULT 15
METK_CAEEL
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Best Local:
                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBI outstation - the European Bioinformatics institute. There are no restrictions on its work of the EMBI outstation in the collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collaboration of the Collabo
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01-00T-1996 (Rel. 34, Last segmence update)
01-00T-1996 (Rel. 42, Last ammoration update)
Probable 8-demosylmethomine synthetase 006E7 1 (EC 2.5.1.6)
(Methionine adenosyltranoferase) (Adower synthetase).
EMBL; U41009; AAA82280.1;
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STRAIN=Bristol N2;
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P50305;
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SEQUENCE
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PROSITES, P800377, ADOMET SYMTHETHASE 2, 1.
PROSITES, P800377, ADOMET SYMTHETHASE 3, 1.
PROSITES, P800377, ADOMET SYMTHETHASE 3, 1.
MCTAL-Dinding, Multigene family, ATP-binding,
MCTAL-Dinding, Multigene family, ATP-binding,
MCTAL-DIND 131 1.56 ATP (MOTENTIAL).
MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MCTAL MC
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Pfam; PF02772; S-AdoMet_syntD2; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
TIGRFAMs; TIGR01034; metK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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EMBL; AB000716; BAA19170.1; JOINED.
EIR, A37118, A37118.
HSSP; P04384; 1MXB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J05571; AAA42106.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitted (NOV-1995) to the BMEL/GenBank/DDB4 databases.

RETHIONINE AND ATP (BY SIMILARITY).

RETHIONINE AND ATP (BY SIMILARITY).

CATALVITIC ACTUTY: ATP 1—methionine + H(2)O = phosphate + diphosphate + S-adenosyl-1-methionine.

COPACTOR: Birds 2 divalant lons, such as magnesium or cobalt, and processium ion per minunit (By similarity).

POTENTIAL STATEMENT OF THE POTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
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7; Conserv
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2 Dp bacteria:*

3 Dp fungan:*

4 Dp human:*

5 Sp invertobyat!

5 Sp invertobyat!

7 Sp mdo:*

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47.5	47.5	47.5	47.5	47.5	47.5	48.1	48.8	48.8	48.8	48.8	48.8	49.4	49.4	49.4	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	51.2	51.2	51.2	52.5	52.5	52.5
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ALIGNMENTS

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4 YONSEKERAY 13 101 YONSEARRAY 110	Obery Match 152,0%, Score 44, DB 11; Length 120; Best Local Stailarity 80,0% Pred, Mb. 26; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	092088 PRELIMINARY PRT, 120 AA. 092083 PRELIMINARY PRT, 120 AA. 092083 PRELIMINARY PRT, 120 AA. 092083 PRELIMINARY PRT, 120 AA. 092083 PRELIMINARY PRT, 120 AA. 092083 PRELIMINARY PRT, 120 AA. 01.BC-2001 (TERBELTEL 12). Last annotation update) 10.1MR2-2001 (TERBELTEL 22). Last annotation update) 10.1MR2-2001 (TERBELTEL 22). Last annotation variable region 10.1MR2-2001 (Nouse). 10.1MR2-2001 PROWN A. 10.1MR2-2001 PRELIMINARY PRELIMINARY PRELIMINARY PRELIMINARY PROBLEM PROPORTION FOR THE EMBL/GemBank/DDBJ databases. 10.1MR2-2000 PRELIMINARY PROPORTION FOR THE PROPORTION FROM THE PROPORTION FOR THE P	ISS

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BMELT AND 2172: BAC 27741.1, 200740-42BA4A60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
Bukaryota; Metazoa; (
Mammalia; Butheria; F
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STRAIN=C57BL/60; TISSUB=Olfactory brain,
MEDLINE=23354683; PubMed=12468851;
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SEQUENCE 205 AA; 22603 MW;
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Q93233;
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Science 28:2012-2018(1998).
EMBL; Z81037; CAB02750.1; -.
WormPep; C17E4.5; CE08254.
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MEDLINE=99069613; PubMed=9851916;
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NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. SEQUENCE FROM N.A. Chretien N. MEDLINES-9812579; PubMed-9462747; Rochefort D.L., Chretien N. Errais B., Bouchard J.P., Xio Y. G., Roomens J.M., Uyama E., Nohita O., Tome P.M.S., Latteniers B.G., Romens J.M., Duranceau A., Blumen S., Korcyn A.D., Heutik P., Mathieu J., Duranceau A., Blumen S., Korcyn A.D., Rouleau G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            043484
043484;
01-JUN-1998
Strausbegg R.;
Submitted (UIL-2001) to the EMBL/GenBank/DDBJ databases
SMBL, ARC05029, ARC03556.1; -.
EMBL, BC010939, AH10939.1; -.
Genew; HGMC.8665, PABPM.;
Genew; HGMC.8665, PABPM.
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035935,
01-JAN-1998
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               dystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TremBLrel.
01-OCT-2002 (TremBLrel.
Poly(A) binding protein
nuclear 1).
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                                                                                                                                                                                      TISSUE=Skin
                                                                                                                                                                                                                                                                                             Nat. Genet.
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Lee Y.J., Lee J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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01-OCT-2002
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(TrEMBLrel. 22, I
(TrEMBLrel. 22, I
ding protein II (s
                                                                                                                                                                                                                                                                                       18:164-167(1998).
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Last sequence update)
Last annotation update)
(Similar to poly(A)-binding protein,

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

cause oculopharyngeal muscular

Created)

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Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                 EMBL; U93050; AAC00210.1; -. MGD; MGI:1859158; Pabpn1. InterPro; IPR000504; RNA_rec
                                                                                                                                                                                                                                                                                                                                                                                            Poly(A) binding protein PABPNI OR MPABII.
Mus musculus (Mouse).
                                                                                                                                                                                                                 Biochim. Biophys. Acta 1395:40~46(1998)
EMBL; U93050; AAC00210.1; -.
                                                                                                                                                                                                                                                        Lee Y.J., Lee J., Yang "Genomic structure and
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                 3; PS50102; RRM; 1.
3; PS00030; RRM RNP 1; 1.
302 AA; 32296 MW; 2
                                                        Similarity
7; Conserv
CDKFSGHPKGPAY 213
                         CXXYGNSPKGFAY 13
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
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                                                                                                                                                                                                                                                                        PubMed=9434149;
Yang I.C., Hahn
                                                                    53.8%;
                                                                                                                                                                                                                                                          I.C., Hahn Y., Lee Y., Chung expression of murine poly(A)
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                                                                      Pred. No. 6.9;
                                                                                  Score 44;
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                                                                                                               2F0F6F7CC19C1986 CRC64;
                                                        Mismatches
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binding protein
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Best Local
                                                                                                                                           ORNNE! PRELIMINARY, PRT;
ORNNE! OCCUPATION (TEMBERE! 20, Created)
01-WAR-2002 (TEMBERE! 20, Last seq
01-WAR-2003 (TEMBERE! 2, Last and
PRODADLE beta-91/COSYltransferase.
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Best Local :
                                                                                   Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium....
             SEQUENCE FROM N.A.
STRAIN=13 / Type A;
PubMed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     028165;
01-NDV-1996 (TERNBLYEL 01, Created)
01-NDV-1996 (TERNBLYEL 02, Last sequence update)
01-MRR-2003 (TERNBLYEL 23, Last annotation update)
PolyA binding protein II.
                                                                         NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS500030; RRM; RNP 1; 1.
SEQUENCE 306 AA; 3766 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000504; RNA_rec_mot Pfam; PF00076; rrm; 1.
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EMBL; X89969; CAA62006.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Thymus, Aorta, Muzzle epithelium, a
MEDLINE=96071160; PubMed=7479061;
Nemeth A., Krause S., Blank D., Jenny A.,
Hahle E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         028165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation of genomic and cDNA clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
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SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM;
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nes 7; Conserv
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7; Conserve
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                                                                                                                                                                                                                                                                                                                                CDKFSGHPKGFAY 217
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PS00030; RRM_RNP_1; 1.
306 AA; 32749 MW;
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53.8%;
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Last annotation update
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Pred. No. 7;
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Pred. No. 7;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 306;
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RESULT 9
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Matches 7
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Best Local
  SEQUENCE FROM N.A. STRAIN=968 h90;
MEDLINE=20223868; P
Ding D.Q., Tomita Y
Hiraoka Y.;
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                                                                                                 NCBI_TaxID=4896;
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01-MAR-2003 (TrEMBLrel 23,
01-MAR-2003 (TrEMBLrel 23,
Organic anion transporter E
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               PubMed=10759889;
Y., Yamamoto A.,
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43.8%;
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             Yamamoto A., Chikashige Y., Haraguchi T.,
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MRDL/He-4/2-3-10.
The PANTON Consortium,
The PANTON Consortium,
The RIEDN Ganome Exploration Research Gr
'Nhallysis of the mouse transcriptome bas'
60,770 full-Length Chlans.",
1 60,770 full-Length Chlans.",
1 MRTURE 420:563-573 (2002).
R BIEL; AK032589; BAC43879.1, - 6687507E
                                                                                      GUTTLI) (TEMBLE). 13, Created)
01-WAY-2000 (TEMBLE). 13, Created)
01-WAY-2000 (TEMBLE). 13, Last sequence update)
01-WAY-2003 (TEMBLE). 23, Last annotation update)
Hypothetical 18.1 kba protein (Fragment).
25,7512.
Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Pungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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STRAIN=C57BL/6J; TISSUE=Cecum;
MEDLINE=22354683; PubMed=12466851;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shidariur 7. Ohtenik K., Hirakawa H., Ohtehima K., Yemashite A.,
Shida T., Ogashawara M., Hattori M., Khihara S., Hyyashi H.,
"Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-aater.",
Proc. Natl. Acad. Sci. U.S. A. 99:996-1001(2002).
BMBL, APO01165, BAB00183.1.-
BMBL, APO01165, BAB0183.1.-
InterPro. IFRO1173, Glycor transf.
Fransferase; Complete Procesome. 27: 1
Eamly Pr00315, Glycos transf. 27: 1
SEQUENCE 29:94 Ah.; 33358 MF; 3908F593B712CA35 CEC64;
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01-MAR-2001
01-MAR-2001
01-MAR-2003
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BMBL ABOO20013 BBA970711...
ThreePro. IPP0002504, RNA_rec_mot.
PFam. PFO007504, RNA_rec_mot.
PFAm. PFO007504, RNA_I.
PFO007751, RESULT.
PFO007751, RNA_I.
PFO007751, RESULT.
PFO007751, 
                   Xenopus laevis (African clawed frog).
Ebkafyota: Metazoa; Chordata; Craniata; Vertebrata; Eutaleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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PROSITE; PS00030; RRM RNP 1; 1.
SEQUENCE 166 AA; 18461 MW;
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SPBC16E9.12C.
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Q9BZB7;
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EMBL, AF329403, AAK01240.1, -.
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PROSITE; PS50102; RRM; 2.
SEQUENCE 491 AA; 54162 MW; 56
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MEDLINE-21125222; PubMed=11223249;
Welk J.F. (Charlesworth A., Smith G.D., MacNicol A.M.;
Tidentification and characterization of the gene encod
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Mammalia; Eutheria; Primates;
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PROSITE; PS00030; RRM RNP 1;
SEQUENCE 296 AA; 32449 MW;
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InterPro; IPR000504; RNA_rec_mot.
Pfam; PP60076; rrm; 1.
SMART; SM00360; RRM; 1.
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"Developmental expression of Poly(A) Binding Protein II in Xenopus
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(TrEMBLrel. 10,
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element-binding protein
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Pred. No.
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Pred. No. 16;
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Suzuki H., Maegawa S., Murakawa M., Hoshijima K., Yasuda K., Inoue K.;

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SEQUENCE FROM N.A.

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Matches 7
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P70166;
01-FEB-1997
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01-MAR-2001
01-MAR-2003
Elkaryota; Metazoa; Chordata; Craniata; Vertebrata; Bureleostomi;
Memmalia; Butheria; Rodentia; Schirognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
[1]
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                                                                                                                                                                                                              Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kateu Y. Yamashita M., Ogawa K., Nagahama Y.;
"Goldfish cytoplasmic polyadenylation element binding protein
(CPEB) lite interaction with CPS of cyclin B mRNA and phosphorylation
by cdk and Egg protein kinases.";
Submitted (JUN-2000) to the EMEL/GenBank/DDBJ databases.
EMBL, ABO4451, BAB19551, I.
EMBLY, ABO4451, BAB19551, I.
SMRTY, SMO3567, RBM, 18-C_mot.
SMRTY, SMO3567, RBM, 10-C
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SEQUENCE 559 AA; 62122 MW;
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Actinopterygii; Neopterygii; Teleostei;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
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ZFIN; ZDB-GENE-990927-1; zorba.
InterPro; IPR000504; RNA_rec_mot.
SMART; SM00360; RRM; 1.
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PROSITE; PSG0102; RRM; 1.

SEQUENCE 559 AA; 62255 MW; 36CF42BlAC70A377 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 CPPKGNMPKGYVY 356
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                                                                                                 SEQUENCE
                                                                                                          MGD; MGI:108442; Cpeb.
InterPro; IPR005504; RNA rec_mot.
SMART; SM00360; RRM; 1.
PROSITE; P850102; RRM; 2.
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TISSUB=Ovary;
350 CPPKGNMPKGYVY 362
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                       CXXYGNSPKGFAY 13
                                                                                                 561 AA; 61917 MW;
                                                Conservative
                                                            53.8%;
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                                                            Score 42; DB
Pred. No. 31;
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Job time : 6.37637 secs Search completed: November 7, 2003, 07:34:37

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein search, using sw model

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Run on: November 7, 2003, 07:21:17; Search time 6.89987 Seconds (without alignments) 368.069 Million cell updates/sec

Title: Perfect score: US-09-661-992B-105 CXXYGNSPKGFAYXXC 16

Scoring table: Searched: BLOSUM62 Gapop 10.0 , 1107863 seqs, 158726573 residues Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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1 SIDSI/gegdata/genesed/genesed-embl/AA196. DAT:

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22 SIDSI/geddata/genesed/genesed-genesed-embl/AA

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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HCV El antigen mon	-		50.0	40	9
Drosophila melanog	22 ABB64427		51.2	41	00
Protein encoded by	22 AAB66460	626	52.5	40	7
	23 ABP62216		52.5	42	0
Human novel secret	23 ABG95556		55.0	44	. v
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Anti-FIX/FIXa anti	22 AAB20433		82.5	66	N
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ABU61105	ABU67445	ABU65941	ABU65608	ABU71151	AAM38889	AAU29063	AAY57273	AAY57272	AAY57270	AAB44275	AAY41719	AAW86276	ABP71366	ABB58914	AAE09692	AAY43866	AAR82982	AAR82981	AAR82986	AAR82980	AAR82979	AAR82977	AAB62753	ABP71368	AAB62780	AAW31724	AA018433	ABG77145	ABG03182	ABP08836	ABG22854	AAY95075	ABB63366	ABP43671	ABP62206
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ALIGNMENTS

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Rector IX; FIX; Rector IXa; FIXa; antibody; procoagulant; Factor VIII ocfactor; blood coagulation disorder; haemophilia h; haemorrhagic disthesis; haemostatic, adolytic; therapy; mouse; complementarity determining region; CDR.

PF	383	E E	ž 3	FT	3	33	Ę	Ļ	F	H	ž	S	ğ	Š	ž	Š	₹	ž	H	≵ ∶	3 }	Ş	a A	ij	AAB2	RESULT
13-SEP-2000; 2000WO-EP08936.	22-MAR-2001.	WO200119992-A2.	/note= "any amino acid	•	ς,	/note= "any amino acid Misc-difference 14			c-difference	Key Location/Qualifiers		Mus musculus.		ity determin	rhagic diathesi	VIII cofactor; blood coagul	FIX; Facto:		Anti-FIX/FIXa antibody CDR3.	er-com-room (retroc direct)	(£: mar		AAB20444;	AAB20444 standard; Peptide; 16 AA.	AAB20444	FLT 1

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of complementarity determining region 3 (CRR3) of an anti-body having anti-Factor IX (FIXa) activity. Such anti-bodies anti-activated Factor IX (FIXa) activity. Such anti-bodies (CRR3 pspilde) have Factor VIIIa (FFIIIa) cofactor activity or FIXa (CRR3 pspilde) have Factor VIIIa (FFIIIa) cofactor activity or FIXa octivating activity. Anti-secration for the anti-bodies or their activity of the such activity of their complete of their secretary. Anti-secration for the case of FVIII inhibitors patients. The anti-bodies or their derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially hamophila had administrative for the case of FVIII inhibitors and composition for treating patients with blood coagulation disorders, especially hamophila had and hemorrhagic dathereis.
                                                                                                                                                                                                                                                                                      Factor IX; FIX; Factor IXa; FIXa; sePv; antibody, procagulant; Factor VIII ocfactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB20433 standard; Protein; 242 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilla A and haemorrhayic distinguis
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              22-MAR-2001.
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                                                                                                                                                                                                                                              Chimeric -
                                                                                                                                                                                                                                                            Chimeric -
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120..134
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or the present sequence is that of a single chain Fv (scrv) derivative of antibody 193/AD3, comprising the heavy (vn) and light (vn) chain variable regions of 193/AD3 joined by an artificial, flexible linker to 193/AD3 with the scrv was obtained by PcR amplification of chuka for 193/AD3 vn and vn, regions and cloning in vertex place. 193/AD3 is neamly so of anti-inman factor in (TRI)/ACC traveled Factor IX (FIX) and the scrv was done in the preceding activity of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen of the screen 
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                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diathesis.
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                                                                                                                                                                                         Local Similarity
                                                                                                                        11;
1 CXXYGNSPKGFAY 13
                                                                                                                                                                                                                                                                                                                                                               242 AA;
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99AT-0001576
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                                                                                                                                                                               82.5%;
                                                                                                                        Score 66; DB
Pred. No. 0.00
0; Mismatches
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                                                                                                                                                                               0.0051;
                                                                                                                                                                                                                                       DB 22; Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dorner F;
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RESULT 3 AAB20388

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96

CALYGNSPKGFAY 108

0

AAB20388 standard; Peptide; 10 AA

21-JUN-2001 (first entry)

Anti-FIX/FIXa antibody 193/AD3 CDR3

complementarity determining region; CDR. Factor XX, FXX, Factor XXa, FXXa, antibody, procesquiant, Factor VIII cofactor, blood cosquiation disorder; haemophilia A; haemorrhagic disthesis; haemostatic; amidolytic; therapy; mouse;

Mus musculus.

WO200119992-A2

22-MAR-2001.

13-SEP-2000; 2000WO-EP08936.

14-SEP-1999; 99AT-0001576.

(BAXT) BAXTER AG.

Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;

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RESULT 4
AAW59884
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Best Local :
       New isolated polymucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activating activity. Administration of the antibodies or their derivatives leads to an increase in the proceagilant activity of griza, even in the presence of FVIII a inhibitors. This allows for rapid blood cogulation even in the absence of FVIII or FVIII, an in the case of FVIII inhibitor patients. The antibodies or their derivatives are used in a Calamed pharmacountient composition for treating patients with blood compulation disorders, especially hemosphills a and hemorrhagic dathresis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of complementarity determining region 3 (CRR3) of the heavy chain of an antibody expressed by mouse hybridose 193/ND3. This antibody has anti-Pactor IX (FIX) or anti-activated Pactor IX (FIXA) activity. It is an example of anti-FIX/FIX antibodies of the invention. Such antibodies and their derivatives (including those that comprise the present CRR3 peptide) have Factor VIII at [FVIIIa] confactor activity or FIXR
                                                                     WPI; 1998-414099/35.
N-PSDB; AAV41925.
                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW59884 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                  Feng P,
                                                                                                                                                                                                                           21-JAN-1997;
                                                                                                                                                                                                                                                                                         23-JUL-1998
                                                                                                                                                                                                                                                                                                                       WO9831800-A2
                                                                                                                                                                                                                                                                                                                                                     Omo
                                                                                                                                                                                                                                                                                                                                                                                Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW59884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-290358/30
                                                                                                                                                                   (HUMA-)
                                                                                                                                                                                 (AUCK-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 YGNSPKGFAY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                   HUMAN
                                                                                                                                                                               AUCKLAND UNISERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                  Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGNSPKGFAY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                   GENOME
                                                                                                                                                                                                               97US-0034205.
97US-0034204.
                                                                                                                                                                                                                                                            98WO-US00960
                                                                                                                                     Krissansen GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.5%; Score 58; 100.0%; Pred. No.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; serceted protein; autoimmuse disease; chemotaxis; theumatoid arterities hyperprotiferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebrovascular disorder; subbuun; nervous system disorders, perebrai isofahenia, angloganesis; subbuun; nervous system disorders, Alinbiamer's disease; infection; isoso regeneration; coular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell projiferation; organ cramsplantarion; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of the cDNA clone Bol-like (HACT29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypoptides. They can be used for a g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various altergies, and as anti-linfectious agents. The products can also be used for detection and dispossis.
                                                                                                                                                                                                                                   07-MAR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human novel secreted protein gene 120 polypeptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-2003
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                                                                                                                                                                          11-APR-1997,
                                                                                                                                                                                                                     11-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preservative; nutritional.
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9788-0400334

9788-0403349

9788-0403349

9788-0403569

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9788-0403569

9788-0433129

9788-0433129

9788-0433149

9788-043569

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Pred. No.
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08-JUL-1997;
16-JUL-1997;
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06-JUN-1997;
06-JUN-1997;
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23-MAY-1997;
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97US-047501P
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The invention relates to an isolated procein that is one of 166 human come of the process of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
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12-SEP-1997;
02-OCT-1997;
06-MAR-1998;
                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 103; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endress GA, Yu G,
Duan R, Hu J, Flo
Moore PA, Shi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-634796/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Fischer CL, Soppet DP, Carter KC, Beo, Yu G, Ni J, Feng P, Young PE, Greene JM, Pei tu J, Florene KA, Olsen HS, Ebner R, Brewer LA; Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                            365
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97US-058785P.
97US-061060P.
98WO-US04493.
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23; Length 365;
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Query Match
Best Local
                                     Matches
264 CDKFSGHPKGFAY 276
                 1 CXXYGNSPKGFAY 13
                                     Similarity
7; Conserv
                                     Conservative
                                             53.8%;
                                    Score 44; DB
Pred. No. 35;
1; Mismatches
                                     ۲.
                                     .
                                    Gaps
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0

RESULT 6 ABBESLT 6 ABBESLT ABPE AX ABPE AX ABPE AX ABPE AX ABPE AX ABPE AX ABPE AX ABPE AX Virun BE Huma BE Hu

믕 S

ABP62216 standard; Protein; 132 AA

10-OCT-2002

(first entry)

Human immunopeptide to HCV E2 glycoprotein Fab variable region #63.

Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein; nonetructural protein; hepatitis C virus; HCV, E2 glycoprotein; NS3 protein; viral infection.

Homo sapiens.

01-AUG-2002

WO200259340-A1.

25-JAN-2002; 2002WO-US02303

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RESULT 7
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to human immunopolypeptides, produced by a phage transfected cell library. The present sequence is one such phage transfected cell library. The present sequence is one such immunopolypeptide. The immunopolypeptides have binding specificity or envelope glycopordein E2 and nonstructural process NS3 of hepatitis C virus (HCT). E2 glycoprocein is believed to be responsible for target cell binding and contains neutralising spitopes, while NS3 is thought to get involved in the replication of HCV. The immunopolypertides are useful con taggressing and treating a patient having or suspected to be having the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the 
Screening a mutant library for mutants unable to grow under specific conditions and for identifying loci involved in pathogenicity,
                                                                                      N-PSDB; AAF31627.
                                                                                                                 WPI; 2001-091804/10.
                                                                                                                                                                                                                                                                                          08-JUL-1999;
                                                                                                                                                                                                                                                                                                                06-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis; attenuated microoxeanism, fad26; Rv2930;
signature tagged transposon mutant; mutant library;
mycobacterial infoction; actinomycetales; antibacterial; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Mycobacterium tuberculosis fad26 (Rv2930) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB66460 standard; Protein; 626 AA.
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                                                                                                                                                                                                                               (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCV infection.
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7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 AA;
                                                                                                                                                                        Guilhot C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                          9908-0142833
                                                                                                                                                                                                                                                                                                                9905-0142982
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                                                                                                                                                                            Camacho
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Pred. No. 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 132;
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                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identifying and isolating mutants of actinomycetales and for identifying compounds that have antibiotic activity. The method is used to identify mutants of microorganisms, preferably an actinomycetales, such as M. ubberculosis, M. botts, M. lepras M. avum, M. intracellulatire and M. paratuberculosis, M. botts, M. lepras M. avum, M. intracellulatire and It is especially useful for identifying loci involved in pathogenicity. It is useful in constructing vaccines. The method can be used to screen multiple librarise concurrently. It can screen librarise of different organisms or different examins of the same organism. The present progenicit is encoded by a gene which is disrupted by the insertion of the 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to 18 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence six given in a specification relating to a method for screening a library of mitarts. The method comprises constructing a library with insertions in genes and/or regulatory regions of the organisms of interest, when the insertion contains a teg and/or a transpose associated with a teg. The mitarts are identified by hybridistic or the tags to known sequences. The method is useful for treating an individual suffering from a mycobacterial infection supposed to an infectious Mycobacterium, or having both of the productions Mycobacterium, or having to the productions Mycobacterium, or having to the productions Mycobacterium. It is also useful for any organism of the productions Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Fig 5A; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises using signature tagged transposon mutagenesis
                                                                                     4 YGNSPKGFA 12
                                                                                                                                                                                                                                                                                                                                                     626 AA;
                                                                                                                                                                          Conservative
                                                                                                                                                                                                              52.5%;
                                                                                                                                                                                                              Score 42;
Pred. No.
                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                     1.3e+02;
                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                        Length 626;
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                                                                                                                                                                          Gaps
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73 YGSDPKGFA 81
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RESULT 8
ABB64427
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Drosophila melanogaster polypeptide SEQ ID NO 20073. 26-MAR-2002 Drosophila; developmental biology; cell signalling; insecticide; ABB64427 standard; Protein; 2515 AA (first entry)

Drosophila melanogaster pharmaceutical.

W0200171042-A2

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P

11-JUL-2000; 2000US-0614150

Venter JC, Adams M,

N-PSDB; ABL08530. WPI, 2001-656860/75 Li PWD Myers EW;

New isolated nucleic acid genes from Drosophila and interactions detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell

Disclosure; SEQ ID NO 20073; 21pp + Sequence Listing; English

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Matches
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                                           The invention relates to a human monoclonal antibody or its antigen binding fragments which exhibit immunological binding affilintly for a hepartitis C vitrus (BCY) Et antigen comprising an amino acid sequence bomalogous to the binding portion of a human antibody Fib molecule from a combinatorial antibody library. The vaccine composition comprising the antibodies of antigen binding fragments against BUY ELD or Exhibits of the physraciable region is useful in treating or preventing BUY intestion in a mobject. Sequences METS13-AB076568 represent human monoclonal antibodies against HCV EL antigen.
                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 56; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine comprising a human monoclonal antibody against hepatitis C virus (HCV) El or E2 antigen, useful for treating or preventing HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; HCV; hepatitis C virus; El antigen; monoclonal antibody; vaccine; hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
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The sequence data for this parent did not form part of the printed the sequence data for was obtained in electronic format directly from MIDO at ftp-wipo.in/Pub/pub/shed_pet_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nuclaic acid detection respent capable of detecting 1000 or more genes from Prospobila. The invention is useful in developmental biology and in shufdering cell signalling and call-cell interactions in higher elevances for the development of insecticides, therapeutics and pharmacoutical drugs. The invention discloses genomic DNA sequences (MELIGITA ANGJOSII), expressed DNA sequences (MELIGITA ANGJOSII), expressed DNA sequences (MELIGITA CONTRACTION ANGJOSII).
Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-608502/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drakenberg K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JAN-2001; 2001US-260889P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCV B1 antigen monoclonal antibody #52
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7; Conserv
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107 AA;
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87.5%;
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Pred. No. 8.4e+02;
0; Mismatches 1
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Best Local Similarity Query Match

50.0%;

Score Pred.

No. DB 23; 45;

Length 107;

26-FEB-2003

(first entry)

ABP43671;

ABP43671 standard; Protein; 261 AA

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RESULT 11
ABP43671
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ABP62206
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                                                                                                                                                          Matches
                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                    The present invention relates to human immunopolypeptides, produced by a phage transfected cell library. The present sequence is one such immunopolypeptide. The immunopolypeptides have binding specificity for envelope 3/proprocein E2 and nonstructural protein N33 of hapatitis C virus HUTO; E2 glycoprocein is believed to be responsible for tearer cell binding and contains neutralising spitopes, while N31 is thought to ge involved in the replication of RV. The immunopolypeptides are useful you diagnosing and treating a patient having or suspected to be having your diagnosing and treating a patient having or suspected to be having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human immunopolypeptide with binding specificity for certain of heparitis of (HRV), for diagnosing or treating patients having or suspected o having HCV infection.
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Fig 12; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABQ92705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JAN-2001; 2001US-264451P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nonstructural protein; hepat:
NS3 protein; viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunopeptide to HCV E2 glycoprotein Fab variable region #53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP62206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP62206 standard; Protein; 136 AA
                                                                                                                                                                                                                                                                           HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-599801/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maruyama T, Jones IM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                         Local
                                                                           89 CQQYGPSPPGYTF 103
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                                                                                                              1 CXXYGNSPKGFAY 13
                                                                                                                                                          6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                     136 AA;
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                         46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatitis C virus; HCV; E2 glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burton DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                         Score 40;
Pred. No.
                                                                                                                                                      Mismatches
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                                                                                                                                                                      185
                                                                                                                                                                                            В
                                                                                                                                                                                            23;
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                                                                                                                                                      5,
                                                                                                                                                                                            Length 136;
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                                                                                                                                                      Indels
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Methionine adenosyltransferase II alpha clone MGC:2907

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                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                          Query Match
Best Local :
       Drosophila; developmental biology; cell signalling; insecticide;
                                       Drosophila melanogaster polypeptide SEQ ID NO 16890.
                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to 446 newly isolated polymucleotide seguances. The activity of polymucleotides of the invention may be described as, unlineary, neuroprosective, immunomodulator, cycostatic and anti-inflamancy, coppositions comprising mucleic acids of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; anti-inflammatoxy; gene thexapy; mutritional supplement; wound; burn; ulcer; Alzdeimer's disease; Huntington's disease; amyortophic lateral sclerosis; autoimmune disorder; inflammation;
                                                                                                                                   ABB63366 standard; Protein; 291 AA.
                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                              ampotrophic lateral sclerosis, autoimmume disorders, cancer or inflammation. The nucleic acids and polypoptides are also useful in idiagnostic and research methods. The sequences given in records aparais4. Appriss4. Appriss4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID # 574; 357pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABQ60915.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2000; 2000US-0687527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001; 2001WO-US27760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuroprotective; immunomodulator; cancer; chromosome 2p11.2;
                                                                                                                                                                                                                                                                         Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
                                                                                                                                                                                                              92 YDDSSKGFDYKTC 104
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                                                                                                                                                                                                                                              YGNSPKGFAYXXC 16
                                                                                                                                                                                                                                                                                                                                       261 AA;
                                                                                                                                                                                                                                                                            Conservative
                                                                       (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou P,
Wehrman
                                                                                                                                                                                                                                                                                        50.0%;
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                                                                                                                                                                                                                                                                                        Score 40;
Pred. No.
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Drmanac RT;
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                                                                                                                                                                                                                                                                                          1.1e+02;
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                                                                                                                                                                                                                                                                                                       Length 261;
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pharmaceutical.

14-AUG-1998; 01-MAR-2000 Candida albicans

98GB-0017796 98EP-0310694.

23-DEC-1998; EP982401-A2

(JANC) JANSSEN PHARM NV

Candida albicans infection; growth; survival; medicament; AIDS; vulvovaginitis; immunocompromised patient; treat.

Candida albicans polypeptide sequence # 43.

23-JUN-2000 AAY95075;

(first entry

AAY95075 standard; Protein; 385 AA

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Query Match
Best Local
                                                                                                                                                                                                                                                                              capable of detecting 1000 or more genes from broscophila. The inventuesful in developmental biology and in elucidating cell signalling cell-circle in the inventue for the development of insecticides, therapeutics and pharmaceurical cury. The invention discloses genomic DNA sequence (BALIGITS-BALIGITS) copressed DNA sequences (BALIGITS-BALIGITS).
                                                                                          Sequence
                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 16890; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                          ABB57737-ABB72072
                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                          291 AA;
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                              Length 291;
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alling and
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18

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Matches
119 GKRPKGFAY 127
              5 GNSPKGFAY 13
                                     Similarity
                            Conservative
                                   77.8%;
                                   Pred. No.
                            Mismatches
                          . 1.3e+02;
2;
                            Indels
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                           Gaps
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RESULT 14
ABG22854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a polypeptide that is critical for the survival and growth of Candida abloans. The C. ablicans inclaic acid molecules encoding the polypeptides of the invention may be used as probes and primers for detecting homologous mudalcia catd molecule sequences. The polypeptides and mucleic acid molecules and compounds identified as selectively modulating the expression of the polypeptides, may be used as medicaments or for the preparation of a medicament to treat C.ablicans sections of the polypeptides and not previously the preparation of the polypeptides are sectionally in Alls patients and to treat Cablicans associated diseases have the polyperides to treat C.ablicans associated diseases have seen side effects and less contity than previously used methods such as the solve especially suitable for the polyperides.
                                     New isolated polymucleotide and encoded polymetides, useful ins
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
                           biodiversity
                                                                                                                                                                                                             23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #22845
                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG22854 standard; Protein; 503 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 33, Figure 39; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Essential polypeptides isolated from Candida albicans, treatment of diseases caused by C.albicans, especially
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                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                            31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunocompromised patients, such as AIDS patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunocompromised subjects, e.g., AIDS patients -
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                                                                                                                  2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                              supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 YDDSEKGFDYKTC 94
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                                                                                                                                                  RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                        AAS87041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 AA;
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                                                                                                                                                  Liu C,
                                                                                                                                                                                                                            200008-0540217
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 21;
Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 385;
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                                                                                                                                                                                                                                                                                                                                                                                                forensic;
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Claim 20, SEQ ID No 53213; 103pp; English

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,

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RESULT 15
ABP08836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; peoriasis; benign rumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systematic upus erythematosus; hypertranion; hypertr
                                                                                                                                             WPI; 2002-106308/14.
                                                                                                                                                                                                                Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000; 2000US-206132P-
29-AUG-2000; 2000US-228716P
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                                                                                                              N-PSDB; ABN24588.
                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-2001; 2001WO-US10836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis
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es 7, Conserv
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Pred. No.
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Disclosure; SEQ ID 17654; 1037pp; English.
                                                                          hyperproliferative disorders and autoimmune disorders -
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The present invention describes substantially purified human proceins creating frame. GRYX, where X is 4-1484 (see Table 1 cm in the specification). ABMINFGS to ABMINFGS encode the human GRYX CC proteins given in ABMINFGS to ABMINFGS encode the human GRYX corrections are useful for treating or preventing a pathology associated with an OREX-associated disorder: In humans, and in the manifacture of a medicament for treating a syndrome associated with OREX-associated disorder: OREX polymouthoride expenses can be used in the sequences can be used in the expenses of the process of the proc at ftp.wipo.int/pub/published_pct_sequences.

Sequence 116 AA;

₽ Ş 65 YSNSPDGEA 73 4 YGNSPKGFA 12

Matches

7; Conservative

0; Mismatches Score 39; DB Pred. No. 71;

0; Gaps

0;

Query Match Best Local Similarity

48.8%;

DB 23; Length 116; 2; Indels

Search completed: November 7, 2003, 07:27:04 Job time: 7.89987 secs

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Run on:
                                                                                                                OM protein - protein search, using sw model
November 7, 2003, 07:30:19, Search time 14.0347 Seconds (Without alignments) 195.799 Willion cell updates/sec
                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Total number of	Searched:	Scoring table: BLOSUM62 Gapop 10		Title:
Total number of hits satisfying chosen parameters: 644079	644079 segs, 171749292 residues	BLOSUM62 Gapop 10.0 , Gapext 0.5	1 CXXYGNSPKGFAYXXC 16	US-09-661-992B-105

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

644079

Database

-	Published Applications AA:* 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep: 3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep: 3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
	n2_6/ptodata/2/pubpaa/US07_PUBCOMB n2_6/ptodata/2/pubpaa/PCT_NEW_PUB.
	2_6/ptodata/2/pubpaa/US06_PUBC
	6/ptodata/2/pubpaa/US07 NEW PUE
	/2/pubpaa/PCTUS PUBCON
	6/ptodata/2/pubpaa/US08
	/USO8_PUBCOME
	6/ptodata/2/pubpaa/US09A
	10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB_pep:*
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18:							8	7	
8: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*							/cgn2_6/ptodata/2/pubpaa/US08_PUB(/cgn2_6/ptodata/2/pubpaa/US08	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the accre of the result being printed, and is derived by analysis of the total score distribution.

	No. Sco	Result Qu	
	Score Match Length DB	Query	
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351	351	351	351	351	211	108	108	107	105	105	365	365	306	249	% Query Match Length
11	10	10	10	10	v	15	15	8	10	10	12	H	15	15	88
US-09-978-189-226	US-09-999-832A-226	US-09-978-192A-226	US-09-978-697-226	US-09-978-295A-226	US-09-764-903-39	US-10-269-805-36	US-10-269-805-32	US-08-844-215-10	US-09-828-708-7	US-09-828-708-3	US-09-882-171-696	US-09-809-391-696	US-10-153-668-120	US-10-153-668-118	ID
Sequence 226, App		Sequence 226. App	Sequence 226, App	Sequence 226, App	Sequence 39, Appl	Sequence 36, Appl	<u>س</u>	Sequence 10, Appl	7	ω	Sequence 696, App		Sequence 120, App	Sequence 118, App	Description

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	32	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38
	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5
	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351	351
	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	11	11	11	11	1,1	11	11	11	11	11	11	11	11	1	11
AT TOMMENTO	US-10-173-690-80	US-10-173-689-80	US-10-196-747-80	-10-184-642-8		US-10-194-457-80	US-10-187-749-80	US-10-199-672-80		-10	US-10-002-967A-226	US-10-143-031A-226	US-09-978-298A-226	US-09-978-188A-226	US-09-978-375A-226	-09	1	US-09-978-757A-226	US-09-999-830A-226	US-09-978-193A-226	-09-978-423A-22	US-09-918-585A-226		-09	-09	US-09-978-564A-226	-978-403A-22	US-09-978-191A-226	-978-585	US-09-978-608A-226
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	Appl	Agg.	Appl	App1	P C	Appl	Appl	Appl	App	Ą,	App	App			•	•	App	•	•	•	•	•	Ago	ğ	ρg	App	App	App	Agg	App

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US-10-153-668-118

Ouery Match 55.0%; Score 44; DB 15; Length 249; Best Local Similarity 53.8%; Reed, No. 9.4; Brackles 7; Conservative 1; Wismatches 5; Indels 0, Gaps

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148 CDKFSGHPKGFAY 160

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NUMBER OF SEQ ID NOS: 488
SEQ ID NO 1.0
SEQ ID NO 1.0
LENGTH: 30
TYPE: PRIT
ORGANLEN: Homo sapiens
US-10-133-668-1.20
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CIRRENT PELLORICON WINNERS, 18/60/293,172
PRIOR FLLIN DATE; 200.0-5-24
PRIOR PELLORICON WINNERS, 18/60/293,172
PRIOR PELLORICON WINNERS, 18/60/316,031
PRIOR PELLORICON WINNERS, 18/60/294,403
PRIOR PELLORICON WINNERS, 18/60/294,403
PRIOR PELLORICON WINNERS, 19/2001-15/7043
PRIOR PELLORICON WINNERS, 19/2001-15/7043
PRIOR PELLORICON WINNERS, 19/2001-15/60-81
PRIOR PELLORICON WINNERS, 19/2001-26/681
                                                                                                                                                                              US-09-809-391-696
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANY: Ruben et al.
TTILE OF INVENTION. 166 Human Secreted proteins
FILE REFERENCE: P2002P2
                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local &
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APPLICANT: MATSUD
APPLICANT: MURAMA
APPLICANT: ISHIZA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 120,
                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 696, Application US/09809391
Publication No. US20030049618A1
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPELICANT: MARSUDA, Akio
RPELICANT: MERRAWATSU, Shuji
RPELICANT: ISHIZAWA, Kenya
RTILE OF INVENTION: STATE Activating Gene
RTILE REFERENCE: 1254-0207F
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                            ENGTH: 365
                                                                                   Local Similarity
les 7; Conserv
264 CDKFSGHPKGFAY 276
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                                        1 CXXYGNSPKGFAY 13
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7; Conserva
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o. US20030092616A1
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                                                                                   Score 44; DB 11; Length 365;
Pred. No. 14;
1; Mismatches 5; Indels
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CIREBENT NEIDLYCHTON WINNERS: 105/109/882.171
CURRENT PELING BATE: 2001-06-18
PRIOR PAPILICHTON WUNDERS: 09/809.391
PRIOR PAPILICHTON WUNDERS: 09/809.391
PRIOR PELING BATE: 2001-03-16
PRIOR PELING BATE: 2002-06-109/149.476
PRIOR PELING BATE: 1098-03-06
PRIOR PELING BATE: 1098-03-06
PRIOR PELING BATE: 1098-03-06
PRIOR PELING BATE: 1099-03-06
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR
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ON PRINCATION UNUSER: 60/447-503

ON PILIME DATE: 1997-05-23

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OR FILIME DATE: 1997-05-23

OR FILIME DATE: 1997-05-23

OR APPLICATION WINSER: 60/047,598

OR APPLICATION WINSER: 60/047,613

OR FILIME DATE: 1997-05-23-047,582

OR FILIME DATE: 1998-05-23-047,582

OR FILIME DATE: 1998-05-20-23-047,582

OR FILIME DATE: 1998-05-20-24-25-047,612

OR FILIME DATE: 1997-05-20-7,612

OR FILIME DATE: 1997-05-20-7,612

OR FILIME DATE: 1997-05-20-7,612

OR FILIME DATE: 1997-05-20-7,612
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R APPLICATION NUMBER: 60/047,597
DR FILING DATE: 1997-05-23
R                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R FILING DATE. 1997-05-23
RAPPLICATION NUMBER: 66/047,583
RR FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
RAPPLICATION NUMBER: 66/047,618
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,600
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
                                           APPLICATION NUMBER: 60/047,632
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o. US20030175858A1
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BE APPLICATION NUMBER: 60/056,911
BE PILING DATE: 1997-06-25
BE APPLICATION NUMBER: 60/056,636
BE FILING DATE: 1997-06-26,974
BE PILING DATE: 1997-06-26,974
BE PILING DATE: 1997-06-26,910
BE APPLICATION NUMBER: 60/056,864
BE PILING DATE: 1997-06-22,916,864
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NE APELICATION NUMBER: 60)043,313

NE FILING DATE: 1997-04-11

NE PELICATION NUMBER: 60)043,572

NE FILING DATE: 1997-04-11

NE PELICATION NUMBER: 60)043,315

NE FILING DATE: 1997-04-11

NE PELICATION NUMBER: 60,048,974
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OR FILING DATE: 1997-04-11
OR FILING DATE: 1997-04-11
OR APELICATION WUMBER: 60/043,311
OR FILING DATE: 1997-04-11
OR APELICATION WUMBER: 60/043,671
OR FILING DATE: 1997-04-11
OR FILING DATE: 1997-04-11
OR FILING DATE: 1997-04-11
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NE FILING DATE: 1997-06-3
NE APPLICATION NUMBER: 60/043,580
NE FILING DATE: 1997-04-31,568
NE FILING DATE: 1997-04-31,568
NE FILING DATE: 1997-04-31,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/056,662
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,872
FILING DATE: 1997-08-22
                                                                                             APPLICATION NUMBER: 60/056,631
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,894
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/056,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,903
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APPLICATION NUMBER: 60/056,882
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,630
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APPLICATION NUMBER: 60/056,889
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,877
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APPLICATION NUMBER: 60/043,669
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,845
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,892
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APPLICATION NUMBER: 60/056,878
FILING DATE: 1997-08-22
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Query Match
Best Local
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TOR PILLING DATE: 1997-08-22

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TOR PILLING DATE: 1997-08-22

TOR PILLING DATE: 1997-05-23

TOR PILLING DATE: 1997-05-23

TOR PILLING DATE: 1997-05-24

TOR PILLING DATE: 1997-05-26

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ON APPLICATION UNMSER: 0,075.6 875

ON FILING DATE: 1997-08-22

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ON PILING DATE: 1997-08-22

ON PILING DATE: 1997-08-29

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ON PILING DATE: 1997-08-29

ON PILING DATE: 1997-08-26

ON PILING DATE: 1997-0
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OR FILLING DATE: 1,997-04-11,
OR FILLING DATE: 1,997-04-11,
OR FILLING DATE: 1,997-04-11,
OR FILLING DATE: 1,997-04-17,
OR APPLICATION NUMBER: 60/047,501
OR FILLING DATE: 1,997-06-23,
OR APPLICATION NUMBER: 60/043,670
OR FILLING DATE: 1,997-06-12,
OR FILLING DATE: 1,997-06-12,
OR FILLING DATE: 1,997-06-12,
OR FILLING DATE: 1,997-06-22,
OR FILLING DATE: 1,997-0
                                                                                                                                                                                                                                                                          FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/056,884
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APPLICATION NUMBER: 60/056,876
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,881
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53.8%;
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Score 44; DB 12; Length 365; Pred. No. 14;
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뭉 264 CDKFSGHPKGFAY 276 1 CXXYGNSPKGFAY 13 l Similarity 7; Conserva

Matches

Conservative

Mismatches

0; Gaps

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RESGUT 5 US-09-828-708-3 US-09-828-708-3 Sequence 3, Application US/09828708 Fatent No. US20020146753A1 GENERAL INFORMATION:

APPLICANT: Ditzel, H.

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US-09-828-708-7
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LENGTH: 105
TYPE: PRT
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APPLICANT: Schaller.
TYTLE OF INVENTION: Autointibodies to glucose-6-phosphate isomerase and their particly
TYTLE OF INVENTION: Autoinmune disease
FILE REFERENCE: 1541.00515 US/09/828,708
CURRENT APPLICATION NUMBER: 09/9828,708
CURRENT APPLICATION NUMBER: 09/9828,708
CURRENT PARTICATION NUMBER: 09/9828,708
CURRENT PARTICATION PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTICATION OF THE PARTI
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Best Local Similarity 5%...
Conservative
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Patent No. US20020146753A1
GENERAL INFORMATION:
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Best Local
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APPLICANT: Strice, D.
APPLICANT: Schaller, M.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoimnime disease
FILE REFERENCE: 136.100512.
CURRENT APPLICATION NUMBER: US/09/238/708
CURRENT FILLA DATE: 2001-09-24
MUMBER OF SEQ ID MOSS: 123
MONBER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PERSSON, MATS AXEL
APPLICANT: ALLANDER, TOBIAS ETIK
TITLE OF INVENTION: HUBANITIS C VIRUS (HCV) E2 ANTIGEN
                                                                                                                                                                                                                     STREET: 90 MIDDL
CITY: MENLO PARK
STATE: CA
                                                                                                                               ZIP: 94025
                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                        CA
USA
                                                                                                                                                                                                                                                                                                                   B: ROBINS & ASSOCIATES
90 MIDDLEFIELD ROAD, SUITE 200
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Pred. No. 41;
2; Mismatches
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CURRENT APPLICATION NUMBER: US/10/269,805
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; Sequence 36, Application US/10269805; Publication No. US20030124129A1; GENERAL INFORMATION; APPLICANT: OLINER, JONATHAN D.
                                                                                                                    RESULT 9
US-10-269-805-36
                                                                                                                                                                                                                                                                                                                                                                US-10-269-805-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Sequence 32, Application US/10269905
| Publication No. US20901214129A1
| GENERAL INFORMATION: ONATHAN D. |
| APPLICANT: OLITER, JONATHAN D. |
| TITLE OF INVENTION: ANGLOPOISTIN-2 SPECIFIC BINDING AGENTS |
| FILE REFERENCE: A-712 | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-269-805-32
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/228,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SED ID NOS: 70
SOPTWARE: PatentIn version 3.1
SED ID NO 32
LENGTH: 108
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS FILE REFERENCE: A-722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (650) 325-78
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 19-APR-196
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,215
FILING DATE: 17-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MCCRACKEN, THOMAS P. REGISTRATION NUMBER: 38,548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 47.5%;
Local Similarity 54.5%;
                                                                                                                                                                                                 89 CQHYGSSPRTF 99
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linear
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NO: 10:
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54.5%;
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Pred. No. 42;
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Pred. No. 42;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-36
                                                                                                                                                                                                                                                                                                                                                             US-09-978-295A-226
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US-09-764-903-39
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US-09-764-903-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL IMPORMATION:
APPLICANT, Rosen et al.
TYTHE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 36
LENGTH; 108
                                                                                                                                                                                                                                                                                                               GENERAL
                                                                                                                                                                                                                                                                                                                            Sequence 226, Application US/09978295A Patent No. US20020156006A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Application US/09764903
Patent No. US20020090674A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/764,903
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 211
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 54.
les 6; Conservative
                                                                                                                                                                                                                                                                                                               INFORMATION:
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                                                  Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Gurney, Austin L.
Hillan, Kenneth J
                           KLjavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                   Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                 Gao, Wei-Qiang
                                                                                                                                                                                                  Filvaroff, Ellen
                                                                                                                                                                                                                                                               Botstein, David
            Napier, Mary A.
                                                                                                                                                                                                                                   Eaton, Dan
                                                                                                                                                                                                                                                Desnoyers, Luc
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James;
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Pred. No. 84;
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CURRENT FILING DATE: 200-10-15
PRIOR APPLICATION NUMBER: 09/91855
PRIOR PEPLICATION NUMBER: 09/91855
PRIOR PEPLICATION NUMBER: 00/66220
PRIOR APPLICATION NUMBER: 00/66220
PRIOR PEPLICATION NUMBER: 00/66249
PRIOR PEPLICATION NUMBER: 00/66249
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RRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
RRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
RRIOR FILING DATE: 1998-03-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT:
DR APPLICATION NUMBER: 60/080194
DR FILING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/080327
DR FILING DATE: 1998-04-01
DR PPLICATION NUMBER: 60/080328
DR PPLICATION NUMBER: 60/080328
DR FILING DATE: 1998-04-01
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
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FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078004
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FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077641
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FILING DATE: 1998-03-31
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                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/080105
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FILING DATE: 1998-03-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/079663
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FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/079656
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Williams, P. Mickey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paoni, Nicholas F.
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## 1000 PILLING DATE: 1998-04-01
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## 1000 PILLING DATE: 1998-04-08
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## 1000 PILLING DATE: 1998-04-29
## 1000 PILLING DATE: 1998-04-39
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RESULT 12
US-09-978-697-226
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Best Local :
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ON APPLICATION WHERE: 60/08689

ON APPLICATION WHERE: 60/08689

ON APPLICATION WHERE: 60/08559

ON APPLICATION WHERE: 60/08559

ON APPLICATION WHERE: 60/08550

ON PILLAY DATE: 1998-05-15

ON APPLICATION WHERE: 60/085670

ON PILLAY DATE: 1998-05-15

ON APPLICATION WHERE: 60/08570

ON PILLAY DATE: 1998-05-15

ON APPLICATION WHERE: 60/085697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE APPLICATION NUMBER: 60/085339

RETLING DATE: 1986-05-13

RETLING DATE: 1986-05-13

RETLING DATE: 1998-05-13

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DE FILINO DATE: 1998-05-07
DE APPLICATION NUMBER: 60/08458
DE FILINO DATE: 1998-05-07
DE APPLICATION NUMBER: 60/084600
DE FILING DATE: 1998-05-07
DE APPLICATION NUMBER: 60/084627
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APPLICATION NUMBER: 60/084643
FILING DATE: 1998-05-07
                                                                                                143 HĠVŚPQĠPQWSGC 155
                                                                                                                                                4 YGNSPKGFAYXXC 16
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                                                                                                                                                                                                                             47.5%; Score 38; 46.2%; Pred. No.
                                                                                                                                                                                                         Mismatches
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1.4e+02;
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Sequence 226, Application US/09978697 Patent No. US20020169284A1 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT APPLICANT: APPLICANT Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tunas, Daniel
Williams, P. Mickey
Wood, William I. Ashkenazi, Avi Grimaldi, J. Christopher Gurney, Austin L. Hillan, Kenneth J Kljavin, Ivar J. Baker Kevin P. Botstein, David Pan, James; Godowski, Goddard, Audrey Gerritsen, Mary E. Gerber, Hanspeter Gao, Wei-Qiang Fong, Ferrara, Napoleon Filvaroff, Ellen Kuo, Sophia S. Napier, Mary A. Eaton, Dan Desnoyers, Luc Sherman Tura

CURRENT APPLICATION NUMBER: US/09/978,697 CURRENT FILING DATE: 2001-10-16 PATOR APPLICATION NUMBER: 09/918585 PRIOR FILING DATE: 2001-07-30 TITLE OF INVENTION. Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same ILE REFERENCE: \$2630P1C27 R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080333
R FILING DATE: 1998-04-01
R APPLICATION WUMBER: 60/080334
R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/081070 APPLICATION NUMBER: 60/077641 FILING DATE: 1998-03-17 APPLICATION NUMBER: 60/077649 FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/077791 FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/080327 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080328 APPLICATION NUMBER: 60/080105 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080107 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080165 APPLICATION NUMBER: 60/079920 FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/079923 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079786 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079663 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079728 APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03-26 APPLICATION NUMBER: 60/079664 APPLICATION NUMBER: 60/078939 APPLICATION NUMBER: 60/066364 FILING DATE: 1997-11-21 APPLICATION NUMBER: 60/064249 FILING DATE: 1997-11-03 APPLICATION NUMBER: 60/065311 APPLICATION NUMBER: 60/062250 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/080194 FILING DATE: 1998-03-31 FILING DATE: 1998-03-3: FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/079689 FILING DATE: 1998-03-27 FILING DATE: 1998-03-27 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 FILING DATE: 1998-03-20 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/078936 APPLICATION NUMBER: 60/078886 APPLICATION NUMBER: 60/078004 FILING DATE: 1998-03-13 FILING DATE: 1998-03-12 APPLICATION NUMBER: 60/077632 FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/077450 FILING DATE: 1998-03-10 FILING DATE: 1997-11-13

PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR NE PILING DATE: 1998-04-29
BA APPLICATION NUMBER: 60/083742
BR FILING DATE: 1998-04-30
BR FILING DATE: 1998-05-05
BR FILING DATE: 1998-05-05
BR FILING DATE: 1998-05-05 DR FILING DATE: 1998-04-29
BR APELICATION UNBER: 60/83558
DR FILING DATE: 1998-04-29
BR APELICATION WUNBER: 60/083559
BR EFILING DATE: 1998-04-29
BR EFILING DATE: 1998-04-29
BR APELICATION WUNBER: 60/083500 E FILING DATE: 1998-04-22

MARPHICATION UNMER: 60/083804

MARPHICATION UNMER: 60/083804

MARPHICATION UNMER: 60/083700

MARPHICATION UNMER: 60/083791

MARPHICATION UNMER: 60/083791

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MARPHICATION UNMERS: 60/083796 R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083499
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R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/084598 FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084640
FILING DATE: 1998-05-07 FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084441
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084637 APPLICATION NUMBER: 60/083496 FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/093392
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/093495 FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/083336
FILING DATE: 1998-04-27
APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/092569
FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704 APPLICATION NUMBER: 60/081838 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081952 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081819 APPLICATION NUMBER: 60/081955 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
FILING DATE: 1998-04-09 FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195 APPLICATION NUMBER: 60/081073 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-5-07 APPLICATION NUMBER: 60/084639 FILING DATE: 1998-04-15 FILING DATE: 1998-05-07

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RESULT 13
US-09-978-192A-226
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Best Local
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APPLICANT:
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Patent No. US20020177553A1
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APPLICANT: Thams, biniel
APPLICANT: Hiliams, P. Mickey
APPLICANT: Rood, William I.
TITLE OF INVESTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVESTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT REPERIOR: P630912
CURRENT SPLICATION NUMBER: US/09/978,192A
CURRENT SPLICATION NUMBER: US/09/978,192A
EXIOR APPLICATION NUMBER: 00/918585
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OR FILLING DAY: 1980-05-15

OR APPLICATION NUMBER: 60/085580

OR APPLICATION NUMBER: 60/085573

OR FILLING DAYE: 1980-05-15

OR APPLICATION NUMBER: 60/085704

OR FILLING DAYE: 1988-05-15

OR FILLING DAYE: 1988-05-16

OR FILLING DAYE: 1988-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085689
FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085700
FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085338
FILING DATE: 1998-05-13
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
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APPLICATION NUMBER: 60/084643
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/085339
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6; Conserv
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Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                                                                  Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                             Gurney, Austra -.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                            Gerber, Hanspeter
Gerritsen, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baker Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                      Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                          Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desnoyers, Luc
                                                                                                                                                                                                                                             Paoni,
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                                                                                                                                                                                                                                                                                                                 Kljavin,
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Pred. No. 1.4e+02;
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APPLICATION NUMBER: 60/081071
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203

1998-04-09

PRIOR

FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/081070 FILING DATE: 1998-04-08

APPLICATION NUMBER: 60/080334

FILING DATE:

1998-04-0

APPLICATION NUMBER: 60/ FILING DATE: 1998-04-08

60/081049

PRIOR PRIOR

APPLICATION NUMBER: 60/080327
TILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333

FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080165
FILING DATE: 1998-03-31 FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/080105 FILING DATE: 1998-03-31 FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/079923

APPLICATION NUMBER: 60/080107

APPLICATION NUMBER: 60/080194 FILING DATE: 1998-03-31

PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR DE FILING DATE: 1998-03-11
DR REPLICATION NUMBER: 60/077791
DR FILING DATE: 1998-03-12
DR PELICATION NUMBER: 60/078004
DR FILING DATE: 1998-03-13
DR PELICATION NUMBER: 60/078886
DR FILING DATE: 1998-03-20
DR PELICATION NUMBER: 60/078886 DE APELICATION NUMBER: 60/66250

R FILING DATE: 1997-10-17

R FILING DATE: 1997-10-17

R FILING DATE: 1997-11-03

R FILING DATE: 1997-11-03

R FILING DATE: 1997-11-18

R FILING DATE: 1997-11-18

R FILING DATE: 1997-11-18 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03-26 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/077641 FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/077649 APPLICATION NUMBER: 60/077632 APPLICATION NUMBER: 60/066364 FILING DATE: 1997-11-21 APPLICATION NUMBER: 60/077450 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079663 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079294 APPLICATION NUMBER: 60/078939 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079786 APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079689 APPLICATION NUMBER: 60/079664 FILING DATE: 1998-03-

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PRIOR APPLICATION UNMBER: 60/082569
PRIOR APPLICATION UNMBER: 60/082704
PRIOR PILTMG DATE: 1998-04-21
PRIOR APPLICATION UNMBER: 60/082704
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/061838
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PRIOR APPLICATION NUMBER: 60/081819
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PRIOR APPLICATION NUMBER: 60/083496
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PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
RIOR APPLICATION NUMBER: 60/083495
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PRIOR APPLICATION NUMBER: 60/082797
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PRIOR APPLICATION NUMBER: 60/082700
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BPILING DATE: 1998-05-05
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BRADELING 
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APPLICATION NUMBER: 60/083558
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085338
FILING DATE: 1998-05-13
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FILING DATE: 1998-05-07
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084627
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APPLICATION NUMBER: 60/084640
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FILING DATE: 1998-05-07
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ADDITIONAL WILLIAM WILLIAM CONTROL OF THE SAME POLYPOPTICES and Nucleic PITTLE ON INVESTORS. Social Encoding the Same Polypoptides and Nucleic PITTLE OF INVESTORS. Social Encoding the Same POLYPOPTICS. CURRENT PAPILOXION NUMBER: US/09/999.832A PRICE APPLICATION NUMBER: 09/91855
PRICE RILLIAM DATE: 2001-10-29
PRICE RILLIAM DATE: 2001-10-29
PRICE RILLIAM DATE: 309-10-17
PRICE RILLIAM DATE: 109/910-10-17
PRICE RILLIAM DATE: 109/91-10-17
PRICE RILLIAM DATE: 109/91-11-13
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REXOR FILING ADXE: 1999-05-13
REXOR APPLICANTION NUMBER: 60/085582
REXOR FILING ADXE: 1999-05-15
REXOR APPLICATION NUMBER: 60/085700
REXOR FILING DATE: 1996-05-15
PELOR APPLICATION NUMBER: 60/085689
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Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
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APPLICATION NUMBER: 60/066364
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Godowski, Paul J.
Grimaldi, J. Christopher
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Botstein, David
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Hillan, Kenneth J
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Filvaroff, Ellen
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Pred. No. 1.4e+02;
3; Mismatches 4
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APPLICANT, Williams P. Middey
APPLICANT, MOOA, William I.
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FILE REFRENCE: P2630PIC7
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APPLICANT: Baker Kevin P.
APPLICANT: Bocstein, Davi
APPLICANT: Desnoyers, Luc
APPLICANT: Eston, Dan
APPLICANT: Ferrara, Napol
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Publication No.
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6; Conservation
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Botstein, David
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PRIOR PILLYANION NUMBER: 60/07749

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PRIOR PILLYANION NUMBER: 60/07978

PRIOR PILLYANION NUMBER: 60/08003

PRIOR PILLYANION

PRIOR PILLING DATE: 1998-04-21
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Query Match 47.5%; Best Local Similarity 46.2%; Matches 6; Conservative

Score 38; DB 11; Length 351; Pred. No. 1.4e+02; Pred. No. 1.4e+02; 3; Mismatches 4; Indels

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Search completed: November 7, 2003, 08:16:55 dob time: 15.0347 secs

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                 328717 seqs, 42310858 residues
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-635-109-7
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Sequence 696, App

Sequence 17, Appl

Sequence 19, Appl

Sequence 19, Appl

Sequence 19, Appl

Sequence 21, Appl

Sequence 22, Appl

Sequence 22, Appl

Sequence 23, Appl

Sequence 24, Appl

Sequence 26, Appl

Sequence 27, Appl

Sequence 29, Appl

Sequence 21, Appl

Sequence 21, Appl

Sequence 22, Appl

Sequence 21, Appl

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Sequence 24, Appl

Sequence 26, Appl

Sequence 27, Appl

Sequence 27, Appl

Sequence 28, Appl

Sequence 29, Appl

Sequence 29, Appl
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Result No.

38 35 35 35 36 35 36 36 36

ALIGNMENTS

BARLIER ER FILIMO DATE: 1997-08-22
ER FILIMO DATE: 1997-08-22
ER FILIMO DATE: 1997-08-22
ER PLIMO DATE: 1997-08-22 RE PILIGO DATE: 1997-08-22

RE APPLICATION UNUBER: 60,056,630

RE FILIAN DATE: 1997-08-22

RE PILIGATION UNUBER: 60,056,878

RE PILIGATION UNUBER: 60,056,622

RE PILIGATION UNUBER: 60,056,622

RE PILIGATION UNUBER: 60,056,872

R PILLED DATE: 1997-04-11

ER APPLICATION WUBBER: 0/0/43,311

ER FILMS DATE: 1997-04-11

ER APPLICATION WUBBER: 0/0/43,671

ER PILLED DATE: 1997-04-11

ER APPLICATION WUBBER: 0/0/43,674

ER PILLED DATE: 1997-04-11

ER PILLED DATE: 1997-04-11 ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,596
ER LILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,612
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,632 RE PILING DATE: 1997-05-23
SR APPLICATION NUMBER: 60/047,598
SR PILING DATE: 1997-05-23
SR PILING DATE: 1997-05-23
SR PILING DATE: 1997-05-23
SR APPLICATION NUMBER: 60/047,582 N FILIMO DATE: 1997-04-11
RR APLICATION NUMBER: 60/048,974
R FILIMO DATE: 1997-06-06
RR APLICATION NUMBER: 60/056,886
R FILIMO DATE: 1997-08-22
RR APLICATION NUMBER: 60/056,877
RR APLICATION NUMBER: 60/056,877
RR FILIMO DATE: 1997-08-22
RR FILIMO DATE: 1997-08-28
RR FILIMO DATE: 1997-08-28 RE FILING DATE: 1997-05-23
RE APPLICATION NUMBER: 60/047,601
RE FILING DATE: 1997-05-23
RE FILING DATE: 1997-04-11
RE FILING DATE: 1997-04-11
RE APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,315
FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569 APPLICATION NUMBER: 60/047,500 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,587 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,492 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-1

EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER ARLIER IN APPLICATION NUMBER: 60/055,889
SE FILING DATE: 1997-08-22
SE APPLICATION NUMBER: 60/055,908
SE FILING DATE: 1997-08-25
SE APPLICATION NUMBER: 60/048,964
SE FILING DATE: 1997-06-05
SE FILING DATE: 1997-06-05
SE FILING DATE: 1997-09-05
SE PILING DATE: 1997-09-05
SE APPLICATION NUMBER: 60/057,580
SE APPLICATION NUMBER: 60/057,684
SE FILING DATE: 1997-09-05 APPLICATION N
FILING DATE: APPLICATION NUMBER: 60/056,664
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,876 APPLICATION NUMBER: 60/ PILING DATE: 1997-08-22 APPLICATION NUMBER: 60/043,576
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/047,501
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670 APPLICATION NUMBER: 60/ FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,862 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,875 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ PTT.TNG DATE: 1997-05-23 APPLICATION NUMBER: 60/047,589 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 APPLICATION NUMBER: 60/047,599 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,595 FILING DATE: 1997-05-23 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,892 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-04-11 FILING DATE: 1997-04-13 APPLICATION NUMBER: 60/047,614 APPLICATION NUMBER: 60/047,594 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,585 APPLICATION NUMBER: 60/047,588 APPLICATION NUMBER: 60/043,578 NUMBER: 60/056,894 NUMBER: 60/056,874 NUMBER: 60/056,636 1997-05-23 1997-08-22 1997-08-22 1997-05-23 1997-05-23 1997-05-23 1997-08-22 1997-08-22 1997-08-22 60/056,632 60/047,593 60/047,590 60/057,761 60/056,63

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                                                                           Matches
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Best Local :
                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                 CUERRHY APPLICATION DAWA:
APPLICATION INTHERS: US 109/09/025,7698
PRICK APPLICATION DAWS: 18-FBB-1598
PRICK APPLICATION HOMBER: EP 95 11 3021.0
PRILING DATE: 18-MG-1995
PRILING DATE: 18-MG-1995
PRILING DATE: 18-MG-1995
PRICHEST/PAITION HUMBER: 27,794
PRISTSTPAITION HUMBER: 27,794
PRISTSTPAITION HUMBER: 307.794
PRISTSTPAITION HUMBER: 307.794
PRISTSTPAITION HUMBER: 307.794
PRISTSTPAITION: (1215) 585-5900
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RANLIER FILING DATE: 1997-09-05
RANLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
RANLIER APPLICATION NUMBER: 60/061,060
EARLIER APPLICATION UNMER: 60/061,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                     TELEBAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1251 A
CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 55.0%; Score 44; DB Local Similarity 53.8%; Pred. No. 9.6; hes 7; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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89 CQQYGNSPYTF 99
                                       1 CXXYGNSPKGF 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: James F. Haley, Jr., Ssq. c/o Fish & Neave
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASD
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0,
                                                                                          63.6%;
                                                                        0; Mismatches
                                                                                          Score 39; DB
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30 (EPO)
                                                                                                            DB 4; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 365;
                                                                        4; Indels
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RESULT 3

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; Sequence 7. Application US/08635109

Patent NO. 639114

GENERAL HETORNATION:
APPLICANT: Persoon, Nato A. A.
APPLICANT: Allander, Tokias E.
APPLICANT: Allander, Tokias E.
TITLE OF INVENTION: HIMMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
TITLE OF INVENTION: HIMMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
TITLE OF INVENTION: HIMMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
TITLE OF INVENTION: HEPATITIES C VIEWS (HCV) E2 ANTIGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 327-3400
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        APPLICANT: Scotgen Higharmacentrals
APPLICANT: Menlo Park, California 94025
APPLICANT: Menlo Park, California 94025
APPLICANT: United States of America
APPLICANT: 1345 Avenue of the Americas
APPLICANT: New York, New York 10105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MCCTACKE, Thomas P
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 2300-6146
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19-APR-19:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      APPLICANT: United States of Am
TITLE OF INVENTION: RECOMBINAN
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 107 amino
TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                           STREET: 805 Th
CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 285 Hamilton Avenue, Suite 200 CITY: Palo Alto STATE: California
                                      COUNTRY:
                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: REED & ROBINS
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                     10022
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5646253
                                                           New York
                                                                                                     E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 amino acids
                                                                                                                                                                                                           United States of America
1345 Avenue of the America
New York, New York 10105
United States of America
VBNTION: RECOMBINAT HUMAN ANTI-LK26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.5%; Score 38; DB 4; Length 107; 54.5%; Pred. No. 27;
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US-08-207-996-19
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEPAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
CTTANDERVESCO: circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                     COMPUTER EXEMPALS FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-105/MS-DOS
SOFTMARE: Worlderfect 6.0/ASCII standard
URBERT APPLICATION DATA;
                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-
                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                APPLICATION NUMBER:
FILING DATE: 08-MAR-
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Pasqualini, Patricia A. REGISTRATION NUMBER: 34,894 REFERENCE/DOCKET NUMBER: LUD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1in
                                                                                                                                                                                                                                                                                                                                      ZIP: 10022
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                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 47.5%;
Local Similarity 46.2%;
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5646253
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United States of America
1345 Avenue of the Americas
New York, New York 10105
United States of America
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1014 Hamilton Court
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                                                                                                                                                                                     08-MAR-1994
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Pred. No. 30;
                                                                                               LUD-5363
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RESULT 7

96 CARHGDDPAWFAY 108

1 CXXYGNSPKGFAY 13

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PRICHIT NO. 5646753

GENERAL INFORMATICAL:

APPLICANT: Societa Biopharmaceuticals, Inc.

APPLICANT: Societa Biopharmaceuticals, Inc.

APPLICANT: Hondo Bark California 9005

APPLICANT: United States of Americas

APPLICANT: New York, New York 10105

APPLICANT: United States of America

APPLICANT: UNITEDOLES
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TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
POLECULE TYPE: DNA (genomic)
US-08-207-996-19
                                                                            US-08-207-996-20
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                                                                                                                THESPAY. 212-939-9394
INFORMATION POR SEA ID NO. 20:
SEQUENCE CHARACTERISTICS:
MENOTH: 119 amino acids
TYES: amino acid
STRANDENNESS: single
TOPOLOSY: linear
Matches
                                      Query Match
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                Query Match 47.5%; Score 38; DB 1; Length 119; Best Local Similarity 46.2%; Pred. No. 30;
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                                                                                                                                                                                                                                                                                             APPLICATION DATA.

APPLICATION NUMBER: US/08/207.9

PILING DATE: 08-MAR-1994

CLASSIFFCATON: 530

ATTORNEY/AGENT INFORMATION:
MANE: PAGGRAIAIN: PRELICIA A.
REGISTRATION WINBER: 34,894

REGISTRATION WINBER: 34,00-53
                                                                                                TOPOLOGY: 1i
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MEDIUM TYPE: 3.5 inc
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ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0/ASCII standard
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CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                         TELEPHONE:
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Local Similarity 46.2%;
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Y: U.S.A.
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Conservative
                                                                                                                                                                                                                                                             212-688-9200
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2; Mismatches
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Pred. No. 30;
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Retent No. 564653
Retent No. 564653
Retent No. 564653
APPLICANT: Scodeen Biopharmaceuticals, Inc.
APPLICANT: Scodeen Biopharmaceuticals, Inc.
APPLICANT: HOLA Hamilton Court
APPLICANT: Hola Fark, California 94025
APPLICANT: United States of America
APPLICANT: Malo Avenue of the America
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                       TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
TO SECURENCES: 29
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
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STREET: New York
STATE: New York
STATE: " S.A.
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NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING YSUTEM: PC-DOS/M9-DOS
SOFTWARE: MordPerfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207.996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
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APPLICANT: United States Go America
APPLICANT: Not Sevenue of the Americas
APPLICANT: New YORK, New YORK: 10105
APPLICANT: United States of America
APPLICANT: United States of America
TITLE OF INVENTION: ANTIDOLIES
TITLE OF INVENTION: ANTIDOLIES
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                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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     STREET:
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CLASSIFICATION: 530
                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 CARHGDDPANFAY 108
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3: Felfe & Lynch
805 Third Avenue
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1014 Hamilton Court
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US-08-207-996-27
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MEDIUM TYPE: 35 inchall FORM:
MEDIUM TYPE: 35 inchall
COMPUTER: INFE: 35 inchall
OCMPUTER: 35 inchall
OCMPUT
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TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 2
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APPLICANT: 1014 Hamilton Court
APPLICANT: Wanto Park, California 94025
APPLICANT: United States of America
APPLICANT: 1345 Avenue of the Americas
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NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REALDABLE FORM:
MEDIUM TYPE: 3.5 Anch
COMPUTER: IH PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: MC-OXOS-TSC-G O/ASCII standard
CURBENT APPLICATION DATA:
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APPLICANT: 135 Avenue of the Americas
APPLICANT: New York, New York 10105
APPLICANT: Hoted States of America
ATTLE OF INVENTION: ANTIONIES
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LENGTH: 119 amino acid
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
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FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
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nes 6; Conserv
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STRANDEDNESS: sin
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STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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Gaps 0;

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; NOLECULE TYPE: protein
US-08-760-840A-18
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US-08-760-840A-18
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US-08-207-996-27
                                                                  Matches
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/08760840A Patent No. 5952484
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 18:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APELICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: PCT/US 95/0309
FILING DATE: 08-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compat
OPERATING SYSTEM: PC-DC
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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APPLICANT: LAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                   TYPE: amino
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hanson, No. 5952484man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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1 CXXYGNSPKGFAY 13
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Similarity 46.2%;
6; Conservative
                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                      119 amino acids
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805 Third Avenue
                                                                  Conservative
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212-838-3884
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                        unknown
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                                                                                           47.5%;
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                                                             Mismatches
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                                                                                           Score 38; DB
Pred. No. 30;
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                                                        Gaps
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Sequence **. ***.

Patent NO. 59928494
GENERAL INFORMATION.
GENERAL INFORMATION.

APPLICANT: Milliam J. HARRIS;
APPLICANT: Milliam J. RETTIG;
APPLICANT: Pollar GARIN-CHESA;
APPLICANT: Pilar GARIN-CHESA;
APPLICANT: Lloyd J. OLD

**TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK28 ANTIBODIES

**TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK28 ANTIBODIES
                                                                                                                                                                                                                                RESULT 12
US-08-760-840A-20
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US-08-760-840A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 19:
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FILING DATE: 05-DEC-1996

PELOR APELCATION DATA:
APELCATION NUMBER: PCT/US 95/03094

FILING DATE: 08-MAX-1995

CLASSIFICATION: 536

CLASSIFICATION: 536
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STREET: New York
CITY: New York
TTATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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CURRENT APPLICATION DATA:
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APPLICANT: L10yd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Match 47.5%; Score 38; Local Similarity 46.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hanson, No. 5952484man
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                          96 CARHGDDPAWFAY 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 119;
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MAMIS HARSON, NO. 956
REGISTRATION NUMBER: 10,946
REGERENCY/DOCKET NUMBER: LUD 545
REGERENCY/DOCKET NUMBER: LUD 545
REGERENCY/DOCKET NUMBER: LUD 545
REGERENCY/DOCKET NUMBER: LUD 545
REGERENCY/DOCKET NUMBER: LUD 545
REGERENCY/DOCKET NUMBER: LUD 545
SEQUENCY CHARACTERISTICS:
SEQUENCY CHARACTERISTICS:
SEQUENCY CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/08760840A Patent No. 5952484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                                          APPLICANT: PAUL WALLACE;
APPLICANT: WALLACE;
APPLICANT: WALLACE;
APPLICANT: HOLIGANG J. RESTIG;
APPLICANT: LIOYd J. OLID
APPLICANT: LIOYd J. OLID
APPLICANT: LIOYd J. OLID
APPLICANT: LIOYd J. OLID
APPLICANT: LIOYd J. OLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O:
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                              MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                       STREET: 805 Th
CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US 95/03094
FILING DATE: 08-MAR-1995
CLASSIFICATION: 536
                                                                                                                                                                                ZIP: 10022
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                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 47.5%;
Local Similarity 46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 CARHGDDPAWFAY 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 119 amino acids
amino acid
                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                              805 Third Avenue
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                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                     Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                       US/08/760,840A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 2; Length 119;
Pred. No. 30;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUD 5363.1 DIV. - JEL/NDH/SLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08760840A Patent No. 5952484 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                      MEDIUM TYPE KEADAMLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SETEM: FO-CDS/MS-DOS
SOFTMARE: MO-CDPETECC
CURRENT APELICATION AND SETEM: US/08/760,840A
APELICATION MOMBER: US/08/760,840A
LILING DATE: 05-US-1996
PEIDE APELICATION MATH.
APELICATION MOMBER: PCT/US 95/01094
APELICATION MATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APELICATION DANH.

APELICATION UNUBER: PCT/IS 95/030:
PILIND DATE: 08-MAR-1995

CLASSIFICATION: 556
APTONEMY/AGENT INFORMATION:
NAME: Hamenon No. 525-2864man D.
REGISTHAUTION UNUBER: 09-96
REFERENCE/DOCKET NUMBER: 01. UD 5363
TELEOPHONE: 12. 2869-2900
TELEOPHONE: 3. 2. 2869-2900
TELEOPHONE: 3. 2. 2869-3900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 21;
SEQUENCE CHARACTERISTICS;
                                                                        TELEPHONE: 212-688-920
TELEPAX: 212-838-3884
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORRESPUN.
ADDRESSES: ENGRESSES: 805 Thira STREET: New York
STATE: New York
STATE: New York
U.S.A.
                                                                                                                                   CLASSIFICATION. 536
ATTORNEY/AGENT INFORMATION:
NAME: HARBON, No. 5952464man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: JUD 53
TELECOMMUNICATION INFORMATION:
                                SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 46.2%;
ses 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TYPE: amino acid
STRANDEDNESS: un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 CARHGDDPAWFAY 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 amino acids
                                                                                                                  212-688-9200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 119;
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Search completed: November 7, 2003, 07:30:11 Job time: 2.3498 secs
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; MOLECULE TYPE; protein
US-08-760-840A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-760-840A-28
                                                                                                                                                                                                                                                                                                                Query Match 47.5%;
Best Local Similarity 46.2%;
Matches 6; Conservative
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GENERAL INFORMATION;
APPLICANT PAUL NALLACE;
APPLICANT PAUL NALLACE;
APPLICANT WOLEGAM J. HARRIS;
APPLICANT WOLEGAM J. HARRIS;
APPLICANT HOLEGAM J. RETTIG;
APPLICANT, LIJOH JOAN CHESA;
APPLICANT, LIJOH JOAN CHESA;
APPLICANT, LIJOH JOAN CHESA;
APPLICANT, LIJOH JOAN PRINCHESS;
ITHE OF INVESTIGN. RECOMBINANT HUMAN ANTI-LKZ6 ANTIBODIES
NUMBER OF SEQUENCES;
31
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CURRENT APPLICATION ON THE MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MINN / MI
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Best Local Similarity 46.2% Pred: No. 30;
Matches 6; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/08760840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 28;
SEQUENCE CHARACTERISTICS:
LENGTH; 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS,
ADDRESSEE: Pelfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
21P: 1002.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
NOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                     96 CARHGDDPAWFAY 108
                                                                                                                                                                                                                                   1 CXXYGNSPKGPAY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXXYGNSPKGFAY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212-688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                Score 38; DB 2; Length 119;
Pred. No. 30;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LUD 5363.1 DIV. - JEL/NDH/SLH
                                                                                                                                                                                                                                                                                                          5; Indels
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                                                                                                                                                                                                                                                                                                   Gaps
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18; Search time 2.0721 Seconds (Without alignments) 742.581 Million cell updates/sec

Sequence: Title: Perfect score: US-09-661-992B-106 82 1 FRNRGMTALLKVSSCD 16

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

203308 segs, 96168682 residues

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum DB seq length: 2000000000 Minimum DB seq length: 0

Database : PIR 76: Maximum Match 100% Listing first 45 summaries pir3:* pir1:*

pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*			SUMMARIES	
Regult No.	Score	Query	Length	ВВ		ription
۲	82	100.0	2351	ь	EZHU	coagulation factor
2	76	92.7	2319	N	A47004	
ω	70	85.4	869	N	A25945	
۵	70	85.4	2133	N	T42763	
Ŋ	44	53.7	275	ы	283412	3
6	42	51.2	220	N	\$44966	
7	41	50.0	873	N	B86471	hetical p
8	41	50.0	1120	N	T14275	myosin-like protei
9	40	48.8	76	N	A97957	hypothetical prote
10	40	48.8	536	N	B81319	N-acylneuraminate
11	40	48.8	573	N	B96639	protein T1F9.16 (i
12	39	47.6	157	N	A87117	probable phosphopa
13	39	47.6	160	Ŋ	T44703	lipopolysaccharide
14	39	47.6	505	N	A97642	
15	39	47.6	512	N	AB2865	hypothetical prote
16	39	47.6	558	N	T19269	
17	39	47.6	1058	N	D82654	•
18	39	47.6	1099	N	A59311	
19	39	47.6	1208	N	T34469	•
20	38.5	47.0	455	N	AD2620	
21	38.5	47.0	467	N	D97402	hypothetical 53.7K
22	38	46.3	300	N	T21149	
23	38	46.3	485	N	T03426	sucrose phosphoryl
24	38	46.3	485	N	AE3244	sucrose phosphoryl
25	37.5	45.7	172	N	B75368	hypothetical prote
26	37.5	45.7	376	N	T42673	hypothetical prote
27	37	45.1	58	N	AB2880	
28	37	45.1	129	N	F82515	₩.
29	37	45.1	151	N	E71547	hypothetical prote

36	36	36	36	36	36	36.5	37	37	37	37	37	37	37	37	37
			43.9			44.5	45.1	45.1	45.1	45.1	45.1	45.1	45,1	45.1	45.1
89	68	89	89	89	89	650	1243	776	772	772			456	323	304
2 F90779	2 858344	2 A60279	2 169156	2 801033	1 542609	2 A34498	2 860138	2 T29064	2 G98327	2 AF2955	2 H72208	2 T33760	2 T48291	2 T25948	2 A45989
	Shiga-1	shiga-1	shiga-l	Shiga-1	shiga-1	glycopr	sex factor	hyaluronate	hypothetica	GGDEF f	conserved	sphingo	hypothetical	hypother	peroxisome
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ALIGNMENTS

coagulation factor VIII precursor (walidated) - human
NyAlternate names antihemophilic factor A, coagulation factor VIIIc; procoagulant con
C;Species; Homo sapiens (man)
C;Becies; 82-May-1985 #equance_revision 38-May-1985 #text_change 08-Dec-2000
C;Accession: I54318; A00525; T8059; A23584; A25174; A42348; A43986; 863527; 866445; E
R;Gitechiar, J., Wood, W.I.
Hum. Mol. Genet. 1, 199-200, 199-200;

A, Status: preliminary; translated from GB/EMBL/DDBJ

A.Title. Expression of active human factor VIII from recombinant DNA clones A.Reference number: A0525; MUID:85061548; PMID:6438526 A.Accession: A00525 A;Rodacule 'type: DNA:
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s, D.N.; Hewick, R.M. Nature 312, 342-347, 1984 A;Molecule type: mRNA A;Molecule type: mRNA A;Grose-references: BMSL:X01165; BMSL:X01166; BMSL:X01179 R;Toole, J.J.; Knopf, J.L.; Wozney, J.M.; Sultzman, L.A.; Buecker, J.L.; Pittman, D.D.

A.Pitila: Molecular cloning of a cDNA encoding human antihaemophilic factor. A.Raference number: I58059, MUID:85061550, PMID:6438528 A.Accession: I58059

Ajacons references: GB:MD1740; NID:g183807; EDDM:AAA52484.1; PID:g182803 A;Cross references: GB:MD1740; NID:g183807; EDDM:AAA52484.1; PID:g182803 A;Trustr, M., ; Bickher, R., ; Barke, R.L.; Coppt., D.; Chu, C.; Diaha, D.; Hartog, K.; K.; K.; K.; And, Diaha, D.; Hartog, K.; K.; K.; K.; Barke, D.; Dahl, H.H.; Favalaro, J.; Harsen, J.; M.; V.; M.; Barke, D.; Barke, J.; Barke, J.; Barke, J.; K.; K.; Barke, J.; Barke, J

A.;Polsecule type: mRNA A.;Polsecule type: mRNA A.;Crose-references: GB:M1413, NID:g182817, PIDN:AAA52485.1, PID:g182818 R.;Earon, D.; Rodrignez; H.; Vehar; G.A. Sichhenkery 25, 505-512, 1386 A.;Pittle: Proteopytte processing of human factor VIII. Correlation of specific cleavage

A.Reference number: A26174, MUID:86159740, PMID:1082357 A.Reference number: A26174 A.Reference number: A26174 A.Reference number: A26174 A.Reference number: A26174 A.Reference number: A26174, A26174 R; Pittman, D.D.; Wang, J.H.; Kaufman, R.J.

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AlContents: amportation; diantitâs bonds
AlContents: amportation; diantitâs bonds
AlContents: 239-079, 711-079, and 2019-079 were shown to have free sulfhydryls
R.K.dialko, M.; Hedding, A.; Talbo, G.; Bersson, E.; Thomsen, J.; Ebbn, M.
Bur, J. Bicchen, 234, 773-779, 1955
Bur, J. Bicchen, 234, 773-779, 1955
Bur, J. Bicchen, 234, 773-779, MUD1:6564559; PHID:857844
AlEsference namber: 854577, MUD1:6564559; PHID:857844
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A, Residues: Y, 547-52;1853-1860, 'X', 1862-1364, 'X', 1866 cFNY>
G, Layer, A., van Sonjindal, H.B.; Niehrs, C.; Buttnar, W.B.; Verbeet, M.P.; Wartens, K.,
G, Layer, A., van Sonjindal, H.B.; Niehrs, C.; Buttnar, W.B.; Verbeet, M.P.; Wartens, K.,
J. Biol. Chem. 266, '740-746, 1991
A, Miller: Shifation of Tyy(1680) of human blood coagulation factor VIII is essential for Niederabone number: NS-1869, px(1):1519-3266; PNID:189875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;20-740/Product; coagulation factor VIIIa heavy chain #status experimental <ACH:
F;20-356/Domain: A1 <DA1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Keywords: eoute phase; blood coagulation; duplication; glycoprotein; hemophilia A, pla
F:1-19/Domain: signal seguence #status predicted 4310-
F:20-2351/Product: coagulation factor VIII #status experimental «MAT»
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C; Superfamily: coagulation fa
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AvIntrons: 48/2; 69/1; 130/1; 201/1; 224/1; 263/1; 337/1; 424/2; 401/3; 513/1;
C.Function:
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A;Molecule type: protein
A;Residues: 168-1685 <LIN>
C;Comment: Factor VIII is at
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Lind, P.; Larsson, K.; Spira, J.; Sydow-Baeckman, M.; Almstedt, A.; Gray, E.; Sandber, Bur. J. Biochem. 232, 19-27, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 733-752;753-759 < KJA>
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Protesin Sci. 4, 740-746, 1946 bonds and free cysteines in the heavy and light chains
A./Ritle: Locations of disulfide hydroj95338127; PMID:7631471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Contents: amnotation; sulfation
R.Gitschier, J., Mood, M.T., Goralka, T.M.; Wion, K.L.; Chen, B.Y.; Raton, D.H.; Vehar,
Nature 312, 326-330, 1984
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                                                                                                                                                                                                                                                                                                                                                                             F;392-759/Domain: A2 <DA2>
F;402-730/Domain: ferroxidase repeat homology <FO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;23-348/Domain: ferroxidase repeat homology <FOl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: acts as a cofactor, with calcium and phospholipid, for the factor IXa pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:119124; OMIM:306700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:F8C
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                                                                                                                                                                                                                                                     )1668-2351/Product: coagulation factor VIIIa light chain #status experimental <ACL>
                                                                                                                                                                                                                                                                                                                                                  ;760-1667/Domain: B <DB0>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: coagulation factor VIII; discoidin I amino-terminal homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comment: Factor VIII is activated by factor Xa and thrombin, but prolonged exposure p
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9,1667-1669/Chaevege site; Axy-Giu (midentified proteinase) #status experimental F;1768-1709/Chaevege site; Axy-Gav (congulation factor Xa, thrombins) #status experime F;1740-1741/Chaevege site; Axy-Ala (coegulation factor Xa) #status experimental F;1740-1741/Chaevege site; Axy-Ala (coegulation factor Xa) #status experimental F;1740-1741/Chaevege site; #status produced
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A;Molecule type: protein A;Molecule type: protein A;Rasidues: 20-6;356-371,392-408;582-594;1668-1669;'X',1671;1672-1692;1693-1708;1709-1 A;Experimental source: recombinant material from Chinese hamster ovary cells Biochemiatry 31, 3315-3325, 1992 A,Tille: Identification and functional importance of tyrosine sulfate residues within re A,Reference number: A42348 MUID:9207952; PMID:1554716 A,Recession: A42348

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16;
Conservative
       100.0%; Score 82;
100.0%; Pred. No.
9
 Mismatches
       1.3e-06;
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 Indels
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716 FRURGMIALLKVSSCD 731
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Computation Sector VIII, discoldin I amino-terminal homology; Servoxid
S; Stetun; Preliminary
Computation Sector Preliminary
Fig. 30; Preliminary
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Genomics 16, 374-379, 1993
A; Title: Sequence of the murine factor VIII cDNA F;2160-2313/Domain: discoidin I amino-terminal homology F;1686-2006/Domain: ferroxidase repeat homology <FO3>F;2007-2156/Domain: discoidin I amino-terminal homology C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Jun-1999 coagulation factor VIII precursor - mouse C; Species: Mus musculus (house mouse) A; Accession: A47004 A;Reference number: A47004; MUID:93300511; PMID:8314577 Matches Query Match Accession: A47004 Local 15; 1 FRNRGMTALLKVSSCD 16 Similarity Conservative 92.7%; Score 76; 93.8%; Pred. No. 0; Pred. No. 1.7e-05; Mismatches DB 2; 1; Indels Length 2319; 0 Gaps o;

716 FRKRGMTALLKVSSCD 731

C./Accession; 152945 Pattenn, D.D.; Orr. E.C.; Murtha, P.; Wasley, L.C.; Kaufman, R.J. Proc. Marl, Acad. Sci. U.S.A. 83, 5939-5947, 1986 Proc. Marl, Acad. Sci. U.S.A. 83, 5939-5947, 1986 A; Title: A large region (U.S.A. 83), 5939-5947, 1986 Proc. Wall is dispensable for in v A; Reference number: A55945; MUID:86287369; PMID:3016730 A; Accession: A52945 C:Species: 16:Aug_1988 #sequence_revision 16-Aug-1988 #text_change 21-Jul-2000 A. Status: nucleic acid sequence not shown; not compared with conceptual translation A. Molecule type: DNA A. Residues: 1-65 < TOO>

Matches Query Match Local 14; Conservative Similarity 85.4%; Score 70; 93.3%; Pred. No. 0, Mismatches DB 2; 7e-05; Length 869; Indels

0;

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lmäR protein - Streptomyces ilmoolnensis
C:Spacies: Streptomyces ilmoolnensis
C:Pate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Oct-1999
C:Paccession: 869825; 844966
R;Pewonke, U.; Schmidt, H.; Zhang, H.Z.; Piepersberg, W.
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C;Pates: 11-dan-2000 #sequence_revision 11-dan-2000 #text_change 09-dun-2000
C;Pacession: 192763
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A; Residues: 1-275 <STO>
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A;Reference number: A8250, MUID:20437337; PMID:10984043
A;Accession: B39442
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Mature 405, 59-544, 2000
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C;Species: Pseudomonas aeruginosa
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Al,Reference number: Z2269
Al,Accession: 742763
Al,Status: preliminary; translated from GB/EMBL/DDBJ
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Nol. Microbiol. 16, 1137-1156, 1995
A.Title: Molecular claracteriation of the lincomycin-production gene cluster of Strep
A.Reference number: 65805; MUID:96020646; PMID:8577249
A.Rocession: §59825
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A, Status: preliminary, nucleic acid sequence not shown; translation not shown A, Molecula: type: DNA A, Residues: 1-220 < PE2>

A; Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994 A;Cross-references: EMBL:X79146; NID:g499194; PIDN:CAA55765.1; PID:g581696

C; Superfamily: Bacillus subtilis 23K phosphoprotein orfu A,Start codon: GTG A;Gene: lmbR

Query Match Matches Local Similarity Conservative 64.3%; Pred. Score 42; Mismatches No. DB 2; Ç, Length 220 Indels 0 0,

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Accession: B86471 hypothetical protein T32G9.38 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons

Maturie 408. 816-820, 2000

A.A.Michore: Hunter, U.L., Vankins, U.J., Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.A., Li, J.H., J.K., Y., Lin, X., Liu, S.X., Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Edizo, M.; Rouney, T.; Rowchey, D.; Sakano, H.
A.Anthore: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Nu, D.; Tu, G.; Fraser, C.M.; Vencer, U.C.; Davis, R. M.
A.; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.; Roterone number: A86141; MUDI:21016713; BWID:11130712

A;Status: preliminary A;Molecule type: DNA

Residues: 1-873 <STO>

A,Cross-references: GB:AE005172; NID:g11386301; PIDN:AAG35092.1; GSPDB:GN00141 C;Genetics:

A; Map position: 1 C; Superfamily: Arabidopsis thaliana hypothetical protein F26C24.7

Matches Query Match Local Similarity Conservative 50.0%; Score 41; DB 2; Pred. No. 25; Mismatches ۲. Length 873 0 Gaps 0

624 FKNRGLTQLVK 634 1 FRURGMTALLK 11

mysin-like protein myl - common sunflower
mysin-like protein myl - common sunflower
Myliteriale names: AFM homolog protein my; unconventional myosin
C;Spacies: Halanthus annuus (common sunflower)
C;Pate: 20-8ep-1999 #sequence_revision 20-8ep-1999 #text_change 08-8ep-2000
C;Accession: T14275

A;Description: Functional analysis of an unconventional myosin from sunflower express submitted to the EMBL Data Library, March 1997

A.Reference number: 217957
A.Recession: 1914275
A.Status: preliminary, translated from GB/EMBL/DDBJ
A.Wolecule type: m&W.
A.Wolecule type: m&W.
A.Wolecule type: m&W.
A.Wolecule type: m&W.

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A)Cross-references: GB:ALI39077; GB:ALI11168; NID:96968444; FIDN:CAB73398.1; FID:9696857
A)Experimental Gource: serotype O2; strain NCTC 11168
C)Genetics: 1
C)Genetics: A)Come newAj; C;1143
A)Gene: newAj; C;1143
C)Keywords: nucleotidyltransferase
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B83.13

M-exylmetraninate cytidylyltransferase (EC 2.7.7.43) Cj1143 [imported] - Campylobacter Cispecies: Campylobacter jejuni trision 31-Mar-2000 #text_change 03-Jun-2002 Cibocession B83.13
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A;Molecule type: DNA
A;Residues: 1-536 <PAR>
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A.Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals by A.Fetteren number: A81250, MUID:20150912; BMID:10688204

A.; Recession: 891319
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C;Specias: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession. A97957
R;Boakins, J.A.; Alborn dr. M.; Arnold, J.; Blasscrak, L.; Burgett, S.; Peloff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.M.; LeFkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.;
J. Bacteriol. 183, 5703-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Taltie: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Taltie: Genome of the Sacterium Streptococcus pneumoniae Strain R6.
A;Taltie: Genome of the Sacterium Streptococcus pneumoniae Strain R6.
A;Taltie: Genome of the Sacterium Streptococcus pneumoniae Strain R6.
A;Taltie: Genome of the Sacterium Streptococcus pneumoniae Strain R6.
A;Taltie: Genome of the Sacterium Streptococcus pneumoniae Strain R6.
A;Taltie: Genome of the Sacterium Strain R6.
A;Taltie: Genome of the Sacterium Strain R6.
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C;Genetics:
A;Gene: spr0681
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C;Superfamil; myosin heavy chain 95F; myosin motor domain homology
F;120-782/Domain: myosin motor domain homology cMO>
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A; Residues: 1-76 < KUR>
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C,Genetics:
                                                                                      Query Match
Best Local S
Matches 7
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Best Local
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Matches
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les 7, Conserv
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                                                                                      Similarity
7; Conserv
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FKNENSNALISVVECD 449
                                           FRURGMTALLKVSSCD 16
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                                                                                      Conservative
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                                                                                                        48.8%;
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                                                                                                        Score 40;
Pred. No.
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Pred. No. 3.4;
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Pred. No. 31;
                                                                                      Mismatches
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                                                                                                                              Length 536
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                                                                                  Indels
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A87117
                                                         T44703
                                                                           RESULT 13
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B96639
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C;Genetics:
A;Gene: TIP9.16
A;Map position:
Cipopolyser/accharide core biosynthesis protein [imported] - Mycobacterium leprae
Cipopolyser/accharide leprae
Cipate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeggr, K.; Simon, S.; Simmonds, M.;

A;Tille: Massive gene decay in the leprosy bacillus.

A;Reference number: A85909; MUID:21128732; PMID:11234002

A;Accession, A87117

A;Bectus; preliminary
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A; Alathors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Waiti, R.; Marzial, Rizzoo, M.; Rooney, T.; Rowley, D.; Sakamo, H.
A; Althors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallor Kar, M.; Wu, D.; Yu, G.; Fraeer, C.W.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A; Reference number: A66141; MID: 21016719; PMID: 11130712
                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: coaD
C; Superfamily: lipopolysaccharide core biosynthesis protein kdtE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL450380; NID:g13093433; PIDN:CAC30616.1; GSPDB:GN00147
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-157 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.COLe, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; wheeler, P.R.;
R.; Davies, R.M., Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyean, M.A.; Rutherford, K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: A87117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable phosphopantetheine adenylyltransferase [imported] - Mycobacterium leprae
C;Species: Mycobacterium lebrae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references:
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A; Residues: 1-573 <STO>
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: B96639
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                     47.6%;
70.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                            Mismatches
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A, Scatus; preliminary
A, Molecule type: DNA
A, Residus; 1-512 CUUD>
A) Cross-reference: GB1,E008688; PIDN:AMI43336.1; PID:g17740829; GSPDB:GN00186
A) Experimental source: strain CS8 (Dupont)
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein ggul (imported)
Cispecies: Agrobacterium tumefaciens (strain C59, Dupont)
Cispecies: Agrobacterium tumefaciens (classics)
Cipace: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
CiAccession. 182865
R: Nood, D.W.; Setubal, J.C.; Kaal, R.; Noods, D.; Chen, L.; Nood, G.E.; Chen, V., Noocearge, G.; Gillet, W.; Jerant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Noccearge, G.; Gillet, W.; Jerant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Noccearge, G.; Gillet, W.; Jerant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; M.; M.; Noccearge, G.; Gillet, W.; Jerant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; M.; Gordon-Kamm, A; Nathors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A; Nathors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, etc.; S. W.
                                                                                                                                                                                                                                                                          A/Title: The Genome of the Matural Genetic Engineer Agrobacterium tumefaciens CS8
A.Reference number: AB2577, MUID:21608550; PMID:11743193
A/Accession: AB2865
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A;Molecule type: DNA
A;Residues: 1-505 <KUR>
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A./ Title: Genome Sequence of the Flant Pathogen and Biocechnology Agent Agrobacterium tum A. Reference number: A97359, MUID:21608551, PMID:11743194

A./ Recession: A97362
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C,Superfamily: lipopolysaccharide core biosynthesis protein kdtB
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A;Molecule type: DNA
A;Residues: 1-160 cPAR>
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R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EWBL Data Library, May 1998
A;Reference number: Z22830
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A/Experimental source: cosmid B1243
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Title: Perfect score: Scoring table: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-661-992B-106 82 1 FRNRGMTALLKVSSCD 16

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greates than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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- I- RUNCTION: FACTOR VIII, ALONG WITH CALCIUM AND PHOSEMOLIPID, ACTS

AS A COMPACTOR FOR FACTOR IXA WHEN IT COMPERTS EACTOR X TO THE

C -1. SUPCELLULAR L'OCATION: Extracellular.

- I- SUPLIABRIT: CONCLUING 3 FT/6 Type A domains.

- I- SIMILARIT: CONCLUING 3 FT/6 Type A domains.

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01-JUN-1994 (Rel. 29, Last sequence update)
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08-SEP-2018 Rev. 7111 Precursor (Procespilant
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Mammalia; Eutheria; R
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Sus scrofa (Pig).
Eukaryota; Metazoa; (Mammalia; Eutheria; NCBI_TaxID=9823;

Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;

Euteleostomi; Sus.

precursor (Procoagulant component)

SEQUENCE FROM N.A. Healey J.F., Lubin I.M., Lollar P.;

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the European Bioinformatics institute, There are no restrictions on its use by non-profit institutions a long as its context is not the profit institutions along as its context is context in modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial centricies requires a license agreement (See http://www.isb-sib.ch/armounce/or send an email to license@isb-sib.ch).
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PROSITE; PS01286; PASSC_2; 2.
PROSITE; PS0027; PASSC_3; 2.
PROSITE; PS0079; MULTICOPERS OXIDASE; 3.
Blodd cosgulation; Repeat; Plasma; Acute p
Signal; Glycoprotein; Sulfation.
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InterPro; IPR000421; FA58 C.
Pfam; PF00394; Cu-oxidase; 3.
Pfam; PF00754; F5 F8 type C; 2.
SMART; SM00231; FA58C; 2.
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"Elimination of a major inhibitor epitope
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Kaufman R.J.;
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SIMILARITY: Contains 3 F5/8 type A domains.
SIMILARITY: Contains 2 F5/8 type C domains.
SIMILARITY: STRONG, TO COAGULATION FACTOR V.
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FUNCTION: FACTOR VIII, ALONG W
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A25945; }
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nan D.D., Orr E.C.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Shimmin L.C.
Shimmin L.C. (Mouse) Chordata; Rodentia; Last sequence update)
Last annotation update)
precursor (EC 4.2.1.1) Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus PRT; 324 ğ (Carbonate dehydratase

"Characterization and evolution of two new members of the alpha-carbonic ambydrase gene family in mouse: Caril and Caris.", Submitted (FEB-2000) to the EMBI/GenBank/DDBV databases. STRAIN=C57BL/6; T. Hewett-Emmett D.,

TISSUE=Kidney; SEQUENCE FROM N.A.

XX MEDILINE-22386257; PubMed-12477932;

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AN Altschuld S.F., Zeeberg B., Bascow K.H., Schaefer C.F., Blakt N.K.,

AN Hopkins R.F., Jozdam H., Moore T., Max S.I., Wang J., Hsish F.Y.,

AN Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.B.,

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AN Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.B.,

AN Bonals S.S., Loquallano N.A., Pecers G.J., Abramson R.D., Mullahy S.J.,

Bonak S.A., McChann D.J., McKernan K.J., Maleb J.A., Gunzarne P.H.,

AN Bonak S.M., McChann D.J., McKernan K.J., Maleb J.A., Gunzarne P.H.,

B. Pabaylon D.M. McChann D.J., Schercher B.J., Lux Y., Glaber R.J.,

AN Whitling M., Medan A., Wond A.A., Wohler B.M., Mohre S., Sannbez A.,

Mitting M., Medan A., Wond A., Wond A., Sherchenko Y., Bouffard G.G.,

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39-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Leated)
30-MAY-2000 (Rel. 39, Leated)
10-SEP-2003 (Rel. 42, Leat amontation update)
11-SEP-2003 (Rel. 47, Leated)
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NEDITINE-3128713; PubMeda1124002;
Cole S. T. Bisjaneker K. Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Beslam D., Brown D., Krillingworth T., Commor R.,
Mungall K., Beslam D., Brown D., Chillingworth T., Commor R.,
Davies R.M., Devlin K., Duchoy S., Feitvell T., Fraser A., Hamlin N.,
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RMBL, BC019975, ANH19975.1;

HSSP, G614444; Z2NC.

MXD; WGI.1931124; Garl5.

Comhd.

Ffam, PF00134; carb anhydrase; 1.

Fracbom; PF00134; anb, Gonnhd.

FROSITE; P800154; BC, COanhd.

FROSITE; P800154; BC, COanhd.
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or send an email to licensesisb-sib.ch).
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The Buropean Bioinformatics Institute. There are no restrictions on its use by non-positif institutions as long as its content is in no way use by non-positif institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.idb-sbi.ch/aumounce/entities requires a license agreement (see http://www.idb-sbi.ch/aumounce/entities requires a license agreement.
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Proc. Natl. Acad. Sci. U. S.A. 99:16899-16903 (2002).
1- FUNCTION: Reversible hydration of carbon dioxide
1- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
1- COPACTON: Zinc (By Similarily).
1- SUBCELULLA LOCATION: Secreted (Focential).
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                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     Corynebacterineae;
                                                                                                                                                                                                                                                             Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Rodriguez A.C., Getimwood J., Schmitz J., Wyers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skaliska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marza M.S.,
Generation and initial analysis of more than 15,000 full-length
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2; Mismatches
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ZINC (CATALYTIC) (BY SIMILARITY).
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Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales; Acidithiobacillaceae; Acidithiobacillus.

STRAIN=ATCC 33020; MEDLINE-95047244; PubMed=7958772; Brown L.D., Denneby M.E., Rawling "The P1 genes of the F1F0 ATP syn Thiobacillus ferrooxidans complem

Rawlings D.B.; ATP synthase f

Microbiol.

Lett.

122:19-26(1994)

complement Escherichia coli F1 unc

from the acidophilic bacterium

SEQUENCE FROM N.A. NCBI_TaxID=920; 01-FEB-1995 01-FEB-1995 28-FEB-2003

(Rel

. 31, Created)
. 31, Last sequence upo
. 41, Last annotation u
ha chain (EC 3.6.3.14).

update) 514 AA update)

ATPA_THIFE P41167;

STANDARD;

PRT;

ATP synthase

alpha

Thiobacillus ferrooxidans.

뭉 S

78 N

RSRGMTAIVK

87

Matches Best Query Match

Local

Similarity RNRGMTALLK 11

47.6%;

Score 39; DB Pred. No. 3.4;

DB 1; 0; Length 160

Mismatches

Indels

0

Gaps

0;

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Conservative

SEQUENCE

proteome.

160 AA;

17496 MW; 1F762492F3C0676C CRC64

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This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outeration the EMPOPAN ENGLA THE THREE AT THE THE THE THREE AT EACH THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THE THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THREE AT THR
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                                                                                 REMITS, PRO1020, LEGBOONTHSS.
TIGRPAMS; TIGR01510; coad_prev_kdtB; 1.
TIGRPAMS; TIGR010125; cyt_tran_rel; 1.
Transferase; Mucleotidyltransferase; Coenzyme A biosynthesis;
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PIR; T44703; T44703.
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-- PATHHAY: Comrayme A (CoA) biosynthesis; fourth std.
-- SIRDITT: Homobecamer (By similarity).
-- SIRDITLAIN LOCATION: Ofroplasms (By similarity).
-- SIMILARITY: Belongs to the bacterial coad family.
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TIGRENMS; TIGROSOS; ATPASS ALEMA, BETA; 1.
PROSTTE; PS00152; ATPASS ALEMA, BETA; 1.
APP synthesis; Cf(1); APP binding; Hydrolase;
Hydrogen ion transport.
MP BIND 170 177:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib-ch/announce/
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last nnotation updat)
16-0CT-2001 (Rel. 40, Last nnotation updat)
Peroxisome assembly factor-1 (PAF-1) (Perox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro IPR000793; ATPase a/bC.
InterPro IPR000194; ATPase a/bC.
InterPro IPR000194; ATPase a/bN.
InterPro IPR000790; ATPase a/bN.
InterPro IPR000790; ATPase a/bN.
InterPro IPR005294; ATPaynThF1_alpha.
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SEQUENCE FROM N.A.
MEDLINE=94309666; PubMed=8035823;
Tsukamoto T., Shimozawa N., Fujik
                                                                                                          Thieringer R., Raetz C.R.H.;
"Peroxisome-deficient Chinese hamster ovary cells with
mutations in peroxisome assembly factor-1.";
J. Biol. Chem. 268:12631-12636(1993).
                                                                                                                                                                                                                                                                                                                                                                                                  Cricetulus griseus (Chinese hamster)
Bukaryota; Metazoa; Chordata; Crania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q06438;
01-JUN-1994
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Pfam; PF00306; ATP-synt_ab_C; 1.
Pfam; PF02874; ATP-synt_ab_N; 1.
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                                                                                                                                                                                                                MEDLINE=93286102; PubMed=7685346
                                                                                                                                                                                                                                             TISSUE=Ovary;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                       Cricetulus.
                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PXMP3 OR PEX2 OR PAF1 OR PMP35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT:
CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) = ADP + phosphate +
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    Shimozawa N., Fujiki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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BY SIMILARITY.
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Sciurognathi; Muridae; Cricetinae;
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8349B6BC651BCB6B CRC64;
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(Peroxin-2) (Peroxisomal membrane
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RESULT 8

TRYGRAN STANDARD; PRT; 419 AA.

PRADE OF CONTROL OF CON

inwardly

Kir5.1

(BIR9).

CNJ16

Rattus norvegicus (Rat).

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.

CCCRTT ARP RELEASE

STRAIN=Sprague-Dawley; MEDLINE=95179470; PubMe NCBI_TaxID=10116; Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

rley; TISSUE=Brain; PubMed=7874445;

SEQUENCE FROM N.A.

Adelman J.P Bond

Pessia

3

Xia X.-M., Lagrutta

inward rectifier potassium

A., Kavanaugh M.P.,

"Cloning and expression of a family of channels.";

Channels 2:183-191(1994)

Tucker S.J., Imbrici P., Salvatore L., D'Adamo M.C., "pH dependence of the inwardly rectifying pocassium and localization in renal tubular epithelia.";
J. Biol. Chem. 275:16404-16407(2000)

MEDLINE=20287495; PubMed=10764726;

SEQUENCE FROM N.A. recept. channers

-!- FUNCTION: INWARD RECTIFIER K+

CHANNELS ARE CHARACTERIZED BY

channel, Pessia M.;

Kir5.1,

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123

FRNRHLASFGKVKQC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Pegroxisoma assembly factor 1: nongenee mutation in a peroxisome deficient Chinese hameter ovary cell mutant and deletion analysis. Nol. Cell. Biol. 14:5458-5465(1994).
HOLICIBIN SOMEHHAY INCLOATED IN THE BIOGENESIS OF PEROXISOMES -1- FUNCTION: SOMEHHAY INCLOATED IN THE BIOGENESIS OF PEROXISOMES -1- SUBCELULLAR DIOCATION: Integral membrane protein. Peroxisomal. -1- SUBCELULLAR DIOCATION: Integral membrane protein.
                                                                                                                                                                                      SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
Transmembrane; Peroxisome; Zinc
                                                                                                                                                                                                                                                       InterPro; IPR001841; Znf ring.
Pfam; PF04757; Pex2 Pex12; 1.
Pfam; PF00097; zf-C3HC4; 1.
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InterPro; IPR001841; Znf_ring.
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PIR; A45989; A45989.
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1 FRNRGMTALLKVSSC
                                                   Similarity
                                                                                                    304 AA;
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                                                Score 37;
Pred. No.
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C->Y: LOSS OF FUNCTION.
; 84EC5FA613C148BF CRC64;
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BY SIMILARITY.
                                   Mismatches
                                                                   DB 1; Length 304;
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SUBMAXILLARY GLAND, SIMILARITY: BELONGS FAMILY.
                                                                                                                                SUBUNITY SEEMS TO FORM HETERODIMER WITH KIR4.1/KCNJ10 KIR2.1/KCNJ2.
SUDCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: IN THE BRAIN, TESTIS, LIVER, SPLEE
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TO THE INWARD RECTIFIER-TYPE K+ CHANNEL
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InterPro; IPR001838; K+channel_IR.
InterPro; IPR001822; K+channel_pore
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371
                                                                                                                                                                    channel; Ion transport;
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7; Conserv
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RRRSPSAVAMVSSCE 385
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                               Score 37; DB
Pred. No. 24;
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                                                                                                                      CYTOPLASMIC (POTENTIAL)
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M1 (POTENTIAL).
H5 (PORE-FORMING) (POTENTIAL).
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P20736;
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Glycoprotein antigen BM66 precursor (Protective
Boophilus microplus (Cattle tick).
Bukaryora; Metazoa, Arthropoda; Chelicerata, Ara
Barastt.formes; Ixodida, Ixodidae; Boophilus.
        MEDLINE=90099323;
Rand K.N., Moore T
Willadsen P., Cobc
                                                                                                                                                                 TISSUE=Gut
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(Rel. 17, Last sequence up
(Rel. 35, Last annotation
                        Cobon G.S.;
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Milladeen P., Riding G.A., McKenna R.V., Kempl Mielsen J.W., Lahnsein J., Cobon G.S., Gough Timmunologic control of a parasitic arthropod. protective artiger from Boophilus microplus. J. J. Immunol. 143:1246-125. (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and expression of
Boophilus microplus.";
Proc. Natl. Acad. Sci. U.S.
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SIGNAL
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PROSITE; PS01186; EGF_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00181; EGF;
PROSITE; PS00022; EG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00008; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A34498; A34498.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=2745982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; EGF-like domain; Repeat; GPI-anchor.
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01-MAR-1989 (Rel. 10, Last sequence update)
028-FEB-2003 (Rel. 41, Last annotation update)
SHIGA-1ike toxin II subunit B precursor (Verotoxin
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EMBL; Y10775; CAA7148.1; -.
ETR; S01033; S01033.
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Jackson M.P., Weill R.J., O'Brien A.D., Holmes R.K., Newland J.W.; 
"Nucleotide sequence analysis and comparison of the structural genes 
for Shiga-like toxin I and Shiga-like toxin II encoded by 
bacteriophages from Escherichia col. 93.";
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Lambda-like viruses
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Pred. No.
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SHIGA-LIKE TOXIN II SUBUNIT
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                                                                                                                                            the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions a long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensessb-sib.ch).
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P38337;
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Hypothetical protein SEQUENCE 142 AA; :
                                                           06); GO:0118024; F:histone-Lysine N-methyltransferase activity; IDA
06); GO:016551; P:histone methylation; IDA
Pfam; PF05205; Cpsi5; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete sequence of a 19,482 bp segment located arm of chromosome II from Saccharomyces cerevisiae.", Yeast 9,189-199(1993).
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Bukaryota; Fungi; Ascomycota; Saccharocotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Bukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicoty; ecore eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.

SEQUENCE FROM N.A. NCBI_TaxID=3702;

REPRESENTATION OF THE PROPERTY Nakamura Y., STRAIN-CV MEDLINE=98162728; Columbia; 2728; PubMed=9501997; Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,

Tabata S.,

"Structural analysis of Arabidopsis Sequence features of the regions of physically assigned Pl clones."; thaliana chromosome 5. 1,191,918 bp covered b covered by seventeen

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REALITE 13

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InterPro, IF8007227; Rtbosomal 319,
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InterPro, IF8007271; S15_enk arch.
Pfam, Pf00013, Rtbosomal 319, 1
PRINTS, P800175, RIBOSOMALS19,
ProDom, P8001012, Rtbosomal 319, 1
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073943; Q9YAM2;
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30-MAY-2000 (Rel
                           MEDILNE-9910399, PubMed-1032966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takhinashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Mishijiana K., Makaawa H.,
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Nomura N., Sako Y., Uchida A.;
Nomera N., Sako Y., Uchida A.;
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-1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS
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Plant Physiol. 127:398-415(2001)
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Barakat A. Szick-Miranda K., Chang I.-F., Guyot R., Blanc G.,
COoke R., Delseny M., Balley-Serres J.;
The organization of cytoplasmic ribosomal protein genes in the
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Score 36; DB Pred. No. 17; 3; Mismatches

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P47087;
01-FEB-1996
                                                                                     EMBL; X87611; ChA60934.1; -.
EMBL; Z49512; ChA89536.1; -.
PIR; S55200; S55200;
SGD; S0003773; YUR012C.
Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                              This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ZMIS outstation - the Burpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in own modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an enail to license@ib-sib.ch/).
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01-FEB-1996 (Rel. 33) . Last sequence update)
01-CTT-1996 (Rel. 34) . Last amnotation update)
Hypothetical 23.2 kDa procein in SPCI-IDV3 in
VR0101C OR J1440 OR URB3.25.
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DNA Res. 6.63-101(1999)
-i- FUNCTION: ENDONUCLEASE INVOLVED IN RRNA INTRON I-GAMMA HOMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Haan M., Smits P.H.M., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
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Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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EMBL; AP000062; BAA80926.1; -.
PIR, A72560; A72580.
InterPro; IPR001982; Endonuc_LAG/HNH.
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Yamazaki J., Kushilda N., Sako Y., Kikuchi H.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
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Pred. No. 14;
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52D500B57FBC75CB CRC64;
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SWART, SMOOIS; RHOD, 1.
SWART, SMOOIS; RHOD, 1.
PROSITE; PSSOOG; RHOD, 1.
PROSITE; PSSOOG; TYR PHOSPHATASE 1; 1.
PROSITE; PSSOOG; TYR PHOSPHATASE DUAL; 1.
PROSITE; PSSOOG; TYR PHOSPHATASE DUAL; 1.
                                                                                                                                                                                                                                         EMBL, ARL67296, AAD46556.1;
HSSP, QL6281 SHXP.
InterPro, 1FR000340, DS, phosphatase.
InterPro, 1FR000340, Bb, danase-like.
InterPro, 1FR000387, TYR, phosphatase.
Ptam, PF00782; DSP, TYR, phosphatase.
£am, PF00782; DSP, E
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-1- FINGTION: BEGULATES MITOCENIC SIGNAL TRANSDUCTION BY

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BRIL AND ENGZ (BY SIMILARITY)
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MEDLINE=20379359; PubMed=10918612;
Eu.S.-L., Waha A., Vogt P.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Bukaryota; Metazoa; Chorddta; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is-OCT-2001 (Rel. 40, Created)
15-OCT-2001 (Rel. 40, Last sequence update)
16-EBS-2003 (Rel. 41, Last annotation update)
Dual specificity protein phosphatase 4 (EC 3.1.3.48) (EC 3.1.3.16)
(Micogen-activated protein kinase phosphatase-2) (MAP kinase
phosphatase-2) (MC-2).

    phosphate.
    SINCLARITY. BELONGS TO THE NON-ESCEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATRASE FAMILY. DULL SEGCIFICITY SUBFAMILY.
    SIMILARITY: CONCALIS 1 THOOSINES COMMAIN.

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Q9PW71;
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DOMAIN
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                                                                               Nuclear protein.
25 143
178 375
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178
361
375 AA;
     Conservative
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                                                                  41052 MW;
43.9%; Score 36; DB 1; Length 375;
80.0%; Pred. No. 33;
tive 1; Mismatches 1; Indels
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                                                                            RHODANESE.
PROTEIN-TYROSINE PHOSPHATASE.
BY SIMILARITY.
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                                                                  179290D0C2BEEEF1 CRC64;
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202 GITALLNVSS 211
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Search completed: November 7, 2003, 07:28:11 Job time : 3.15354 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                            Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                          SPTREMBL 23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
                                                                                           830525 seqs, 258052604 residues
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Gapop 10.0 , Gapext 0.5
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82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                            sp_mhc:*
sp_organelle:*
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                                                                                      sp_plant:*
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sp_vertebrate:*
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47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	48.8	48.8		48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	49.4	49.4	49.4	49.4	50.0	50.0	50.0	50.0	50.0
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1 FRUNGWITALLAVSSCD 16 - - - - - - - - - - - -	Onery Match 93.9%; Score 77; DB 6; Length 2343; Best Local Similarity 93.6%; Pred. No. 8e-05; Indels 0; Gaps 0; Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	PS00079; 2343 A	PROSITE; PS01285; PA58C 1: 2. PROSITE; PS01285; PA58C 1: 2. PROSITE; PS01286; PA58C 2: 2.	Pfam: PP00754; FS Type C; 2.	InterPro; IPR000421; FA58 C.	HSSP; P00451; 1CFG. InterPro; IPR001117; Cu-oxidase.	EMBL; AF049489; AAC05384.1; .		"Characterization of the canine factor VIII cDNA.";	TISSUE=Kidney, and Spleen;	SEQUENCE FROM N.A.		Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		•		1998	O62730 PRELIMINARY; PRT; 2343 AA.	0 1

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RESULT
Q9I2N7
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Best Local S
Matches 15
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InterPro, 1P800117, Oscardase.
Fram, PR00759; On-oxidase.
PR00759; On-oxidase.
PR00759; PS507 72.
PS50772; PS001259; PS507 72.
PR05172; PS01255; PS5807 72.
PR05172; PS01255; PS5807 72.
PR05173; PS01255; PS5807 72.
PR05174; PS01255; PS5807 72.
PR05175; PS01255; PS5807 72.
PR05175; PS01255; PS5807 72.
PR05175; PS01255; PS5807 72.
                                                             STPAINS-CC 15632 / PAOL 1

MEDLINE-204737]; Pubbed-10984043;
MEDLINE-204737]; Pubbed-10984043;
MEDLINE-204737]; Pubbed-10984043;
MECOVER C.K., Pham X.-Q.T., Exvin A.L., Mizoguchi S.D., Warrener P.,
Mickey M.J., Strimman F.S., L., Huffngle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolantino E., Westbrook-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larthig K., Lim R. M.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.,
Complete genome sequence of Pseudomonas aeruginosa PAOI, an
Opportunistic pathogen. 1

Debute 406:1953-584(2001)

Debute 406:1953-584(2001)
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Q912N7;
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01-MAR-2001 (TERMELTE1. 16, Last sequence update)
01-MAR-2003 (TERMELTE1. 23, Last annotation update)
Streptomyoin_3'.-phosphotransferase.
            InterPro; IPR006748; APH 6 hur.
Pfam; PF04655; APH 6 hur; 1.
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Submitted (NOV-1997) to the REML/CHARINK/DEM databases.
-- SIMILARITY: COMPAINS 2 F5/8 TYPE C DOMAINS.
BMB1, AF016234; AABSF412.1;
BSSP, PO0451; ICE.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Giles A., Lillicrap D.
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Mammalia, Eutheria;
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Canis familiaris (Dog).
Canis familiaris (Dog).
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1; Mismatches
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If OsMAPKS, in Tice;

If Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, PAY-1984, ALL-799-1,

R HSSP, PAY-11, ISUH.

R Grammen; QBSTF6;

R InterPro. | TROUOVIJ-9 | Prot. kinase.

R Pfam, PF00051; Phinase; 1.

R Pfam, PF00051; Phinase; 1.

R Pfam, PF00051; PROTEIN MINNS AMP; 1.

R PFAM, PF00051; PROTEIN MINNS AMP; 1.

R PGSTTS; BS0011; BROTEN MINNS AMP; 1.

R PGSTTS; BS0012; ROSEN CALL-FREE CHESCON; 1.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                               Q8NGL0;
   receptor genes.", receptor genes.", to the EMBL/GenBank/DDBJ databases SMBL; ABG65782; BAC06105.1; .
InterFor, IER00276; GECR_Rhodpsn.
                                                                                                        SEQUENCE FROM N.A. SELOT., Okouchi I., Arita Suwa M., Sato T., Okouchi I., Asai K., Tsutsumi S., Aburatani H., Asai K., "Genome-wide discovery and analysis
                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Last se
01-MAR-2003 (TrEMBLrel. 23, Last an
Seven transmembrane helix receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elwaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta; Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEME
MAP kinase MAPKSb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8S3T6;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xiong L., Qi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAPKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8S3T6
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53.3%;
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22, Last sequence update)
23, Last annotation update)
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Pred. No. 5.7;
                                                                                                                                                                                                                                                 Catarrhini;
                                                                                                                                                                                                                                                                      Craniata;
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                                                                                                        M., Futami
, Akiyama Y.;
of human se
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                                                                                                                                                                                                                                                 Hominidae; Homo.
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Q8VGA8
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Best Local
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Q54372;
MEDILINE—50020646; PhiMeds=857742,
Paschke U., Schmidt H., Chang H.Z., Piepersberg W.;
"Molecular characterization of the lincomycin-production gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                          NCBI TaxID=1915;
                                                                                                                                                                                                                                                                                                                     Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                    Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces lincolnensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LmbR protein.
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                                                                                                                                                          STRAIN=78-11;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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PROSITE;
PROSITE;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olfactory receptor MOR174-1.
Mus musculus (Mouse).
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01-MAR-2002 (TrEMBLrel. 20, 
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor;
SEQUENCE
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Similarity 75.0%;
9; Conservative
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PS00237; G PROTEIN_RECEP_F1_1; 1.

PS50262; G PROTEIN_RECEP_F1_2; 1.

r; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRGMTALLKVSS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLGMTALIQVSS 53
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                                                                                                                                                                                                                                                                                                                                                       Actinobacteria; Actinobacteridae; Actinomycetales;
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(TrEMBLrel.
(TrEMBLrel.
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75.0%;
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9AA8CD0E70E0A274 CRC64;
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annotation update)
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10;
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Q933W2
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STRAIN=81-176;

SEQUENCE FROM N.A. NCBI_TaxID=197;

NEDA1.
Campylobacter jejuni.
Bacteria, Proteobacteria, Epsilong
Bacteria, Campylobacter.

Epsilonproteobacteria; Campylobacterales;

CMP-NeuNAc synthetase (CMP-NeuSAc

Last sequence update)
Last annotation update)
NeuSAc synthetase).

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Created)

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Guarry P., Szymanski C.M., Prendergast M.M., Hickey T.E., Bwing C.P. Petertrii D.I., Woran A.P. "Phase Variation of Campylobacter jejuni 81-176 Lipooligosaccharide Affects Virulence.";

Hickey T.B., Ewing C.P.,

Q933W2 Q933W2; Q1-DEC-2001 01-DEC-2001 01-WAR-2003

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Q93MP7
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Q1-DEC-2001
01-DEC-2001
01-MAR-2003
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InterPro; IPR053229; CSylidylyl trans.
Pfam; PF02348; CTP transf. 3; 1-
SEQUENCE 221 AA; 24915 MW; CC7F77
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Mol. Mcrobiol. 15-1137-115-(1995).
BBHL, Y79146, CAASTGS. 11.-1.
InterPro. 1P800185, Transidolase.
PEam, PRO0223 Transidolase.
PEAM, PRO0223 Transidolase.
PEOSITE, P801054; TRANSILIONES 1; 1.
SEQUENCE 200 AA; 2349 MM; 59159145A16A4EF7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campylobacteraceae; Campylobacter NCBI_TaxID=197;
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Bacteria; Proteobacteria;
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YKNSNANALISVSECD 133
                                                PRINTALLKYSSCD 16
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1 (TrambLrel. 19,
3 (TrambLrel. 23,
                                                                                                    Conservative
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                                                                                                                    51.2%;
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Last annotation update)
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                                                                                                                                                Score 42,
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Pred. No.
                                                                                                                            Pred. No. 11;
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                                                                                                                                                                                                    CC7F77F601A28684 CRC64
                                                                                                Mismatches
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                                                                                                                                                Length 221;
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RESULT 11
Q9FOM6
ID Q9FOM
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Cunningham A.-M., Wu Y., Young N M., McKarchuk W W.,
"Blosynthesis of ganglioside manics in Campylobacter jejuni Odlaja4,
identification of the jlycosyltransferase genes, enzymatic synthesis
of model compounds, and Characterization of nanomole amounts by 600-
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J. Biol., Chem. 275:3896-3906 (2000).
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OSSN23,
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O1-UUN-2001 (TYENGLICE). 17, C:
O1-UUN-2001 (TYENGLICE). 17, L:
O1-UUN-2002 (TYENGLICE). 21, L:
Carbonic anhydrase XV (EC 4.2
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Q938X3;
01-DEC-2001
                                                                                                      CAR15.
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Submitted (DML-2001) to the BMS/GenBank/DDBJ databases.
BMBL, AVG4688; AMX8604.1; -3.
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Pfam; PF02348; CTP_transf_3; 1.
SEQUENCE 221 AA; 25014 MW; FC3A3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gilbert M., Michniewicz J., Wakarchuk W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC
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NCBI_TaxID=197;
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STRAIN=ATCC 43432;
Gilbert M., Michniewicz J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Campylobacteraceae; Campylobacter.
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of Campylobacter
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Sukaryota, Metazoa, Chordata, Craniatu, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus MCBI TaxID=10090,

Mus musculus (Mouse)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9KYI4;
                                                                                                                                                                                                                                                                                                                    Kinashi H., Hopwood D.A., Kinashi H., Hopwood D.A., Bet of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces consiloziox A3(2) Chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
Bentley S.D., Parkhill J.,
Submitted (WAY-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riboflavin-specific deaminase.
RIBD OR SCO2688 OR SCC61A.09.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenbach M., Kieser H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oliver K., Harris D.;
Submitted (MAY-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
Bacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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InterPro; IPRO01148; Eby Coanhd.
Pfam; PF00194; carb anhydrase; 1.
ProDom; PD000865; Ebk_Coanhd; 1.
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Submitted (DEC-2001) to the
EMBL; AF231122; AAK16671.1;
EMBL; BC019975; AAH19975.1;
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carbonic anhydrase gens family in mouse: CB13 and CB15.";
Submitted (PEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL; TISSUE=Kldney;
Hewett-Emmett D., Shimmin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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e EMBL/GenBank/DDBJ databases.
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Pred. No.
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red. No. 25;
Mismatches
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STRAINEYS-314 AN 12310 / DSN 44549 / JCN 11189;
KRAWATERDAYSES Y., Yamazaki J., Hino Y., Kikuchi H., Makamura Y.,
Iraco K., Suruki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Isuda Y., Suginco S.;
Irac Hiller General Corymebacterium efficiens YS-314.";
Irac Manitted (MAY-2001) to the EMBL/Gensank/DDBJ databases.
MMLJ, AROUSZIS; BAC18374.1;
Complete Proteome.
SEQUENCE S37 AA; 57162 MM; 1B1067CF463ADBF2 CRC64;
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Q8FTK2;
Q1-MAR-2003
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Pfam: PR01872; RibD c; 1.
TIGREPAMS; TIGR00326; eubact zibD; 1.
TIGREPAMS; TIGR00227; ribD CTerm; 1.
PROSITE; P800903; CYT_DCMF_DEAMINASSS;
                                                                                                                                                                                                                           NCBI_TaxID=152794,
                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacter
Corynebacterineae; Corynebacteriaceae;
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InterPro; IPR002125; dCMP/cyt des
IntexPro; IPR004794; Eubact ribb.
InterPro; IPR002734; Ribb_C.
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"Complete genome sequence of the model actinomycets Streptomyces ocelicolor M(2),",

Nature 417:141-147(2002).

ERBL, AL359:113; CAB9224-1; -.
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                                                           Local Similarity
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                                              Conservative
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153
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                                            Score 41; DB
Pred. No. 43;
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SUMMARIES

Result No.	נע	N	ω	4.	u	6	7	00	9	10	11	12	13	14	15
Score	82	82	82	82	82	82	82	82	82	82	77	76	76	70	70
Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	93.9	92.7	92.7	85.4	85.4
Length	1438	1438	1438	1471	2332	2332	2332	2351	2351	2351	1431	2319	2319	368	368
DB	14	14	15	14	10	12	15	12	15	15	14	12	15	12	15
ID	US-10-006-091-1	US-10-047-257-1	US-10-225-900-1	US-10-095-718-2	US-09-957-641-2	US-10-131-510A-2	US-10-187-319-2	US-10-133-907-4	US-10-132-829-4	US-10-172-712-27	US-10-095-718-4	US-10-131-510A-6	US-10-187-319-6	US-10-131-510A-4	US-10-187-319-4
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	GENERAL	Sequence	Seguence
ı	1, Appli	1, Appli	1, Appli	2, Appli	2, Appli	2, Appli	2, Appli	4, Appli	4, Appli	27, Appl	4, Appli	6, Appli	' INFORMA	4, Appli	4, Appli

RESULT 2
US-10-047-257-1
US-10-047-257-1
; Bequence 1, Application US/10047257
; Publication No. US20020115152A1
; GENERAL INFORMATION:

45	44	43	42	41	40	39	38	37	36	35	34	33	32	32	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	42	42	42	42	42	42	43	43	70	70	70	70
49.4	49.4	49.4	49.4	49.4		49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4		51.2					52.4	52.4	85.4	85.4	85.4	85.4
1160	1160	1160	1160	1160	1160	1160	1160	1160	1160	1160	1160	1160	1160	1160	1160	1160	1160	221	221	221	221	221	221	311	311	2133	2133	1443	1443
12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	φ	15	z	15	12	15	12
145	US-10-144-994-234	-10-143-032	-10-142	-10-142-435	-10-142-	US-10-141-704-234	US-10-141-702-234		US-10-140-926-234	US-10-140-924-234	US-10-140-922-234	US-10-140-807-234	US-10-140-471-234	-10-	US-10-140-021-234	US-10-140-018-234		-10-303-162-	US-10-303-134-37	US-10-303-128-37	US-10-303-118-37	US-10-303-161-37	US-09-816-028A-37	US-10-023-597-52	US-10-017-161-284	US-10-187-319-37	US-10-131-510A-37	-10-	US-10-131-510A-39
	æ	Sequence 234	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	37	37	37	37	7	37,	N	28	37	37	39	Sequence 39,
, Apr	, App	, App	, App	, App	, App	, App	, App	, App	, App	, App	, App	, App	, App	, App	, App	, App	, App	App1	, Appl	Appl	Appl	Appl	App1	App1	, App	Appl	Appl	Appl	Appl

ALIGNMENTS

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US-10-006-091-1
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US-10-006-091-1
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL IMPOSMATION:
APPLICANT: Chan, Sham-Yuan
APPLICANT: Chan, Sham-Yuan
APPLICANT: Chan, Sham-Yuan
APPLICANT: Yee, Helana
APPLICANT: Yee, Helana
TITLE OF INVENTION: Expression System for Factor VIII
FILS REFERENCE: MSB-7255.1
CURENT APPLICATION NOWES: 200.-12-06
UNRENT PELING DATE: 200.-12-06
ANDMERG OF SEQ 11, 1063: 2
ANDMERG OF SEQ 11, 1063: 2
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1438
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10006091
Publication No. US20020102730A1
                                                                                                00.0%; Score 82; DB 14; Length 1438; Best Local Similarity 100.0%; Pred. No. 4.8e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
PENTURE:
WIFFERMATION: Description of Artificial Sequence: Derived from
OTHER INFORMATION: bussen factor VIII sequence
697 FRNRGMTALLKVSSCD 712
                                                  1 FRNRGMTALLKVSSCD 16
                                                                                                0,
                                                                                                Gaps
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GENERAL INFORMATION:
APPLICANT: Walsh, Christophe
APPLICANT: Chao, Hengjun
APPLICANT: Burstein, Haim
APPLICANT: Lynch, Carmel
APPLICANT: Stepan, Tony
                                                                                                                                                   RESULT 4
US-10-095-718-2
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                                                                                                               Sequence 2, Application US/10095718
Publication No. US20020131956A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10225900 Publication No. US20030077752A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/225,900 CURRENT FILING DATE: 2002-08-22 PRIOR APPLICATION NUMBER: US/09/209,916 PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cho. Myung-Sam
APPLICANT: Chan. Sham-Yean
APPLICANT: Kelesy, William
APPLICANT: Kelesy, William
APPLICANT: Kep. Helana
TITUS OF INVENTION: Expression System for Factor VIII
FILE REFERENCE: MSB-7215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/047,257
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yee, Helena
TITLE OF INVENTION: Expression System for Factor VIII
FILE REFERENCE: MSB-7255.2
FILE REFERENCE: MSB-7255.2
                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: human factor VIII sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kelsey, William APPLICANT: Yee, Helena
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: human factor VIII sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 1438
                                                                                                                                                                                                                               697 FRNRGMTALLKVSSCD 712
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                                                                                                                                                                                                                                                                      1 FRNRGMTALLKVSSCD 16
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Chan, Sham-Yuen
                                                                                                                                                                                                                                                                                                              Conservative
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                                                                           Christopher
                                                                                                                                                                                                                                                                                                                          100.0%; Score 82; DB 15;
100.0%; Pred. No. 4.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 82; DB 14; 100.0%; Pred. No. 4.8e-06;
                                                                                                                                                                                                                                                                                                       0,
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                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                            Length 1438;
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US-09-957-641-2
                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Homo sapiens BDD FVIII US-10-095-718-2
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Musen, Keith
TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CINERER FAPELICATION NUMBER: US/10/095,718
CINERER FILLOR DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/689,40
PRIOR APPLICATION NUMBER: 09/689,40
PRIOR MINISTER: 09/689,40
PRIOR MINISTER: 09/10-08-22
PRIOR MATER: 0901-08-22
NUMBER OFFENDATE: 0901-01-12
NUMBER OFFENDATE: 0901-01-12
NUMBER OFFENDATE: 0901-01-12
SEQ ID NO 2 SEGEQ for Windows Version 4.0
Sequence 2, Application US/09957641
Publication No. US20020182670A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Homo sapiens B-domain deleted factor VIII
                                                                                                                                                          1 FRNRGMTALLKVSSCD 16
|||||||||||||
716 FRNRGMTALLKVSSCD 731
                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                    100.0%; Score 82;
100.0%; Pred. No.
                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                    4.96-06;
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                                                                                                                                                                                                                                                                                     Length 1471;
                                                                                                                                                                                                                                              Indels
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-641-2
                                                                                                      NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/957,641
CURRENT FILING DATE: 2001-09-16
PATOR APPLICATION NUMBER: US 60/234047
PATOR FILING DATE: 2000-09-19
PATOR FILING DATE: 2000-09-19
PATOR APPLICATION NUMBER: US 60/236460
PATOR FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                          APPLICANT: Emory University
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: 75-00
                                                                              LENGTH: 2332
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Sequence 3. Application US/1013510A
PEDLICANT: NO. US2003016636A1
GENERAL IMPORMATION:
APPLICANT: LOLIAR, JOHS
APPLICANT: LOLIAR, JOHS
FILE REPERANCE: 75-55
FILE REPERANCE: 75-55
CURRENT APPLICATION NUMBER: US/10/131,510A
CURRENT APPLICATION NUMBER: US. 09/315,779
PERIOR MEDLICATION NUMBER: US. 09/315,779
PERIOR PLICAN DATE: 1999-05-20
                                                                                                                                                                                                                                     RESULT 6
US-10-131-510A-2
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                         1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 82; DB 10; illarity 100.0%; Pred. No. 8.2e-06; Conservative 0; Mismatches 0;
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Length 2332;

0;

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RESULT 7
US-10-187-319-2
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PRIOR FILLING BATE: 1399-06-26
PRIOR PELLING BATE: 1399-06-26
PRIOR PELLING BATE: 1394-11-15
PRIOR PELLING BATE: 1394-01-11
PRIOR REPLICATION NUMBER: U.S. 08/212,133
PRIOR RELING BATE: 1394-01-11
PRIOR REPLICATION NUMBER: U.S. 07/864,004
PRIOR REPLING BATE: 1392-04-07
NUMBER: 0F 280 ID NOS: 40-07
NUMBER: 0F 280 ID NOS: 40-07
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Publication No. US20030068785A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
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PRIOR APPLICATION NUMBER: U.S. 08/670,707
PRIOR FILING DATE: 1996-06-26
                                                                                                                                                                                                  TELEFAX: 303/499-8089 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Lollar, John S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
ANNE: Greenlee, Lorance L.
REGISTRATION NUMBER: 27,894
REFERENCE/DOCKET NUMBER: 75-95K
TELEPHONE: 303/499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION UNMER: US/10/187,319
PILING DATE: 27-Aug-2002
CLASSIFICATION: <UNICOMN-
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIF: 80303
COMPUTER READABLE FORM:
WEDLIM TYPE: F199y disk
OVENTURE: 1189 FC compatible
OVERATING SYSTEM: EC-D59/WS-D09
OVERATING SYSTEM: EC-D59/WS-D09
OVERATING SYSTEM: EC-D59/WS-D09
OVERATING SYSTEM: EC-D59/WS-D09
OVERATING SYSTEM: EC-D59/WS-D09
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ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Hybrid Human/Animal Factor VIII NUMBER OF SEQUENCES: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/523,656
FILLING DATE: 2000-03-10
APPLICATION NUMBER: US 09/037,601
FILLING DATE: 1998-03-0
APPLICATION NUMBER: WO PCT/US97/11155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boulder
STATE: Colorado
                                        LENGTH: 2332 amino acid
TYPE: amino acid
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APPLICATION NUMBER: US 08/670,707
FILING DATE: 1996-06-26
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STRANDEDNESS: single
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US-10-132-829-4
                                                                                                                                                                  CONSEAL INFORMATION:

APPLICANT: Gita; Kammath R.

APPLICANT: Hochijima, Masahiko
TITLE OF INVERTION: which do treat hemophilia by hepatic gene transfer of Factor \
TITLE OF INVERTION: which wested a vector
File REFERENCE : 6627-8112.05/10/132.829
COMMANT APPLICATION NOMER: US/10/132.829
DEBUG TAND DATE: 802-01-25
DEBUG TAND DATE: 802-01-25
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SOFTMARE: PARENTIA VERSION 3.1
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APPLICANT: Chian, Kenneth R.
APPLICANT: Hoshijian, Masahiko
1717LB OR INVARIZON: Merbod to treat hemophilia by hepatic gene transfer of Factor v
1712 BOR INVARIZON: Merbod to Creat hemophilia by hepatic gene transfer of Factor v
1713 RESIDENTIAL STATES OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF
                                                                                                                                                           SEQ ID NO 4
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Publication No. US20030044982A1
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Best Local Similarity
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Publication No. US20030195223A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 16; Conser
                         LENGTH: 2351
TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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MOLECULE TYPE: protein
HYPOTHETICAL: YBS
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 82; DB 15;
100.0%; Pred. No. 8.2e-06;
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RESULT 10
US-10-172-712-27
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                                                                                                                                                                                      US-10-095-718-4
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US-10-172-712-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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SEQ ID NO 27
LENGTH: 2351
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Publication No. US20030125232A1
       Query Match 93.9%, Score 77; DB 14; Length 1431;
Best Local Similarity 93.8%, Pred. No. 3.9e-05;
Matches 15; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Walsh, Christopher
APPLICANT: Chao, Hengjun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10095718
Publication No. US20020131956A1
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Best Local Similarity
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APELICANT: GREFORP, BLIZABETH D.

APELICANT: GETFORP, STABILIZED PROTEINS WITH ENGINEERED DISULFIDE BONDS

FILE REFERENCY, 4,190-40,018

CURRENT PILING DATE: 0002-09-30

FRIOR FILING DATE: 2001-06-48

FRIOR FILING DATE: 2001-06-58

WINDERS OF SEQ ID NOS: 33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and TITLE DOF INVENTION: Methods of Using the Same FILE REFRENCE: 35052/04375 CUREARY TAPEL/CONTON HOWERS: US/10/095,718 CURRENT TAPEL/CONTON HOWERS: US/20/20-21 PRIOR APPLICATION NUMBER: 09/689,430 PRIOR RELING BATE: 2001-08-24 89,430 PRIOR RELING BATE: 2001-08-24 89,430 PRIOR APPLICATION NUMBER: 69/689,780                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                         LENGTH: 1431
TYPE: PRT
ORGANISM: canine B-domain deleted factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
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Lynch, Carmel
Stepan, Tony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Munson, Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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Gaps
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US-10-187-319-6
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US-10-131-510A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 6
LENGTH: 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/10131510A
Publication No. US20030166536A1
GRMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lollar, John S
TITLE OF INVENTION: Modified Factor VIII
FILE REFERENCE: 75-95J
                                                                                                                                                                                                                                                                                                                    GENERAL MEYOMATION:
APPLICANT. LOLIA: John S.
TITLE OF INVENTION: Horid Haman/Animal Factor VIII
NUMBER OF SEQUENCES: CORRESSONDERGE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
                         MEDIUM TYEE: Floppy disk
COMMUTES: INP NC COMMONTAL
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTHABE: Detentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/187,319
FILING DATE: 27-MMG-2002
CLASSIF MATION: CHIMOMONIA
PELICATION NUMBER: US 09/523,656
PELICATION NUMBER: US 09/523,656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 92.7%;
Local Similarity 93.8%;
                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        716 FRKRGMTALLKVSSCD 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FRWRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                      CITY: Boulder
STATE: Colorado
                                                                                                                                                                                                                                                                                       ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle Suite 201
APPLICATION NUMBER: US 09/037,601 FILING DATE: 1998-03-10
                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Pred. No. 0.0001;
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CHRESHY FELLOATION WINGER: US. 09/315,179
PRICE REPLICATION WINGER: US. 09/315,179
PRICE RELIEN BATE: 1399-05-20
PRICE RELIEN BATE: 1399-05-20
PRICE RELIEN BATE: 1399-05-20
PRICE RELIEN BATE: 1399-03-10
PRICE RELIEN BATE: 1399-03-10
PRICE RELIEN BATE: 1399-06-26
PRICE RELIEN BATE: 1399-06-26
PRICE RELIEN BATE: 1399-06-26
PRICE RELIEN BATE: 1399-11-15
PRICE RELIEN BATE: 1399-41-15
PRICE RELIEN BATE: 1399-41-15
PRICE RELIEN BATE: 1399-03-10
PRICE RELIEN BATE: 1399-03-10
PRICE RELIEN BATE: 1399-03-11
PRICE RELIEN BATE: 1399-03-11
PRICE RELIEN BATE: 1399-03-11
PRICE RELIEN BATE: 1399-03-11
; Sequence 4, Application US/10187319
                       RESULT 15
US-10-187-319-4
                                                                                                                                                                                                                                                                        US-10-131-510A-4
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SEQ ID NO 4
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Best Local (
                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lollar, John S
TITLE OF INVENTION: Modified Pactor VIII
FILE REFERENCE: 75-95J
                                                                                                                                                                                                                                                                                     ORGANISM: Sus scrofa
                                                                                                                                                                                                                                                                                                                                LENGTH: 368
                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 TO 2319 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: MO PCT/US97/11155
PILING DATE: 1997-06-26
APPLICATION NUMBER: US 08/670,707
PILING DATE: 1996-66-26
ATTORNEY/AGENT INFORMATION:
                                                                                                      326 RNRGMTALLKVYSCD 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         716 FRKRGMTALLKVSSCD 731
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                                                                                                                                          2 RNRGWTALLKVSSCD 16
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TITLE: Sequence of the Murine Factor VIII cDNA
JOURNAL: Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Greenlee, Lorance L.
REGISTRATION NUMBER: 27,894
REFERENCE/DOCKET NUMBER: 75-95K
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                                                                                                                                                                                     0,
                                                                                                                                                                                                      Score 70; DB 12;
Pred. No. 0.00016;
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Pred. No. 0.0001;
                                                                                                                                                                                     Mismatches
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GENERAL INFORMATION:
                                                                                            Matches
                                                                                                                                          Query Match
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SEQUENCE CHARACTERISTICS:
                                                                                                                       Tecar
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ORBATINA SETTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATH.
CUMBET APPLICATION BATH.
APPLICATION NUMBER: US/10/187,319
FILING OBJES 27-Bag-2007
CLASSIFICATION: CUMBOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Greenlee, Lorance L.
REGISTRATION NUMBER: 27,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/523,656
PILLING DATE: 2000-03-10
APPLICATION NUMBER: US 09/037,601
PILING DATE: 1998-03-10
APPLICATION NUMBER: NO PCT/US97/11155
FFILING DATE: 1997-06-26
                                                                                                                                                                                                           LOCATION: 1.368

O'THER INFORMATION: /notes "Predicted amino acid seguence of porcine factor VIII Az domain, defined as residues asogenence of porcine factor VIII, amino acids 373-740. Residues homologous to human factor VIII, amino acids 373-740. Residues the factor beschrifton: 8EQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 80303
COMPUTER READABLE FORM:
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ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                     PEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 40
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TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
326 RNRGMTALLKVYSCD 340
                                      2 RNRGMTALLKVSSCD 16
                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 368 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 303/499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/670,707 FILING DATE: 1996-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE: spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 303/499-8080
                                                                                            Conservative
                                                                                        85.4%; Score 70; DB 15; Length 368; 93.3%; Pred. No. 0.00016; tive 0; Mismatches 1; Indels
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Search completed: November 7, 2003, 08:16:56 Job time : 15:0347 secs

Residues

Run on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
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seg length: 2000000000
              protein search, using sw model
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100.0
100.0
93.9
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82
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1. /ogp2 6 | prodate // 1/iaa/5A, COMB. pep;*

2. /ogp2 6 | prodate // 1/iaa/5A, COMB. pep;*

3. /ogp2 6 | prodate // 1/iaa/5A, COMB. pep;*

3. /ogp2 6 | prodate // 1/iaa/6B, COMB. pep;*

3. /ogp2 6 | prodate // 1/iaa/6B, COMB. pep;*

5. /ogp2 5 | prodate // 1/iaa/6B, COMB. pep;*

5. /ogp2 5 | prodate // 1/iaa/backflast, pep;*
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          23194 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1199 A 1
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(c) 1993 - 2003 Compugen Ltd.
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                                                 US-09-324-867-2
US-08-882-083-2
US-08-588-107-2
US-09-243-539-2
US-09-224-867-4
US-08-212-133-6
US-08-670-7078-6
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US-08-683-839B-3
US-07-864-004B-4
US-08-251-937A-4
US-08-212-133A-2
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PCT-US94-13200-2
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US-09-315-179-2
US-09-523-656-2
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US-08-474-503-2
US-08-670-707A-2
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                                                                                                                                                                                                                       Sequence 1, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 6, Appli
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Result

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85.4	85.4	85.4	85.4	85.4	85.4	85.4				85.4	85.4	85.4	85.4	85.4	85.4	92.7	92.7	
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US-08-670-707A-39	PCT-US93-03275-6	US-08-212-133A-3	US-08-251-937A-6	US-07-864-004B-6	US-08-121-202-4	PCT-US94-13200-4	US-09-523-656-4	US-09-315-179-4	US-09-037-601-4	US-08-670-707A-4	US-08-474-503-4	US-08-212-133A-6	PCT-US93-03275-2	US-08-251-937A-2	US-07-864-004B-2	PCT-US94-13200-6	US-09-523-656-28	
Sequence 39, Appl	Sequence 6, Appli	•	Sequence 6, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 28, Appl							

ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT Cho, Mung-Sam
APPLICANT Cho, Sham-Yhen
APPLICANT Choa, Sham-Yhen
APPLICANT Keley, William
APPLICANT Keley, William
APPLICANT Keley, William
APPLICANT Keley, Helena
TITUS OF INVESTION Expression System for Factor VIII
FILE REFERENCE, MS1-7255
CURRENT APPLICATION ANDERS: US/09/209,916
CURRENT PLING DATE. 199-12-10
MONTHARS: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-09-209-916-1
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                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08683839B Patent No. 5744326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09209916
Patent No. 6358703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                  GENERAL IMPOSMATION: Use of Viral Cis-Acting Post-Transcriptional TITLS OF INVESTION: Use of Viral Cis-Acting Post-Transcriptional TITLS OF INVESTION: Use of Viral Cis-Acting Post-Transcription of TITLS OF INVESTION: Intronless Genes Containing Mear-Consensus Splice Sites NUMBER OF SECURIORS: INTERNAL SPRINGERORS SECURIORIES CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: human factor VIII sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                      STREET: 60 State Stre
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                 ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                          697 FRNRGMTALLKVSSCD 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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02109-1875
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100.0%; Pred. No. 1.4e-06;
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US-07-864-004B-4
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Best Local Similarity
                                                      TELEFAX: 404-815-6555: INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jame E.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: TT-
TELECOMMUNICATION INFORMATION:
TBLEFHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                               CONFITER READABLE FORM:
MEDIUM TIPE: 10ppy disk
COMBUTE: 1DM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
OPTIMATE: PACENTIA REAGES #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION MOMBER: US/07/964,004B
FILMED DATE: 07 APRIL 1992
                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: PADST, PALTCAL I,
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EM
TELECOMOUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nollar, John S.
APPLICANT: Noge, Marcchall S.
TITUE OF INVENTION: Hybrid Human/Portine Factor VIII
NUMBER OF SAGINACES:
CORRESSONDENCE ADDRESS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 11-MARCH-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
STRANDEDNESS:
                                                                                                            TELEPHONE: 404-815-6508
                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Application US/07864004E 5364771
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Y: US
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                                    2332 amino acids
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1100 Peachtree Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08251937A
Patent No. 5583209
        HYPOTHETICAL: NO
ANTI-SENSE: NO
PRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISH: Homo sapien
TISSUE TYPE: Liver cDNA:
                                                                                                                                                                                                                                                                   PETUBESPILIAN IN 1879
APPLICATION DATA:
APPLICATION HOMBER: US 07/864,004
APPLICATION HOMBER: US 07/864,004
APPLICATION HOMBER: US 07/864,004
APPLICATION HOMBER: 29,476
HER SENSATION HOMBER: 29,476
HER SENSATION HOMBER: HOMBER: HOMBER: HOMBER: 404-615-5047
TELEBHOMBE: 444-615-5047
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                                                                                                                                                                                             TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino acids
                                                                                                                    TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Ploppy disk
COMPUTER: IR NO COMPALTIME
OPERATING SYSTEM: PC-DOS/No-DOS
SOFTWARE: PC-TOS/No-DOS
SOFTWARE: PC-TOS/No-DOS
SOFTWARE: PC-TOS/NO-DOS
COMPANY APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Kilpatrick & Cody
STREET: 1100 Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPB: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Liver cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 Per
CITY: Atlanta
STATE: Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/251,937A
FILING DATE: 31-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    697 FRNRGMTALLKVSSCD 712
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           Homo sapien
E: Liver cDNA sequence
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                                                                                                   . protein
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Query Match 100.0%; Score 82, DB 1, Length 2332; Best Local Similarity 100.0%; Pred. No. 2.5e-0; Matches 16; Conservative 0; Mismarches 0; Indels

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; Sequence 2, Application US/08276594A; Patent No. 5693499; GENERAL INFORMATION:
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US-08-276-594A-2
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US-08-212-133A-2
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Patent No. 5663060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/
PILING DATE: 07-APR-1992
ATTORNEY/ABENT INFORMATION:
NAME: PADS: Natrea 11.28
REGISTRATION NUMBER: 11.28
REGISTRATION NUMBER: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 30303
COMPUTER REALDRELE FORM:
MEDIUM TYPE: Floped dick
COMPUTER: IN FC compatible
COMPUTER: IN FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: TRAGENTIN Balease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lollar, John S.
APPLICANT: Mugg, Marschall S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SUGMENCES: 12
COMERSSONDEMICE ADDRESS:
ADDRESSES: Kilpatrick & Cody
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                         MOLECULA I
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: PIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 404-572-6508
                                                                                                                                                                                                                                                                                                           ORGANISM: HO
                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 404-572-6555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/2
FILING DATE: March 11, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                    697 FRNRGMTALLKVSSCD 712
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                                                                                                                                                                                          1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                   Similarity
YONEMURA, Hiroshi
TAJIMA, Yoshitaka
SUGAWARA, Keishin
MASUDA, Kenichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2332 amino acids
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ilarity 100.0%;
Conservative 0
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E: Liver cDNA sequence
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                                                                                                                                                                                                                                                Score 82; DB 1;
Pred. No. 2.5e-06;
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                               Length 2332;
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US-08-474-503-2
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Fatent No. 5744446
GENERAL INFORMATION:
APPLICANT: Emory University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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APPLICATION NUMBER, US/08/276,594A
PILING DATE: 18-JUL-1994
CLASSIFICATION: 43
PRIOR APPLICATION DATA.

APPLICATION DATA: US 07/950,191
PILING DATE: 24-SEP-192
PRIOR APPLICATION MINDER: US 07/950,191
PILING DATE: 24-SEP-192
PRIOR APPLICATION MINDER: US 07/950,191
PILING DATE: 44-SEP-192
PRIOR APPLICATION MINDER: US 07/950,191
PILING DATE: 44-SEP-193
APPLICATION MINDER: US 07/950,1091
PILING DATE: 44-SEP-193
PRIOR APPLICATION DATE: 44-SEP-193
PRIOR APPLICATION MINDER: US 07/950,1091
PRIOR APPLICATION DATE: 44-SEP-193
PRIOR APPLICATION MINDER: US 07/950,1091
PRIOR APPLICATION DATE: 44-SEP-193
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PRIOR APPLICATION DATE: 44-SE
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INFORMATION FOR SEQ ID NO:
                                                ZIP: 30309

COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC COMPACTABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: DEFILIA REALDABLE
CURRENT PEPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: EMOLY University
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSES: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CITY: Washington
STATE: D.C.
                              APPLICATION NUMBER:
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REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FRNRGMTALLKVSSCD 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202) 672-5399
07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 82; DB 1;
100.0%; Pred. No. 2.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROCESS FOR PREPARING HUMAN COAGULATION FACTOR VIII PROTEIN COMPLEX
                        US/08/474,503
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CRIGINAL SOURCE;
7 TASUE TYPE; Liver CDNA sequence
US-08-474-503-27
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                                                                                                                                                                                                                                                                                                                                                                                  CURRENT NETWINSTER. US/08/670,/v/A
APPLICATION NUMBER: US/08/670,/v/A
FILING DATE: 26-UUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA: NO PCT/US94/13200
FILING DATE: 15-NOV-1994
PRIOR APPLICATION DATA: 15-NOV-1994
PRIOR APPLICATION NUMBER: US/08/212,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08670707#
Patent No. 5859204
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APPLICATION NUMBER: US 08/212,133
FILING DATE: 11-WAN-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/ADSTO INFORMATION:
NAME: Greenlee, Lovance L.
REGISTRATION NUMBER: 75-95F
TELECOMMUNICATION HISCHARION:
TELEFRUME: 303/499-8090
TELEFRUME: 303/499-8090
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ATTORNEY/AGENT IMPORMATION:
NAME: Pratt, John S.
REGISTRATION NIMESER: 29.476
REGERENCE/DOCKET NUMBER: BMUL
TELECOMMUNICATION INFORMATION:
TELECHTONE: 494-415-6500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIP: 80300
COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lollar, John S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
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Pred. No. 2.5e-06;
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US-09-037-601-2
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Best Local Similarity 100.0%;
Matches 16; Conservative 0
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Patent No. 6180371
                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
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APPLICANT: Lollar
                                                                                                                                                                                                                                                                                                  APELICATION NUMBER: US 08/212,133
FILING DATE: 11-MAR-1994
PRIOR APELICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-ARR-1992
ATTORNER/JAGENT IMPORMATION:
NUMBER: VAGENT IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPALIAL

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/097,601

FILING DATE: 26-UNN-1996/037,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US94/13200
FILLING DATE: 15-NOW-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Hybrid Human/Animal Factor VIII NUMBER OF ESQUENCES: 40
CORRESPONDENCE ADDRESS:
                                    MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                         NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
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                     ANTI-SENSE:
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FRAGMENT TYPE: N-terminal
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LENGTH: 2332 amino acids
   RAGMENT TYPE:
                                                                     TOPOLOGY: not relevant
                                                                                       STRANDEDNESS:
                                                                                                            TYPE: amino acid
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TISSUE TYPE: Liver
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TOPOLOGY: no
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Pred. No. 2.5e-06;
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US-09-523-656-2

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CURRENT APPLICATION NUMBER: US/09/523, 656
CURRENT FILTURE DATE: JODO: 03-10
REALIZE FIRTURE DATE: JODO: 03-10
REALIZE FILTURE DATE: J99-03-10
REALIZER FILTURE DATE: J99-03-10
REALIZER FILTURE DATE: J99-03-10
REALIZER DITURE DATE: J99-06-26
ROWHER OF SED ID NOS: 39-06-26
SED ID NO 2 SED ID NOS: SED ID NOS: SED ID NOS: SED ID NOS: SED ID NOS: SED ID NOS: SED ID NOS: SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID NOS SED ID
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US-09-523-656-2
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; ORGANISM: Homo sapiens
US-09-315-179-2
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BARLIER PLINE DATE: 1969-06-26
BARLIER PLINE DATE: 1969-06-26
BARLIER PLINE DATE: 1979-06-26
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BARLIER PLINE DATE: 1979-06-26
BARLIER PLINE DATE: 1979-06-26
BARLIER PLINE DATE: 1989-11-15
BARLIER PLINE DATE: 1999-07-11
BARLIER PLINE DATE: 1999-07-10
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; ORGANISM: Hom
; TISSUE TYPE:
US-09-037-601-2
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SEQ ID NO 2
LENGTH: 2332
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APPLICANT: LO11ar S., John
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: 75-951
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Patent No. 6458563
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Best Local Similarity
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Patent No. 6376463
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CURRENT FILING DATE: 1999-05-20
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TITLE OF INVENTION: Modified Factor VIII
FILE REFERENCE: 75-95H
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ORGANISM: Homo sapiens
                                                                  LENGTH: 2332
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 82; DB 4; Length 2332; 100.0%; Pred. No. 2.5e-06; tive 0; Mismatches 0; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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PCT-US93-03275-4
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                                                                                                                                               Matches
                                                                                                                                                                                                                   Query Match
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IN FC COMPATIBLE
COMPUTER: PLOPPY DISK
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ATTORNEY/AGRAY INFORMATION:
NAMB: PANST, PALTER L.
REGISTRATION NUMBER: 23, 284
REFERENCE/DOCKET NUMBER: 207
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          FRAGKENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Liver cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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ADDRESSE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 404-815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/864004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 19930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Georgia
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hes 16; Conserv
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697 FRNRGMTALLKVSSCD 712
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                                                                    1 FRNRGMTALLKVSSCD 16
                                                                                                                                               16;
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                                                                                                                                                                           100.0%;
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100.0%; Pred. No.
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100.0%; Pred. No. 2.5e-06;
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                                                                                                                                         Mismatches
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                                                                                                                                                                           2.5e-06;
                                                                                                                                                                                                              DB 5;
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RESULT 13 PCT-US94-13200-2

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Sequence 2, Application PC/TUS9413200 GENERAL INFORMATION:

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RESULT 14
US-08-121-202-2
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Patent No. 5563045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Innear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRACKENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patra L.
NAME: Pabst, Namera L.
REGISTRATION NUMBER: 31,284
REFERRENCE/DOCKET NUMBER: EMUL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 2:
COMPUTER EXAMABLE PORM.
MEDIUM TYPE: Plopy disk
COMPUTER: ITM To COMPACHIA
COMPUTER: THM TO COMPACHIA
COMPATRIA STEEM. TO COMPACHIA
SOFTWARF: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER BEADBALE PORM:
WEDTINE TYPE: Floppy disk
WEDTINE TYPE: Floppy disk
COMPUTER: LIN PC COMPACTIVE
COMPUTER: LIN PC COMPACTIVE
COMPACTIVE TYPE: FC-DOS/MS-OOS
SOFTWARE: FS-ESENIT RE-SISSE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMERR: FC-7/US94/13200
FILIND DATE: 13-MOV-1994
                                                                                                                                                                                           REPLICANT: MORMEY, JOHN M.
APPLICANT: MAIGHAIN, RANDAI J.
TITLE OF INVENTION. CHIMERIC PROCOAGULANT PROTEINS
NUMBER OF SEQUENCES. 27
CORRESPONDENCE ADDRESS;
CORRESPONDENCE ADDRESS;
STREET: 87 CARDATAGGEFACK Drive
STREET: 87 CARDATAGGEFACK Drive
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pittman, Debra
APPLICANT: Rehemtulla, Alnawaz
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TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
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                                                                                                                                                          STATE:
                                                                                                                                   COUNTRY:
                                                                                                                                                                          CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapien
TISSUE TYPE: Liver cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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CITY: Atlanta
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STREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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US-08-366-851A-2
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US-08-366-851A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08366851A
Patent No. 5681746
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                                                                                                                                                                                                                                          TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 452-1288
TELEPAX: (619) 452-2616
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NEADOCK INFORMATION:
REGISTRATION NUMBER: 31,544
REGISTRATION NUMBER: GI 5195
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INFORMATION FOR SEQ ID NO: 2:
                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2351 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOPTHARE: Patentin Release #1.0, Version #1.25
CUREMENT APPLICATION NUMBER: US/08/366,851A
RPLING DATE: US/08/366,851A
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 92121
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPS: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
CORRESPINS SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION UNUSER: 34,561
REFERENCE/DOCKET NUMBER: 930049.438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bodner, Mordechai
APPLICANT: He Polo, Micolas J.
APPLICANT: Heu, David Chi-Tang
APPLICANT: Charg, Steven
TITLE OF INVENTION: Retroviral Delivery of Full Length Pactor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: US/08/121,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 100.0%;
Local Similarity 100.0%;
hes 16; Conservative 0
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 11055 ROCITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 14-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B: Viagene, Inc.
11055 Roselle Street
                                                                                                                                               2351 amino acids
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Pred. No. 2.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5195A
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Best Local Similarity 100. Matches 16; Conservative

100.0%; Score 82; DB 1; 100.0%; Pred. No. 2.6e-06; 0;

Length 2351;

0

Gaps

0;

Mismatches

Query Match

8 8

1 FRNRGWTALLKVSSCD 16

Search completed: November 7, 2003, 07:30:12 Job time: 3.3498 secs